Multi-omics data reveal transcriptomes and chromatin accessibility differences between four adipose tissue types in adult Meishan pigs.

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Adipose tissue of pigs is one of the principal organs determine meat-production efficiency. The adipose tissues from the different pig body parts with different function. However, the systematical comparison of gene expression, histone modification and open chromatin states of adipose tissues from different pig body parts were still lacking. In this study, we performed H3K27ac ChIP-seq, ATAC-seq and RNA-Seq on four types of adipose tissues (back fat, belly fat, groin fat and intermuscular fat) in adult Meishan (MS) pigs. In total, 164,347 chromatin accessibility regions, 37,037 putative active enhancers and 24,235 putative active promoters were identified using ATAC-seq and ChIP-seq data. Moreover, 92.86% of H3K27ac peaks, including enhancers and promoters regions, were overlapped with ATAC-seq open chromatin signals. Among the four types of adipose tissues, back fat and groin fat had the most differential H3K27ac ChIP-Seq signal peaks (20,017), the most differentially expressed genes, as well as the most differential ATAC-Seq peaks. Next, we selected the differential ATAC-Seq open chromatin regions between back fat and groin fat for motif analysis, the results showed that back fat were enriched by *PPARA, HNF4A, TCF4* and etc (q<0.01), groin fat were enriched by *NR5A2, FOSL2, FOXF1* and etc (q<0.01). Our study revealed the differences in transcriptome and chromatin accessibility between four types of adipose tissues in adult MS pigs which could help us to better understand the mechanism of fat metabolism and function.

Key words: Pig, adipose tissues, ChIP-Seq, ATAC-Seq, gene expression.