

Multimodal epigenetic and enhancer network remodeling shape the transcriptional landscape of human beige adipocytes

Sarah Hazell Pickering, Natalia M. Galigniana, Mohamed Abdelhalim, Anita L. Sørensen, Julia Madsen Østerbye, Manuela Zucknick, Philippe Collas, Nolwenn Briand

Description of Additional Supplementary Data Files

File name: Supplementary data 1

Description: Differential gene expression between white and beige adipocytes at day15.

File name: Supplementary data 2

Description: ATAC peaks summary statistics (merged replicates).

File name: Supplementary data 3

Description: Hi-ChIP differential loop analysis (HiC-DC+).

File name: Supplementary data 4

Description: Differential ATAC footprinting analysis (TOBIAS).

File name: Supplementary data 5

Description: ChIP primers (NFIL3 ChIP-PCR).

File name: Supplementary data 6

Description: Source numerical data underlying the graphs presented in the figures.