Title:

Interactome of vertebrate GAF/ThPOK reveals its diverse functions in gene regulation and DNA repair

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Supplementary Information
Supplementary Figure S1 Nuclear localization of FLAG-vGAF protein in transfected cells

C2C12 cells transfected with FLAG-vGAF expression plasmids were immunostained with FLAG antibody to detect the localization of FLAG-vGAF. Merged image shows an overlap of FLAG (Red) and DAPI (Blue) signals. (Scale bar 50um).
Panther Gene ontology analysis (GO-Cellular compartment) was performed for proteins identified in vGAF protein IP and negative control IP. X-axis represents the fold enrichment. Top 10 most significant GO categories from vGAF protein IP (blue) and negative control IP list (orange) are plotted on Y-axis.

Supplementary Figure S2 GO-Cellular compartment enrichment analysis of immuno-precipitated proteins
Supplementary Figure S3 Expression of N-terminal GFP tagged constructs of candidate proteins (Cbx5, HDAC1, MBD3, and RBM14)

[A] N-terminal GFP-tagged candidate proteins localize to nucleus. HEK293 cells were transiently transfected with N-terminal GFP tagged construct of candidate protein as indicated. Merged images show an overlap of DAPI and GFP signal (scale bar 50um). [B] N-terminal GFP-tagged constructs express the recombinant protein of expected molecular weight. Western blot analysis of extracts from HEK293 cells transiently transfected with N-terminal GFP tagged construct with GFP antibody.
Supplementary Figure S4

Supplementary Figure S4 GEPIA Analysis for expression data of DNA damage associated proteins in SCM vs. NST

GEPIA is used to analyze the expression data of DNA-repair proteins that interact with vGAF, from 461 SCM and 558 NST samples. The expression levels of above mentioned genes were not found to be statistically different in two groups.