**An approach to identify SNPs in the gene encoding acetyl-CoA acetyltransferase-2**

**(*ACAT*-*2*) and their proposed role in metabolic processes in pig**

Simrinder Singh Sodhi1+, Mrinmoy Ghosh1+, Ki-Duk Song2, Neelesh Sharma1, Jeong Hyun Kim1, Nameun Kim1, Sung Jin Lee3, Chulwoong Kang4, Sung Jong Oh1 and Dong Kee Jeong1,5\*

1Department of Animal Biotechnology, Faculty of Biotechnology, Jeju National University, Jeju-si, Jeju-do, South Korea

2The Animal Genomics and Breeding Center, Hankyong National University, Anseong-si, Gyeonggi-do, South Korea

3Department of Animal Biotechnology, College of Animal Bioscience and Technology, Kangwon National University, Chuncheon, South Korea

4Department of Mechanical and System Engineering, College of Engineering, Jeju National University, Jeju-si, Jeju-do, South Korea

5Sustainable Agriculture Research Institute (SARI), Jeju National University, Jeju-si, Jeju-do, South Korea

+ Authors have contributed equally

\*Corresponding author:

Prof. Dong Kee Jeong,

Department of Animal Biotechnology,

Faculty of Biotechnology, Jeju National University,

Ara-1 Dong, Jeju-Si, Jeju-Do 690-756, South Korea.

Mobile: +82-10-8713-8045, Fax: +82-64-725-2403-3331

 Email: dkjeong@jejunu.ac.kr

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| **SUPPLEMENTARY INFORMATION** |

1. **Table S1……………………………..……………..……p.3**

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| Table S1: Gene ontology analysis suggests the biological processes associated with functioning of the *ACAA2* and *ACAT2* genes in *Sus scrofa* and *Bos taurus.* |
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| GO Class ID\* | **Definitions** | **Counts\*\*** | **Fractions\*\*\*** |
| ***Sus Scrofa*** | ***Bos taurus*** | ***Sus Scrofa*** | ***Bos taurus*** |
| *ACAA2* |
| GO:0006915 | apoptosis | 4 | 4 | 36.36% | 28.57% |
| GO:0008152 | metabolism | 2 | 3 | 18.18% | 21.43% |
| GO:0006629 | lipid metabolism | NA | 2 | NA | 14.29% |
| GO:0016265 | death | 2 | 2 | 18.18% | 14.29% |
| GO:0005739 | mitochondrion | 2 | 2 | 18.18% | 14.29% |
| GO:0042981 | regulation of apoptosis | 1 | 1 | 9.09% | 7.14% |
| *ACAT2* |
| GO:0008152 | metabolism | 2 | 2 | 50.00% | 50.00% |
| GO:0005739 | mitochondrion | 1 | NA | 25.00% | NA |
| GO:0006629 | lipid metabolism | 1 | 1 | 25.00% | 25.00% |
| GO:0009058 | biosynthesis | NA | 1 | NA | 25.00% |
|  |

**\* Go terms/ class IDs:** GO terms into each ancestral term are independent of one another. The counted results may be selectively used and percentages recalculated as the selected terms represent a well-covered spectrum of the scope which helps to avoid redundancy and may make best sense for the data set.

**\*\* Counts :** Number of similar GOs with the current GO

**\*\*\* Fractions :** Share of biological process shown with respect to GO functions