

Supplemental Table 1: Mutants that show increased NA/NAM release

Group I: strong NA/NAM release [scores 5]^a

NAD⁺ metabolism (2)^b – ***pnc1Δ, npt1Δ*** (more NA)
N-terminal acetyltransferase
NatB components (2) – ***mdm20Δ, nat3Δ***

Group II: modestly increased NA/NAM [scores 4]

Cytoskeleton/cell polarization related (1)
Mitochondrial function related (7)
Proteasome component (1)
RNA polymerase component (1)
Sphingolipid metabolism (1)
Trafficking (1)
Uncharacterized (2)

Group III: low to modestly increased NA/NAM [scores 2-3]

NAD⁺ metabolism (2) – *rfm1Δ, yia6Δ*
Amino acid metabolism (2)
cAMP/PKA related (2)
DNA repair (1)
Mitochondrial function related (23)
Peroxisome component (1)
Pyridoxal metabolism (1)
RNA processes (5)
Trafficking (1)
Translation machinery (2)
Transporter (2)
Uncharacterized (3)

^aThe final scores are representative of the secondary screen. All candidates were grouped by the final scores recorded on day 3. ^bThe number in parentheses indicates the number of hits (mutants) found in specific biological process (as defined in the *Saccharomyces Genome Database*).

Note: The BY4742 haploid yeast deletion collection (~4500 strains) was used to screen for mutants with increased NA/NAM release. 2 μ l of each strain was directly taken from the frozen stock and then spotted onto niacin-free SD plates spread with *bnr6Δnrk1Δnrt1Δ* recipient cells, which cannot grow without NA/NAM supplement. After incubation at 30°C for 3 days, we scored the cross-feeding activity (which indicates the level of NA/NAM release) of each mutant by comparing the diameter of the cross-feeding zones to that of the wild type. Mutants were assigned a score of 2 through 5 (WT=1). A higher score represents more NA/NAM release. To eliminate false-positives, mutants with a score of ≥ 3 (81 mutants) were re-examined. A total of 63 mutants passed the secondary screen and are shown in this table.