Figure EV1. Biological functions enriched in key co-expression clusters of human tissues.

A We examined biological functions (i.e., gene ontology biological process terms) enriched in key co-expression clusters identified in metabolically active tissues, such as skeletal muscle, liver, or adipose subcutaneous or omental tissues (hypergeometric test $P < 0.0001$). We found that those tissues were enriched in different biological functions and fatty acid metabolic process was enriched in liver and adipose subcutaneous tissue.

B We examined “fatty acid metabolic process” term among key co-expression clusters of 46 human tissues and found that liver and adipose subcutaneous tissues were most significantly enriched to this term in their key co-expression clusters.

C We showed all biological functions enriched in 46 human tissues (hypergeometric test $P < 0.0001$). The list of the detailed biological functions can be found in Dataset EV3.
Figure EV1.
Figure EV2. Co-expressions of regulatory interactions and their co-regulated gene pairs in skeletal muscle and adipose tissue.

A–H We examined mean co-expressions (red lines) of gene pairs involved in regulatory interactions and compared them with randomly permuted gene pairs by 1,000 times (blue dashed lines) for skeletal muscle tissue and adipose subcutaneous tissue (A and B, respectively). We also examined mean co-expressions of gene pairs that are co-regulated by same transcription factors (TFs) in skeletal muscle tissue and adipose subcutaneous tissue (C and D, respectively). For comparison, we selected gene pairs that do not share TFs binding and examined their mean co-expressions together with randomly permuted gene pairs in skeletal muscle tissue and adipose subcutaneous tissue (E and F, respectively). Finally, we examined mean co-expressions of co-regulated gene pairs according to the number of TFs co-bound in skeletal muscle tissue and adipose subcutaneous tissue (G and H, respectively).
Figure EV3. **Co-expressions of protein–protein interactions and their co-interacting gene pairs in skeletal muscle and adipose tissue.**

A–H We examined mean co-expressions (red lines) of gene pairs involved in protein–protein interactions and compared them with randomly permuted gene pairs by 1,000 times (blue dashed lines) for skeletal muscle tissue and adipose subcutaneous tissue (A and B, respectively). We also examined mean co-expressions of gene pairs that co-interacted with same proteins in skeletal muscle tissue and adipose subcutaneous tissue (C and D, respectively). For comparison, we selected gene pairs that do not interact with same proteins and examined their mean co-expressions together with randomly permuted gene pairs in skeletal muscle tissue and adipose subcutaneous tissue (E and F, respectively). Finally, we examined mean co-expressions of co-interacting gene pairs according to the number of proteins co-interacting in skeletal muscle tissue and adipose subcutaneous tissue (G and H, respectively).