Identification of trait-associated genes related to meat quality using an RNA-seq analysis approach

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A total number of 120 steers born in 2013 and 2014 were analyzed. The animals belonged to the multibreed Angus-Brahman herd from the University of Florida and were classified into six different groups based on their expected Angus composition. Steers were harvested when their subcutaneous fat thickness over the ribeye reached 1.27 cm. Five grams of the *Longissimus* muscle was sampled after splitting the carcass and used for RNA extraction. After 48 hours postmortem, marbling was recorded in the ribeye muscle at the cut surface at the 12th/13th rib interface, and two 2.54 cm steaks from the *Longissimus dorsi* muscle were sampled from each animal, aged for 14 days at 1 to 4°C and cooked at an internal temperature of 71°C. The first steak was used to measure Warner Bratzler shear force (WBSF) and cooking loss, and the second steak was used to measure tenderness, juiciness and connective tissue by sensory panel. A principal component analysis for all recorded phenotypes was performed. The first three principal components were used to construct a meat quality index useful to rank each animal. Eighty animals were selected based on extreme meat quality index. After mRNA isolation and dscDNA synthesis, RNA-seq libraries were sequenced to generate 100 bp paired-end reads. Paired-end reads were mapped using Tophat and Bowtie2 against to the Btau_4.6.1 reference genome. Gene paired-end read counts for all annotated genes were determine using HTSeq including only uniquely mapped paired-end reads to known chromosomes. Robust regression was used for identifying trait-associated genes including the constructed meat quality index as phenotype. The association of gene counts was perform by gene accounting for breed group and year of birth. A total number of 148 genes were associated with the meat quality index (p value < 0.05). In the top twenty, multiple cytoskeletal and transmembrane proteins such as TMEM120B, TMEM186 and SYNJ2 were identified. Additionally, some transcription factors such as WDR77 and NFKB2 were uncovered.