Table S1

Multiple sequence alignment (CLUSTAL W 1.83) of plant NQR sequences from *Arabidopsis*, *Vitis vinifera* (Grape), *Glycine max* (soybean), *Solanum tuberosum* (potato) and *Oryza sativa* (rice). Peptides from the predicted soybean NQR identified by mass spectrometry are underlined. The FMN binding motif is shown in gray.

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                                                  ←  FMN  →
Q9LK88|NQR_ARATH              1 MEAVTAIKP-LIRVAALSGSLRKTSFHTGLLRAAIDLTKESVPGLQIEYI 49
A5AS03|A5AS03_VITVI           1 MAAAIEVQP-VIKVAALCGSLRKASFNRGLIRSAIKISKEAINGMEIEYV 49
PUT-161a-Glycine_max-35276   15 MAAVAGASSSVIKVAALSGSLRKGSYNRALIRSAIELSQGRVEGLQIEYV 64
Q8H9D2|NQR_SOLTU              1 ----MAAQP-VIKVAGLCGSLRKGSYNRGLLNAAMEICKDSITGMEIEYV 45
Q941Z0|NQR1_ORYSJ             1 --MEAAAARPVIRVAAICGSLRKASYNGGLLRAAAGVCEESIPGLRVDHV 48
Q941Y8|NQR2_ORYSJ             1 --MEGSTSPKALRVAAISGSLRRGSANTGLIRAAKEICEESIPGMVIDHV 48
                                           ::**.:.****: * : .*:.:*  : :  : *: ::::

Q9LK88|NQR_ARATH                DISPLPLINTDLEVNGT-YPPVVEAFRQKILEADSILFASPEYNFSVSAP 98
A5AS03|A5AS03_VITVI             DIAPLPMLNTDLEVDGT-YPPAVEAFRQKILEADSILFASPEYNYSVTAP 98
PUT-161a-Glycine_max-35276      DISPLPLLNTDLEVNGT-YPPQVEAFRQKILAADSILFASPEYNYSVASP 113
Q8H9D2|NQR_SOLTU                DISPLPFLNTDLEVNGT-YPPVVEAFRKKIEEADCFLFASPEYNYSITGP 94
Q941Z0|NQR1_ORYSJ               DISGLPLLNTDLETADGGFPPAVEAFRDKVRQADCFLFGSPEYNYSIATP 98
Q941Y8|NQR2_ORYSJ               DIPDLPLLNTDMEVDDG-FPPAVEAFRASVRAADCFLFASPEYNYSISGP 97
                                **. **::***:*. .  :** ***** .:  **.:**.*****:*:: *

Q9LK88|NQR_ARATH                LKNALDWASRPPNVWADKPAAIISTGGGFGGGRSQYHLRQIGVFLDLHFI 148
A5AS03|A5AS03_VITVI             LKNAIDWASRPPNVWADKPAAIISTGGGFGGLSQYHLRQIGVYLDLHFI 148
PUT-161a-Glycine_max-35276      LKNALDWASRAPNVWAGKPAAIVSAGGGFGGGRSQYHLRQIGVFLDLHFI 163
Q8H9D2|NQR_SOLTU                LKNAIDWASRPPNVWADKAAAMVSAGGGFGGGRSQYHLRQIGVFLDLHFI 144
Q941Z0|NQR1_ORYSJ               LKNALDWASRGQNCWADKPAAIVSAGGGFGGGRSQYHLRQVGVFLDLHFI 148
Q941Y8|NQR2_ORYSJ               LKNALDWGSRPPNCWADRAAAIVSASGGSGGSRSMYHIRQVGVFLDIHFI 147
                                ****:**.**  * **.:.**::*:.** **. * **:**:**:**:***

Q9LK88|NQR_ARATH                NKPEFTLNAFQPPQKFDAEGNLVDEVTKERLKQVLLSLQAFTLRLQGK-- 196
A5AS03|A5AS03_VITVI             NKPEFFLNAFQPPAKFDAEGNLIDEDAKKRIKEVILSLQAFTRRLQGK-- 196
PUT-161a-Glycine_max-35276      NKPEFFLNAFQPPAKFNNDGDLIDEDAKNRLKDVLLSLKEFTLRLQGKN- 212
Q8H9D2|NQR_SOLTU                NKPEFFLNAFQQPPKFDSDGVLTDEETKQRLRAVLLALQALALKLKGKCE 194
Q941Z0|NQR1_ORYSJ               NKPELAVKAFEQPPKFDSDGNLIDAQIRERIKQVLLSLQAFTLRLQKKD- 197
Q941Y8|NQR2_ORYSJ               NKPEVFIKAHQPPKKFDSDGNLIDPEIKEELKDMLLSLQAFALRLQGKPA 197
                                ****. ::*.: * **: :* * *   ::.:: ::*:*: :: :*: *

Q9LK88|NQR_ARATH                ------
A5AS03|A5AS03_VITVI             ------
PUT-161a-Glycine_max-35276      ------
Q8H9D2|NQR_SOLTU                ------
Q941Z0|NQR1_ORYSJ               ------
Q941Y8|NQR2_ORYSJ               NSKHAA 203
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