

Additional data file 5: Input dataset for SOM analysis. The variable BS represents the sum of predicted binding strength of n putative medium or strong PPREs (Σbs_n , $bs_i = \max \{bs_{PPAR\alpha}, bs_{PPAR\gamma}, bs_{PPAR\beta/\delta}\}$) found within 20 kB the analyzed region of each gene in human (h) and mouse (m), respectively. The remaining values indicate the number of conserved strong/medium (CS) or weak (CW) PPREs in human and mouse.

Cluster	Gene	BS _h	BS _m	CS _h	CW _h	CS _m	CW _m
IA	<i>ANGPLT4</i>	0.600	0.386	1	1	1	1
	<i>CPT1A</i>	1.000	0.140	1	1	1	1
	<i>PEPCKI</i>	0.600	0.561	1	0	1	1
	<i>LPL</i>	0.350	0.421	1	1	1	0
IB	<i>GK</i>	0.450	0.175	1	1	0	1
	<i>UCP3</i>	0.400	0.491	1	1	0	1
IC	<i>LRP1</i>	0.600	0.632	0	1	1	1
ID	<i>caveolin 1</i>	0.000	0.211	0	1	1	1
	<i>IGFBP1</i>	0.150	0.351	0	1	1	1
IIA	<i>APOC3</i>	0.500	0.596	1	0	1	0
	<i>CPT1B</i>	0.550	0.509	1	0	1	0
	<i>CPT2</i>	0.500	0.211	1	0	1	0
	<i>CYP1A1_E</i>	0.650	0.246	1	0	0	0
	<i>CYP1A1_N</i>	0.650	0.421	1	0	1	0
	<i>HMGCS2</i>	0.575	0.281	1	0	1	0
	<i>SRB1</i>	0.500	0.316	1	0	1	0
IIB	<i>ADRP</i>	0.200	0.316	1	0	1	0
	<i>APOA1</i>	0.300	0.632	1	0	1	0
	<i>G0S2</i>	0.250	0.281	1	0	1	0
	<i>LXRα</i>	0.300	0.421	1	0	1	0
	<i>SSAT</i>	0.200	0.386	1	0	1	0
IIIA	<i>COX2</i>	0.211	0.105	1	0	0	1
	<i>SEMA6B</i>	0.070	0.596	1	0	0	1
IIIB	<i>APOA2</i>	0.450	0.421	0	1	0	1
	<i>APOA5</i>	0.700	0.105	0	1	0	1
	<i>FADS2_E</i>	0.200	0.211	0	0	0	0
	<i>FADS2_N</i>	0.000	0.211	0	1	0	1
	<i>PXR</i>	0.250	0.211	0	1	0	1
	<i>RVRα</i>	0.200	0.298	0	1	0	1
	<i>SLC10A2</i>	0.600	0.105	0	1	0	1
IVA	<i>ACOX1</i>	0.550	1.000	0	0	0	0

IVB	<i>Resistin</i>	0.300	0.246	0	0	0	0
	<i>SULT2A1</i>	0.350	0.404	0	0	0	0
IVC	<i>APOE</i>	0.500	0.105	0	0	0	0
	<i>PPARα</i>	0.350	0.175	0	0	0	0
	<i>CYP27A1</i>	0.350	0.105	0	0	0	0
IVD	<i>GSTA2</i>	0.100	0.281	0	0	0	0
	<i>transferrin</i>	0.100	0.211	0	0	0	0
	<i>UGT1A9</i>	0.100	0.175	0	0	0	0
IVE	<i>CDKN2A</i>	0.000	0.140	0	0	0	0