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

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

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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