

GENETIC AND TRANSCRIPTOMIC ANALYSIS OF INTRAMUSCULAR FAT CONTENT AND FATTY ACID COMPOSITION IN TWO PIG MUSCLES

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Intramuscular fat content (IMF) and fatty acid composition are key traits influencing the sensory, technological and nutritional properties of pig meat. We have carried out a gene expression and QTL analysis to identify genes involved in the genetic variability of these traits in two muscles (*gluteus medius* and *longissimus dorsi*) from a population of 350 Duroc barrows distributed in 5 half-sib families.



EXPRESSION STUDY

88 SAMPLES of 68 animals two muscles × two groups	<i>gluteus medius</i>	<i>longissimus dorsi</i>
HIGH level of lipid parameters	34	10
LOW level of lipid parameters	34	10

RNA

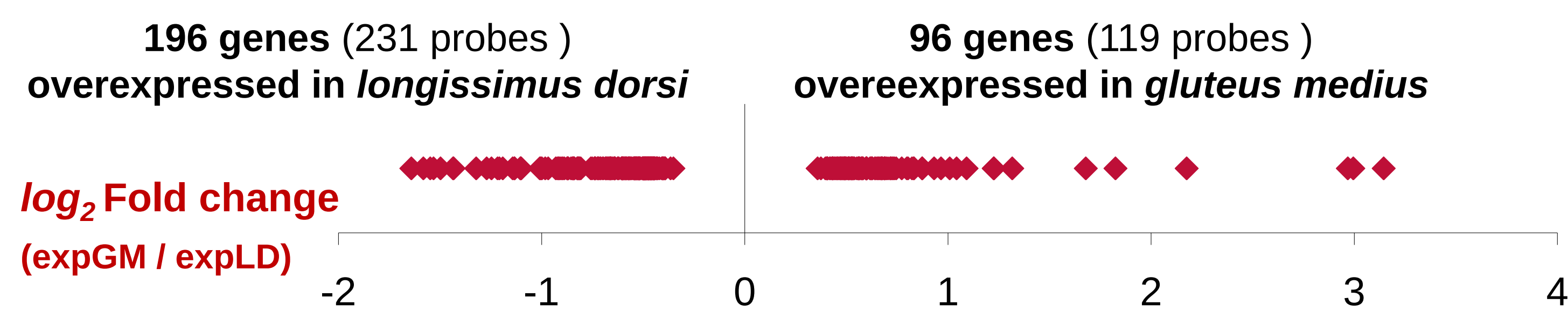


Normalised
expression
data

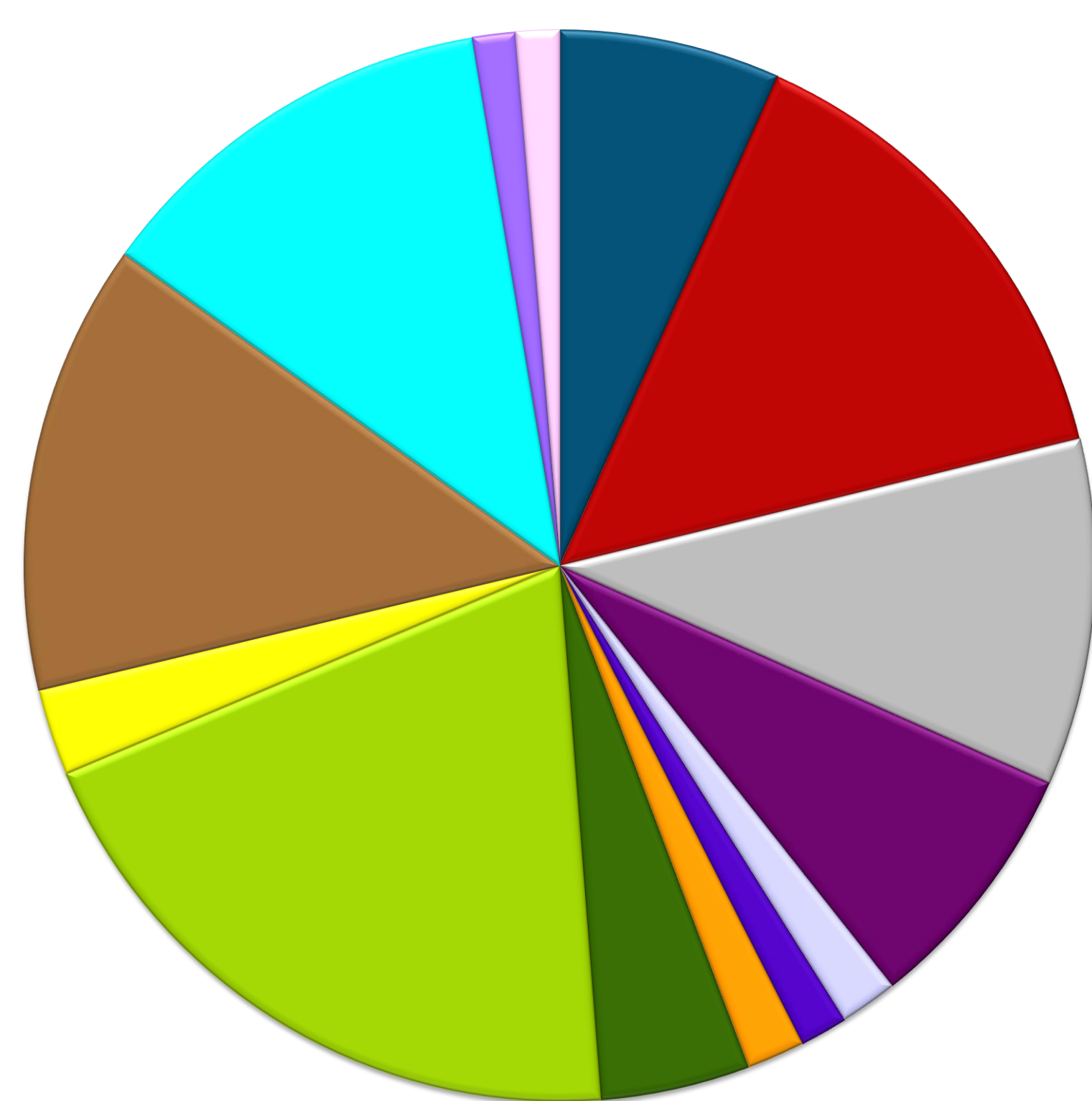
ANOVA (BRB-ArrayTools)
Expression=Muscle+Group+e
(p<0.001 & FDR<0.05)

Gene Ontology Analysis (DAVID)
of genes differentially expressed

292 genes (350 probes Affymetrix) differentially expressed between MUSCLES

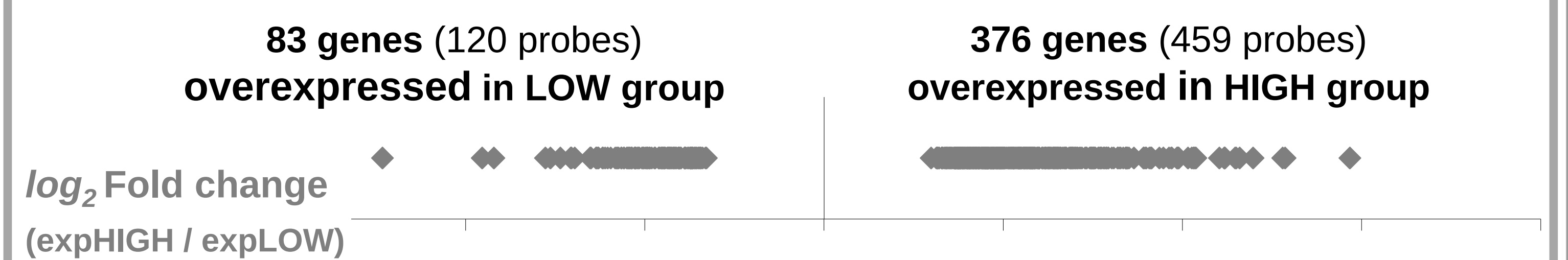


Gene Ontology – Biological GO terms

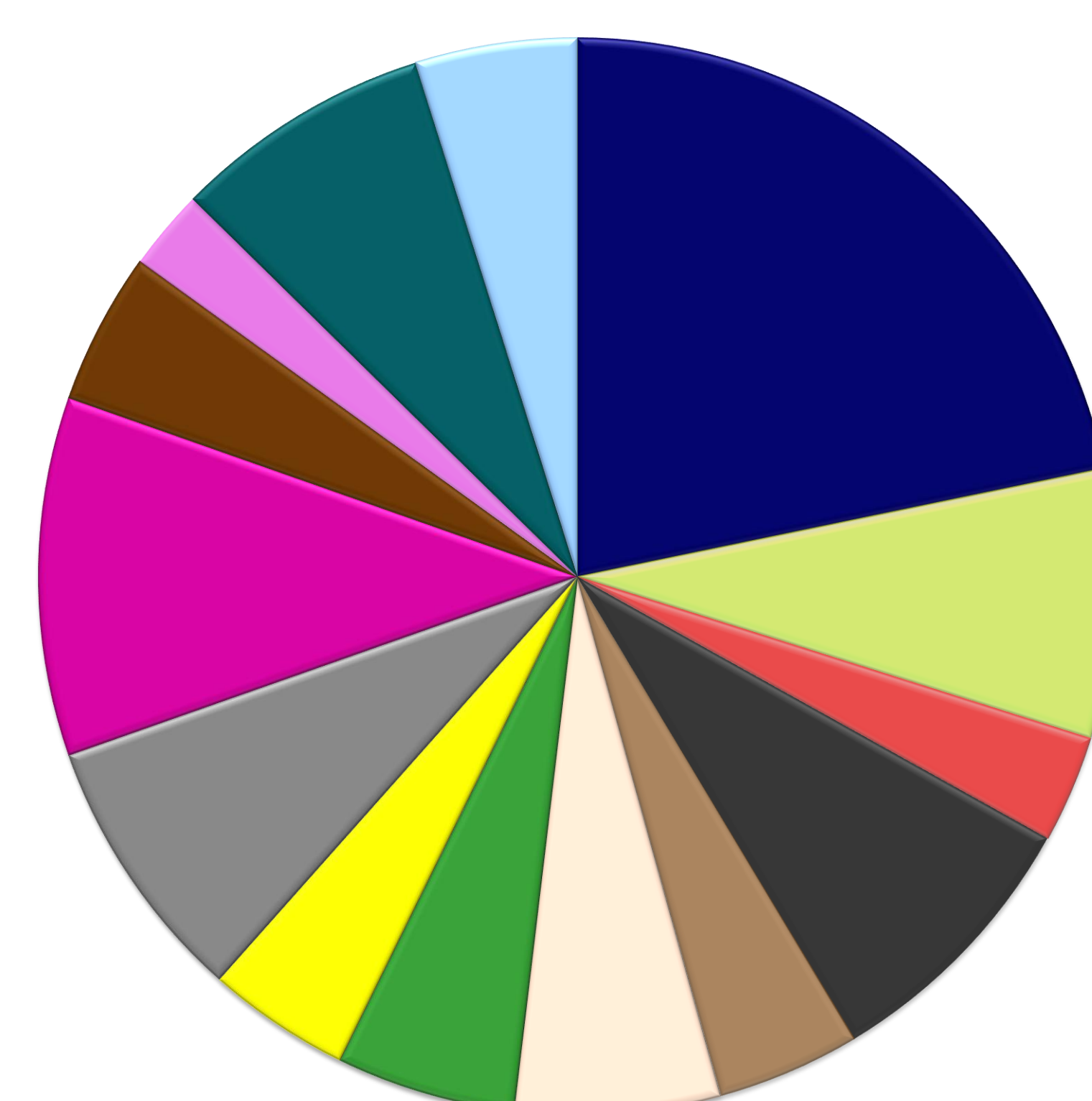


- anatomical structure development
- biological regulation
- developmental process
- multicellular organismal development
- muscle contraction
- muscle development
- muscle system process
- organ development
- primary metabolic process
- protein folding
- regulation of biological process
- regulation of cellular process
- response to protein stimulus
- response to unfolded protein

459 genes (579 probes Affymetrix) differentially expressed between GROUPS



Gene Ontology – Biological GO terms



- cellular component organization and biogenesis
- cellular lipid metabolic process
- fatty acid metabolic process
- lipid metabolic process
- monocarboxylic acid metabolic process
- mRNA metabolic process
- mRNA processing
- protein folding
- response to chemical stimulus
- response to stress
- ribonucleoprotein complex biogenesis and assembly
- ribosome biogenesis and assembly
- RNA processing
- RNA splicing

QTL ANALYSIS

- 350 individuals (5 Half-sib families)
 - 110 microsatellites
 - 15 phenotypes related with IMF and fatty acid profiles of two muscles
- QTL express

28 QTL for *gluteus medius* traits

26 QTL for *longissimus dorsi* traits

MAIN CANDIDATE GENES

Trait	SSC	QTL peak	F-value	Chromosome region	Genes differentially expressed
%Myristic	5	94 cM	13.98	chr.5 (88-118 cM)	GPD1 (<i>Glycerol-3-phosphate dehydrogenase 1</i>)
%Vaccenic	6	95 cM	14.56	chr.6 (84-107 cM)	NPC1 (<i>Niemann-Pick disease type 1</i>)
%IMF	7	133 cM	16.48	chr.7 (100-137 cM)	NPC2 (<i>Niemann-Pick disease type 2</i>)

CONCLUSIONS

- The expression study allowed us to identify 292 genes differentially expressed between *gluteus medius* and *longissimus dorsi* muscles, mainly grouped into GO terms related with muscle development, regulation and function.
- A larger number of genes (459) showed differential expression between the established groups, being most of them overexpressed in animals with HIGH level of lipid parameters, and belonging particularly to GO categories related with lipid metabolism.
- We have detected a number of QTL associated with intramuscular fat content, muscular cholesterol concentration and fatty acid profile of *gluteus medius* and *longissimus dorsi* muscles.
- In a preliminary joint analysis of these results, we have selected three positional and functional candidate genes: *GPD1*, *NPC1* and *NCP2*.