**Supplement S3** Alignment of FAD3A protein sequence of PI 85671 and Williams 82, and Weblogo image showing the conservation of the amino acid region surrounding the residue N110

1. Amino acid sequence of FAD3A protein of PI 85671 compared to that of Williams 82. The amino acid shaded is the change from asparagine residue to aspartic acid (N110D) in PI 85671

PI85671 MVKDTKPLAYAANNGYQKEAFDPSAPPPFKIAEIRVAIPKHCWVKNPWRSLSYVLRDVLV

W82 MVKDTKPLAYAANNGYQKEAFDPSAPPPFKIAEIRVAIPKHCWVKNPWRSLSYVLRDVLV

PI85671 IAALMAAASHFNNWLLWLIYWPIQGTMFWALFVLGHDCGHGSFSDSPFLDSLVGHILHSS

W82 IAALMAAASHFNNWLLWLIYWPIQGTMFWALFVLGHDCGHGSFSDSPFLNSLVGHILHSS

PI85671 ILVPYHGWRISHRTHHQNHGHIEKDESWVPLTEKIYKNLDNMTRLVRFTVPFPLFVYPIY

W82 ILVPYHGWRISHRTHHQNHGHIEKDESWVPLTEKIYKNLDNMTRLVRFTVPFPLFVYPIY

PI85671 LFSRSPGKEGSHFNPYSNLFPPSERKGIAISTLCWVTMFSMLIYLSFITSPVLLLKLYGI

W82 LFSRSPGKEGSHFNPYSNLFPPSERKGIAISTLCWVTMFSMLIYLSFITSPVLLLKLYGI

PI85671 PYWIFVMWLDFVTYLHHHGHHQKLPWYRGKVTKINRK

W82 PYWIFVMWLDFVTYLHHHGHHQKLPWYRGKVTKINRK

b. Weblogo output of the amino acid conservation FAD3A enzyme as part of the BLINK feature at NCBI using GI number 157004277. The top 100 best matched sequences were aligned and used as input for sequence LOGO <http://weblogo.berkeley.edu/logo.cgi> [website](http://www.webcitation.org/query.php?url=http://weblogo.berkeley.edu/logo.cgi&refdoi=10.1186/1471-2229-10-195). The logo consists of stacks of symbols, one stack for each position in the amino acid sequence. The overall height of the stack indicates the sequence conservation at that position, while the height of symbols within the stack indicates the relative frequency of each amino acid at that position. Red circle indicates residue changed due to the N110D FAD3A mutation in PI 85671

