(IKK) complex and 24 pathway components in NF- κ B signalling pathway. Data-base mining of NF- κ B family members and components mRNA expressions are accomplished by querying GEO DataSets profiles under inflammation cytokine stimuli, hypomethylation status, and homocysteine treat. We analysed correlations between gene expression, S-adenosylhomocysteine (SAH), and S-adenosylmethionine (SAM) levels, and SAM/SAH ratios in 7 mouse tissues.

Results Our results showed that (1) NF- κ B family members and pathway components have different expression levels in different tissues, and high expression in mouse, but inactive in human in normal condition; (2) Vascular system has lower response to NF- κ B activity; (3) Tissues can be divided into 3 tiers according to essential molecular of NF- κ B canonical and non-canonical pathway expression level in normal condition; (4) Canonical pathway is activated immediately after inflammatory cytokine TNF- α , IL-1 stimuli, but non-canonical pathway is up-regulated until 4 h treatment; (5) Lymphotoxin β /LIGHT has no effect on NF- κ B family members and components expressions at 4 h; (6) Sca1+ subset endothelial progenitor cells has lower NF- κ B family members and components expressions level than Sca1- subset endothelial progenitor cells; (7) Most of NF- κ B family members and components expressions are down-regulated by hypomethylation status; (8) Most of NF- κ B family members and components expressions are down-regulated by acute homocysteine treat in different cell type.

Conclusions These new results provide an insight on the roles of NF- κ B family members and components in tissues and cross talk between canonical and non-canonical pathway in different cell type, and its relevance to methylation. Our study is the first to make a model of specific tissue gene expression profiles of NF- κ B and regulation of tissue methylation.

GW23-e2636

CROSS TALK OF NF- κ B CANONICAL AND NON-CANONICAL PATHWAY IN HUMAN AND MOUSE TISSUES

doi:10.1136/heartjnl-2012-302920ah.3

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Objectives Nuclear factor- κ B (NF- κ B) family are critical regulators in immunity, stress responses, apoptosis and differentiation, however, tissue NF- κ B metabolism and their relevance to methylation status remain unknown.

Methods We examined gene expression profiles of 5 NF- κ B transcription factors, 6 inhibitory I κ B proteins (I- κ B), 3 I κ B kinase