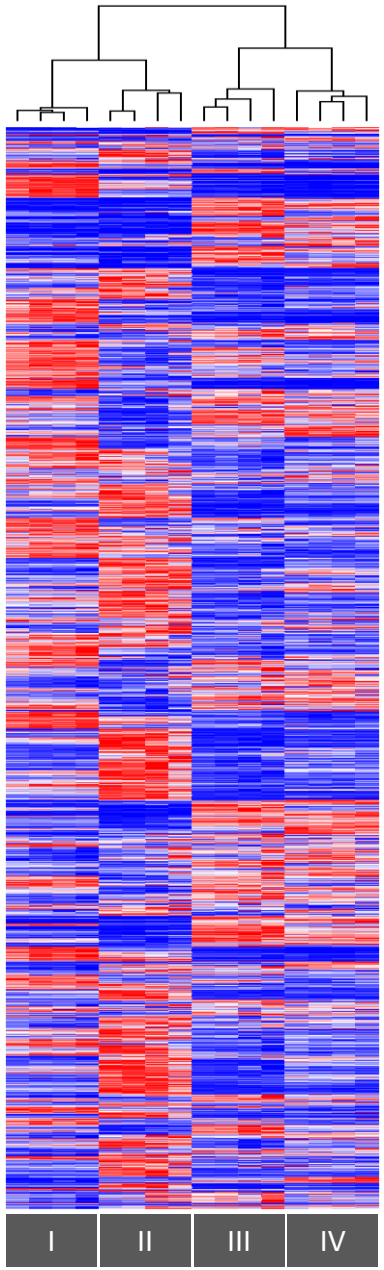
Supplementary figures

Supplementary figure S1

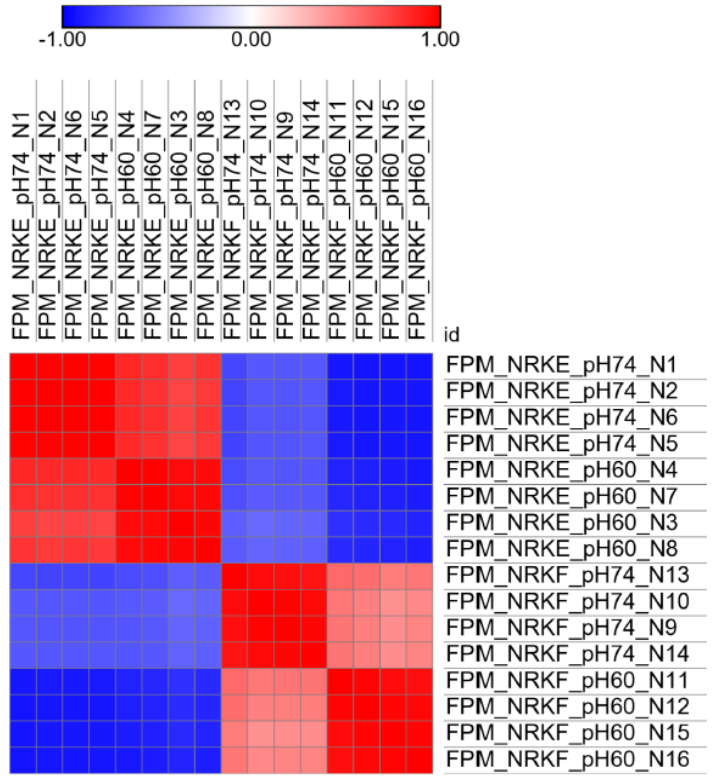
https://software.broadinstitute.org/morpheus/:

Clustering:
Eucledian distance
Linkage method = average

Similarity matrix:
Pearson correlation



all, FPM>10, 11122 genes



Supplementary Table S1. Buffer composition

EDTA buffer	• 136.8 mM NaCl • 2.68 mM KCl • 8.1 mM Na_2HPO_4 x 2 H_2O • 2 mM KH_2PO_4 • 0,7 mM EDTA • pH 7,2
MOPS-Triton buffer	• 10 mM TRIS base • 20 mM MOPS • 100 mM NaCl • 1 mM EDTA • 0.01 % Triton X-100 • pH adjusted to 7.5
6 x Redmix/Lämmli buffer	• 124.8 mM TRIS HCl (AppliChem GmbH, Darmstadt, GER) • 6 % SDS (Carl Roth GmbH&CoKG, Karlsruhe, GER) • 1,42 mM ß-Mercaptoethanol (Sigma-Aldrich Co, St. Louis, USA) • 4,7 mM Glycerol (Sigma-Aldrich Co, St. Louis, USA • 155.2 mM Bromphenol Blue (SERVA Electrophoresis GmbH, Heidelberg, GER) • pH 6.8
running buffer	• 25 mM TRIS

	• 3,5 mM SDS • 192 mM glycine
transfer buffer	• 20 % MeOH • 25 mM Tris • 192 mM glycine
trypsin solution	• 154 mM NaCl • 2.7 mM KCl • 8.2 mM Na_2HPO_4 • 1.5 mM KH_2PO_4 • 0,7 mM EDTA • 0,2 mM streptomycin • 0,18 mM penicillin • 0.02 mM trypsin • pH 7,1-7,3
1xTBS TWEEN	• 3 mM TRIS base • 140 mM NaCl • 0.17 mM TRIS-HCl • 1 % TWEEN 20 • pH 7.4
equilibration buffer	• 10 mM TRIS (pH 7.3)

	• 10 mM KCl • 1.5 mM MgCl • 0.5 mM ß-Mercaptoethanol • 1 : 100 protease inhibitor
lysis buffer	• equilibration buffer • 0.4 % nonidet P40
extraction buffer	• 20 mM HEPES • 0.4 M NaCl • 1 mM EDTA • 1 mM DTT • 1 : 100 protease inhibtor

Supplementary Table S2. Primer sequences and annealing temperatures

Gene name	Accession number	Forward 5′-3′	Backward 5′-3′	Annealing °C
Hprt1	NM_012583.2	ACCAGTCAACGGGG-GACATA	TTGGGGCTG-TACTGCTTGAC	60°C
Nrf2 (Nef2l2)	NM_031789.2	ACTACAGTCCCAG-CAGGACA	GTTTGG-GAATGTGGG-CAACC	60°C
Tkt	NM_022592.2	TCCATACCATGCGC-TACAAG	ATAAGATGG-GAGCTGCATGG	60°C

Abbreviations: *Hprt - Hypoxanthine Phosphoribosyltransferase 1, Nrf2 (Nef2l2) - Nuclear factor erythroid 2-related factor 2, Tkt - transketolase*