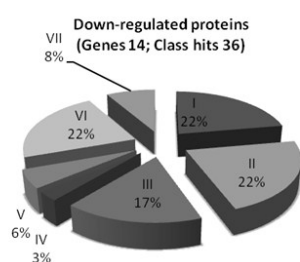
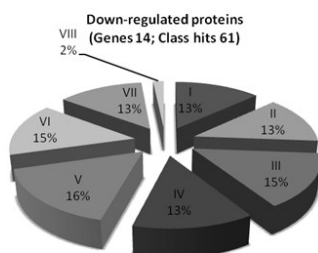


(A) GO Molecular function



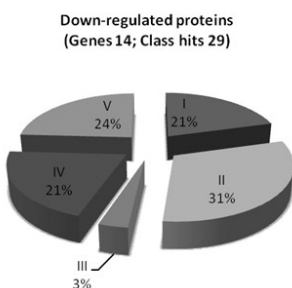
- I. Binding (GO: 0005488)
(MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6, ATP5A1)
- II. Catalytic Activity (GO: 0003824)
(MYH7, MYH2, MYH4, MYH1, MYH13, MYH6, ATP5A1, ATP2A1)
- III. Enzyme regulator activity (GO: 0030234)
(MYH7, MYH2, MYH4, MYH1, MYH13, MYH6)
- IV. Nucleic acid binding transcription factor activity (GO: 0001071)
(LDB3)
- V. Receptor Activity (GO: 0004872)
(RYR1; ATP5A1)
- VI. Structural molecule activity (GO: 0005198)
(ACTA1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6)
- VII. Transporter activity (GO: 0005215)
(RYR1; ATP5A1; ATP2A1)

(B) GO Biological process



- I. Biological regulation (GO: 0065007)
(MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6, ATP2A1)
- II. Cellular component organization or biogenesis (GO: 0071840)
(ACTA1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6)
- III. Cellular process (GO: 0009987)
(ACTA1, RYR1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6)
- IV. Developmental process (GO: 0032502)
(ACTA1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6)
- V. Localization (GO: 0051179)
(ACTA1, RYR1, MYH7, MYH2, MYH4, MYH1, MYH13, MYH6, ATP5A1, ATP2A1)
- VI. Metabolic process (GO: 0008152)
(MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6, ATP5A1, ATP2A1)
- VII. Multicellular organismal process (GO: 0032501)
(RYR1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6)
- VIII. Response to stimulus (GO:0050896)
(RYR1)

(C) GO Cellular component



- I. Cell junction (GO:0030054)
(MYH7, MYH2, MYH4, MYH13, MYH1, MYH6)
- II. Cell part (GO: 0044464)
(ACTA1, MYH7, MYH2, MYH4, LDB3, MYH1, MYH13, MYH6, ATP5A1)
- III. Macromolecular complex (GO: 0032991)
(ATP5A1)
- IV. Membrane (GO: 0016020)
(MYH7, MYH2, MYH4, MYH13, MYH1, MYH6)
- V. Organelle (GO: 0043226)
(MYH7, MYH2, MYH4, LDB3, MYH13, MYH1, MYH6)

Fig. S2 Muscle proteins differently expressed between pigs fed NPD and RPD analysed with the Panther bioinformatics tool (<http://www.pantherdb.org>), using the following gene ontology categories: (A) GO molecular function pie chart shows the number of the down-expressed proteins involved in molecular activity of the cell. (B) GO biological process pie chart indicate the number of the down-expressed proteins involved in each biological process. (C) GO Cellular component pie chart shows the localization of the down-expressed proteins in the cell. For each category the percentage of the total number of proteins in the pie chart is indicated for each Gene Ontology term.