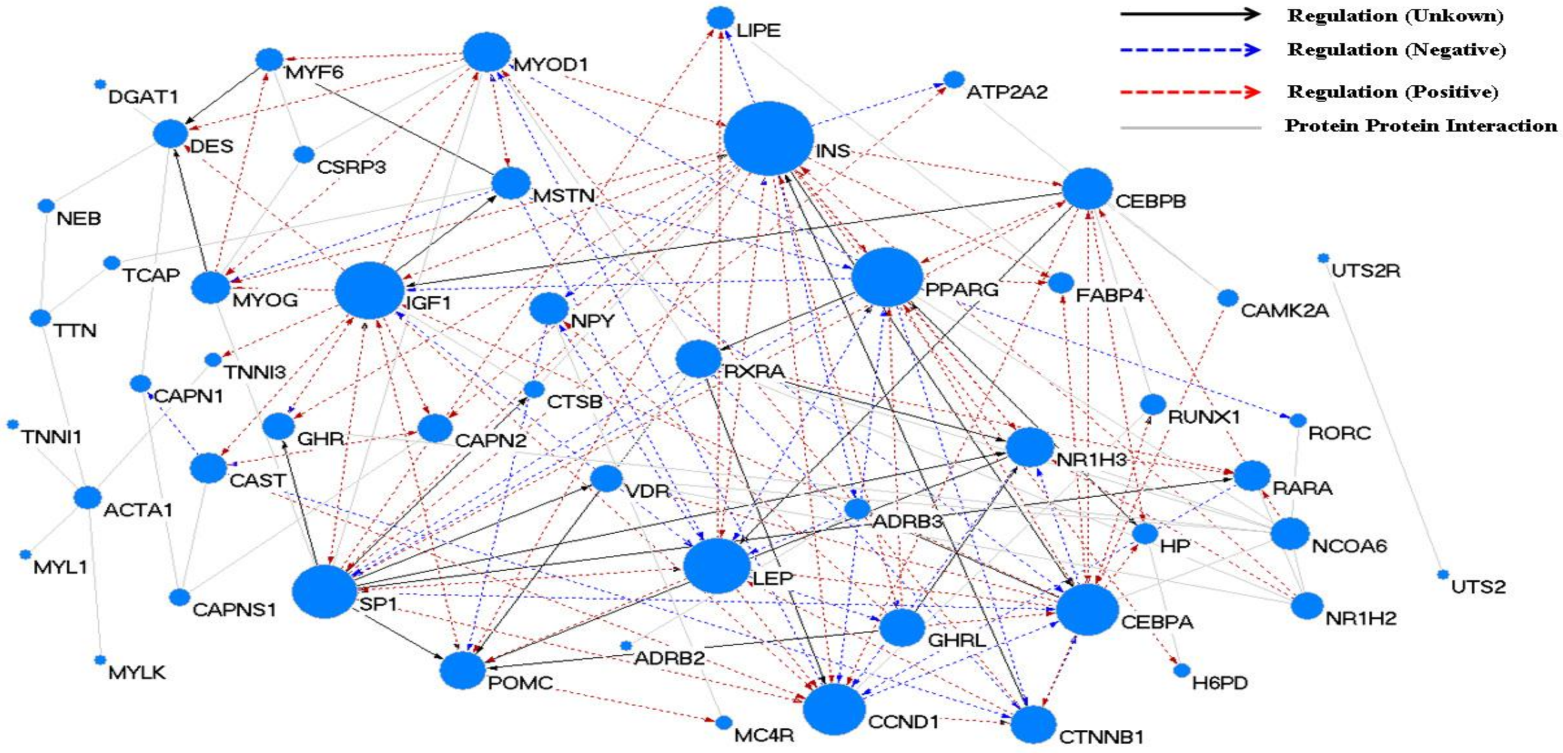
Supplementary Data 2. The important nodes that are not important or do not reveal in the core network, but have a large BC in the extended network

Gene(degree)	Linked proteins	Enriched biological function
CSNK2A1(7)	VDR(33)*, SP1(88)*, PRNP(33), MYF5(10), CTNNB1(135)*, CREM(20), ACACA(7)	adipocytokine signaling(p=0.007), skeletal system development(p=0.0005), regulation of transcription(p=9.88471e-05)
PRKCA(7)	TNNI3(10), RARA(51)*, MYOD1(44)*, MYLK(11)*, FAS(35)*, CREM(20), ACTA1(91)*	signal transduction(p=0.02), regulation of transcription(p=0.018), skeletal muscle fiber adaptation(p=0.0002), myoblast cell fate development(p=0.0004)
RB1(7)	SP1(88)*, NCOA6(37)*, MYOD1(44)*, INS(16)*, CEBPB(49)*, CEBPA(29)*, CCND1(40)*	fat cell differentiation(p=6.1217e-08), adipocytokine signaling(p=0.04), brown fat cell differentiation(p=0.007), insulin action(p=0.01)
SRC(6)	RXRA(80)*, ND2(1), MYLK(11)*, CTNNB1(135)*, ADRB3(3)*, ADRB2(25)*	fat cell differentiation(p=6.1217e-08), adipocytokine signaling(p=0.04), brown fat cell differentiation(p=0.007), insulin action(p=0.01)
ESR1(8)	SP1(88)*, RXRA(80)*, RARA(51)*, NCOA6(37)*, MAPK14(84)*, CTNNB1(135)*, CEBPB(49)*, CCND1(40)*	adipocytokine signaling(p=0.01), liver development(p=2.15431e-09), fat cell differentiation(p=4.17641e-05),

* It is indicated large degree nodes or nodes in the core network.

Supplementary Data 3. The integrated gene networks derived from the result of direct interactions using Pathway Studio software and PPI information of the core network. We constructed the core network 121 genes relate to marbling trait and examined the protein-protein interaction (grey line) among those genes. The pathway studio result contains the four types of regulation that indicate unknown (black arrow), negative (blue dashed arrow) and positive (red dashed arrow) between the direct-interacted genes. The size of node also denotes degree that is the number of connections or edges the node has to other nodes in the core network.



Supplementary Data 4. The gene co-annotation network of the core PPI network. We constructed gene co-annotation network based on the significant terms in the biological processes of Gene Ontology(GO) using 121 nodes of the core network. The result of functional enrichment analysis was carried out from DAVID tool. The size of node means the number of genes sharing the same GO term.