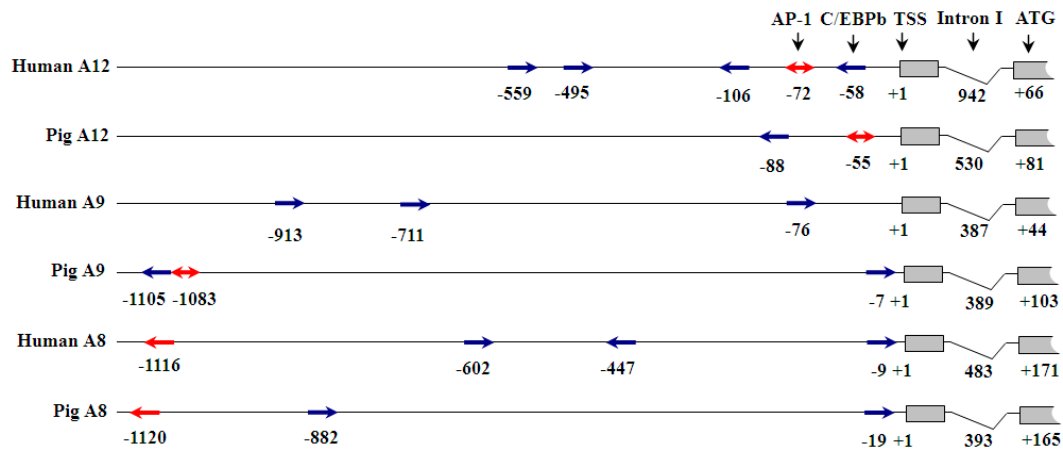


## Supplementary Information

**Figure S1.** The C/EBP $\beta$  and AP-1 binding sites in the -1200 bp region of the promoter of S100A8/A9/A12 genes in humans and pigs. A blue arrow represents the C/EBP $\beta$  binding site. A red arrow represents the AP-1 binding site. The orientation of the arrow represents the direction of transcription factors. The double arrow indicates the transcription factors can bind in both positive and negative directions. TSS, the transcriptional start site; Intron I, the first intron of S100A8/A9/A12 genes; ATG, initiating codon of the gene.



**Table 1.** The primers and probes used in this study.

| Purpose                            | Name                | Sequence (5'-3')                        |
|------------------------------------|---------------------|-----------------------------------------|
| Overexpression vector construction | AP-1L               | GTCAAGCTTGACGGACTGTTCTATGACTGC          |
|                                    | AP-1R               | GTCGAATTCCTCTCTCTCGCAACTTGTC            |
|                                    | C/EBP $\beta$ -LAPL | GTCAAGCTTGCCACCATGGAAGTGGCCAACTTC       |
|                                    | C/EBP $\beta$ -LAPR | GTCGAATTCTAGCAGTGGCCGGAGGA              |
|                                    | C/EBP $\beta$ -LIPL | GTCAAGCTTGCCACCATGGCGGCTGGCTTCC         |
|                                    | C/EBP $\beta$ -LIPR | GTCGAATTCTAGCAGTGGCCGGAGGA              |
| Luciferase analysis                | PL-135              | AGACTCGAGCATGTCGCAGTCAAAGC              |
|                                    | PL-mHSF2            | AGACTCGAGGTTTGAAGTCCCTCTTGAGCAACAGAGC   |
|                                    | PL-mC/EBP $\beta$   | AGACTCGAGGTTTGAAGTTTCTCTTGAGCACGAGAGCAC |
|                                    | PL-mAP-1            | AGACTCGAGCCCCAAGATACATCATAGGAGTTTC      |
|                                    | PL-50               | ATCCTCGAGGTTTCTTCACTTGAGG               |
|                                    | PR                  | AACAAGCTTTTCACCTTCGGAGACAGG             |
| Q-PCR                              | QAP-1L              | TCCAGTAACGGGCACATCAC                    |
|                                    | QAP-1R              | CCCTCCTGCTCGTCAGTCAC                    |
|                                    | QC/EBPL             | GTCCACATCCTCGTCGTCCAG                   |
|                                    | QC/EBPR             | GTTGCGCATCTTGGCCTTGTC                   |
|                                    | QS100A8L            | TGCTGACGGATCTGGAGAGT                    |
|                                    | QS100A8R            | CCCACCTTGATCACCAGTATG                   |
|                                    | QS100A9L            | CGGACCAAATGTGCGAGA                      |
|                                    | QS100A9R            | CCAGGATGTGTTTATGGCTTTC                  |
|                                    | QS100A12L           | GGCATTATGACACCCTTATC                    |
|                                    | QS100A12R           | GTCACCAGGACCACGAAT                      |
|                                    | QRPL32L             | CGGAAGTTTCTGGTACACAATGTAA               |
|                                    | QRPL32R             | GAAGAGACGTTGTGAGCAA                     |

**Table 1.** *Cont.*

| <b>Purpose</b> | <b>Name</b>                   | <b>Sequence (5'–3')</b>      |
|----------------|-------------------------------|------------------------------|
| EMSA analysis  | Consensus C/EBP $\beta$ probe | ACCTGCAGATTGCGCAATCTGCACTC   |
|                | S100A12 C/EBP $\beta$ probe   | AAGTTTCTCTTGAGCAACAGAGCACGGT |
|                | Consensus AP-1 probe          | CGCTTGATGACTCAGCCGGAA        |
|                | S100A12 AP-1 probe            | TTGCCCCAAGATGAATCATAGGAGTTTC |