SUPPLEMENTARY INFORMATION

TRAIN Consortium members:

Surname	First Name	Institution
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Supplementary Table S1: Primers used for RT-qPCR

Gene name	Primer sequence (5'- 3')
hTRIB3	Fw: CTGAGTATCTCAGGTCCCACGT
	Rv: AGGTGGAGCATTTCTCGCGCTA
hPPARG1	Fw: ATGGCATTATGAGACATCCC
	Rv: CATAATGCCATCAGGTTTGGG
36B4	Fw: GGGAAGGTGTAATCCGTCTCCACAG
	Rv: CGAGCGCGAGCATGTGT

Supplementary Table S2: Primers used for ChIP-RT-qPCR.

Gene name	Primer sequence (5'- 3')
PPARG pair 1	Fw: GGATGAGAGCTGGGGAGAAG
	Rv: TCAGCCCAAGACCCCTTCA
PPARG pair 2	Fw: CTGAGGCAGGGTCATGGTC
	Rv: AAGACCCCTTCACCCGGTC
HSCB	Fw: CACTCCCCCTTCAGCTCAAA
	Rv: TGGGTGTTTGGTGGTTCGAA
Neg	Fw: GAGCCAGGGTTTCTCTGATTC
	Rv: CCTCAGTGATCAGCCCTAAATG

Supplementary Table S3: Gene enrichment analysis.

Gene set	Direction	p-Value
Cytoplasmatic ribosomal proteins	Down	$8.42e^{-16}$
Apical junction	Up	0.0044
Cell differentiation index	Up	0.001
Translation factors	Down	0.001
White fat cell differentiation	Up	0.001
Myc target genes	Down	$1.19\,e^{-7}$
Oxidative phosphorylation	Down	0.000027
Kras signaling	Up	0.0013
Fatty acid metabolism	Down	0.066

Supplementary figure S1

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WDR5-Myc   -   WT   S91K   F133A   WT   WT   WT

MLL-Flag   WT   -   WT   WT   R449A   WT   WT

WDR5i

IP: Flag   Myc ab

Flag ab

Input   Myc ab

Flag ab