



Gene expression profiling: identification of genes with altered expression in *Ayu17-449* knockout mice

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Genet. Mol. Res. 10 (3): 1533-1544 (2011)

Received January 8, 2011

Accepted April 10, 2011

Published August 1, 2011

DOI 10.4238/vol10-3gmr1158

ABSTRACT. *Ayu17-449*, a novel gene in mice, has been identified as a tumor-suppressor gene in myeloid malignancy; its product catalyzes the conversion of 5-methylcytosine of DNA to 5-hydroxymethylcytosine. However, *in vivo*, its functional target genes and biological function have remained unclear. Based on the assumption that alterations in the expression of the *Ayu17-449* gene affect the expression of other related genes, we screened a microarray of altered gene expression in *Ayu17-449*^{-/-} and *Ayu17-449*^{+/+} mice. We

identified 4049 genes with altered expression, including 1296 up-regulated (fold change ≥ 2) and 2753 down-regulated (fold change ≤ 0.5) genes in knockout mice compared with control mice. We then used qRT-PCR and RT-PCR to validate the chip data. Gene ontology and pathway analysis were performed on these altered genes. We found that these altered genes are functional genes in the complement and coagulation cascades, metabolism, biosynthesis, transcriptional regulation, proteolysis, and intracellular signaling pathways, such as the peroxisome proliferator-activated-receptor signaling pathway, the TNF- α -NF- κ B pathway, the Notch signaling pathway, the MAPK signaling pathway, and the insulin signaling pathway. The results of our genome-wide comprehensive study could be helpful for comprehending the underlying functional mechanisms of the *Ayu17-449* gene in mammals.

Key words: *Ayu17-449* knockout mice; Gene microarray; *TET-2* (tet oncogene family member 2)