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We have developed a new Affymetrix expression array that has comprehensive coverage of the known pig transcriptome. Expressed sequences (DNA) were collated from public repositories to generate a non-overlapping collection of 52,355 expressed sequences. The final array represents 47,845 expressed transcripts, with a mean probe coverage of 22. Annotation of the array was performed by iterative homology searches across multiple mammalian genomes to assign putative orthology to annotated genes in other species. The new array was used to generate a gene expression atlas of pig tissues. In total, 104 arrays were run on samples derived from 62 tissue/cell types. Following normalization, the data were subjected to correlation network analysis and clustering using the tool BioLayout Express3D. These analyses provide a detailed functional clustering of the pig transcriptome. Based upon this clustering, one can infer the function of a gene of unknown function from the transcriptional company it keeps. For example, we identified a comprehensive set of genes associated with oxidative phosphorylation and with endocytosis. The new array and the gene expression atlas provide a resource for many aspects of future omics research in the pig.

**Key Words:** microarray, annotation, pig

**P2024 Genetic and sex effects on insulin-like growth factor system components in brain of bovine purebred and hybrid fetuses.** A. Javadmanesh<sup>\*1</sup>, K. Kind<sup>1</sup>, C. Fitzsimmons<sup>2</sup>, D. Thomsen<sup>1</sup>, and S. Hiendleder<sup>1</sup>, <sup>1</sup>*JS Davies Epigenetics and Genetics group, School of Animal and Veterinary Sciences, and Robinson Institute, University of Adelaide, Roseworthy Campus, Roseworthy SA 5371 Australia, Adelaide, South Australia, Australia*, <sup>2</sup>*Agriculture and Agri-Food Canada/University of Alberta, Edmonton, Alberta, Canada, Edmonton, Alberta, Canada.*

Insulin-like growth factor (IGF) system components are crucial for pre- and postnatal development as they stimulate cell proliferation and mitogenesis. The IGF system consists of 2 ligands: IGF1 and IGF2; type 1 and 2 receptors: IGF1R and IGF2R; and the 6 binding proteins: IGFBP1–6. IGF system regulation is tightly connected with insulin (INS) and growth hormone (GH), and their receptors, GHR and INSR. IGF1 is highly expressed in brain and essential for normal brain development in human and rodents. Partial inactivation of *IGF1R* in the embryonic mouse brain selectively inhibits GH and IGF1 pathways postnatally which leads to a longer average lifespan. We used quantitative real time-PCR to measure transcript abundance for *IGF1*, *IGF1R*, *IGFBP5* and *GHR* in brain tissue of Day153 fetuses of pure-bred Brahman and Angus cattle and their reciprocal hybrids (n = 74). Expression levels of other investigated transcripts including *INSR*, *IGFBP1*, *IGFBP2*, *IGFBP3*, *IGFBP4* and *IGFBP6* were too low

to measure consistently. Statistical analysis of genetic and sex effects on relative gene expression in hybrids versus pure-breds were performed with a linear model (JMP 4.0, SAS Institute, Inc.). *IGF1R* and *GHR* expression levels were lower in hybrids than in pure-breds ( $P < 0.01$ ). *GHR* transcript was also affected by sex ( $P < 0.05$ ) and by a genetics  $\times$  sex interaction ( $P < 0.01$ ). Other transcripts measured were not significantly different. As *IGF* receptors in brain strongly promote the development of somatotrophic function in the mouse model, this may explain observed developmental differences in hybrid cattle.

**Key Words:** bovine brain, gene expression, IGFs

**P2025 Comparison of the muscle transcriptome between samples with divergent intramuscular fat content in Berkshire by RNA-Seq.** T. H. Kim<sup>\*1</sup>, Y. G. Lee<sup>2</sup>, S. C. Kim<sup>2</sup>, H. J. Jeon<sup>1</sup>, S. W. Lee<sup>1</sup>, K. T. Lee<sup>1</sup>, E. S. Cho<sup>1</sup>, and N. Kim<sup>2</sup>, <sup>1</sup>*National Institute of Animal Science, Suwon, Republic of Korea*, <sup>2</sup>*Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea.*

RNA-Seq has been widely used to understand complex transcriptome landscape of various tissues in mammals. Intramuscular fat content is one of the most crucial variables determining meat quality. A muscle transcriptome analysis was carried out to compare gene expression profiles between loin eye muscles with high and low fat content. We produced an average of 3 Gb from 12 samples by Solexa platform (101bp paired-end sequencing). Tophat and SAMseq were used to identify expression levels of each sample. An expression analysis revealed 55 differentially expressed genes between muscles with high and low intramuscular fat content. Genes within pig QTL database have been compared with differentially expressed genes. Gene Ontology (GO) enrichment analysis and functional analysis also has been performed. This study is a first step toward the development of DNA markers associated with intramuscular fat content. In addition, transcriptome assembly will provide a deep insight into 2 divergent fat muscle tissues such as alternative splicing, polyadenylation, novel genes and transcripts.

**Key Words:** pig, transcriptome, intramuscular fat content

**P2026 Differential expression profiling by deep RNAseq in pigmented and non-pigmented bovine skin.** C. Kuehn<sup>\*</sup>, F. Hadlich, and R. Weikard, *Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.*

Next generation sequencing enables a comprehensive picture of the transcriptome of a specific cell, tissue or developmental stage. Piebald spotting is