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Abstract

Many QTL affecting meat quality and carcass traits have been reported. However, in most of the cases these QTL have been detected in non-commercial populations. Therefore, a family structured population of 457 F2 pigs issued from an inter-cross between 2 commercial sire lines was used to detect QTL affecting meat quality and carcass traits. All animals were genotyped using the Illumina PorcineSNP60 BeadChip platform. Genome-wide association studies were used in combination with linkage disequilibrium-linkage analysis to identify QTL. A total of 32 QTL were detected. Nine of these QTL exceeded the genome-wide 5% significance threshold. We detected 18 QTL affecting carcass composition traits and 16 QTL