SUPPLEMENTARY DATA

**Supplementary Table 1.** Primers

| | **Description and official symbol** | **Forward** | Reverse | concentration |
|---|---|---|---|---|
| ***Ucp1*** | Uncoupling protein 1<br>*Ucp1* | GGGCTGATTCCTTTTGGTCTCT | GGGTTGCACTTCGGAAGTTGT | 300nM |
| ***Adrb3*** | Adrenoceptor beta 3<br>*Adrb3* | ACGCTGAGGCGCAAGAGT | GTAGGGCATATTGGAGGCAAAG | 200nM |
| ***Acc1*** | Acetyl-CoA carboxylase alpha (Acaca)<br>*Acaca* | ACCTCAACCACTACGGCATGA | AGGTGGTGTGAAGGCGTTGT | 200nM |
| ***Cpt1α*** | Carnitine palmitoyltransferase 1a<br>*Cpt1a* | CGGTTCAAGAATGGCATCATC | TCACACCCACCACCACGATA | 200nM |
| ***Rps29*** | Ribosomal protein S29<br>*Rps29* | GCCAGGGTTCTCGCTCTTG | GGCACATGTTCAGCCCGTAT | 300nM |
| ***Hsl*** | Lipase hormone sensitive,<br>*Lipe* | CCCCGAGATGTCACAGTCAAT | GAATTCCCGGATCGCAGAA | 200nM |
| ***Mcad*** | Acyl-CoA dehydrogenase, C-4 to C-12 straight chain<br>*Acadm* | AGCCCTGGACGAAGCTACTA | CTCCTTGGTGCTCCACTAGC | 200nM |
| ***Lcad*** | Acyl-CoA dehydrogenase, long chain,<br>*Acadl* | TCCGCTTCCATGGCGAAATA | CGTAGGCTTTTGCAATCGGG | 200nM |
| ***Cox1*** | Cytochrome c oxidase subunit 1,<br>*Mt-Co1* | GCTTCGTCCACTGATTCCCA | GCAAAGTGGGCTTTTGCTCA | 600nM |
| ***RnaseP*** | Ribonuclease P/MRP 40 subunit,<br>*Rpp40* | TCTGCAACGCGGACCTAAATA | TCTGGCAACACGAAACCTGT | 600nM |
| ***Pgc1α*** | Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha<br>*Ppargc1a* | CTGCCATTGTTAAGACCGAGAA | AGGGACGTCTTTGTGGCTTTT | 200nM |
| ***Cox4i*** | cytochrome c oxidase subunit IV isoform 1<br>*Cox4i1* | TCTACTTCGGTGTGCCTTCG | CCACATCAGGCAAGGGGTAG | 200nM |
| ***Tfam*** | transcription factor A, mitochondrial<br>*Tfam, Mttfa* | GGGGCGTGCTAAGAACACT | CAGATAAGGCTGACAGGCGA | 200nM |
| ***Pparg1*** | peroxisome proliferator-activated receptor gamma 1<br>*Pparg1* | TCGCTGATGCACTGCCTATG | TGATTCCGAAGTTGGTGGGC | 200nM |

| | | | | |
|---|---|---|---|---|
| ***Pparg2*** | peroxisome proliferator-activated receptor gamma 1<br>*Pparg2* | TGCTGGTGATCAGAAGGCTG | AGTGGTTCACAGCTTCTTTCAA | 200nM |
| ***Tbx1*** | T-box 1,<br>*Tbx1* | ACCCTCGAAAAGACAGCGAG | TGCGTGATCCGGTGATTCTG | 200nM |
| ***Pepck*** | phosphoenolpyruvate carboxykinase 1 (soluble)<br>*Pck1* | ATCCCCAAAAGTGGGCAGAG | TACATGGTGCGGCCTTTCAT | 200nM |

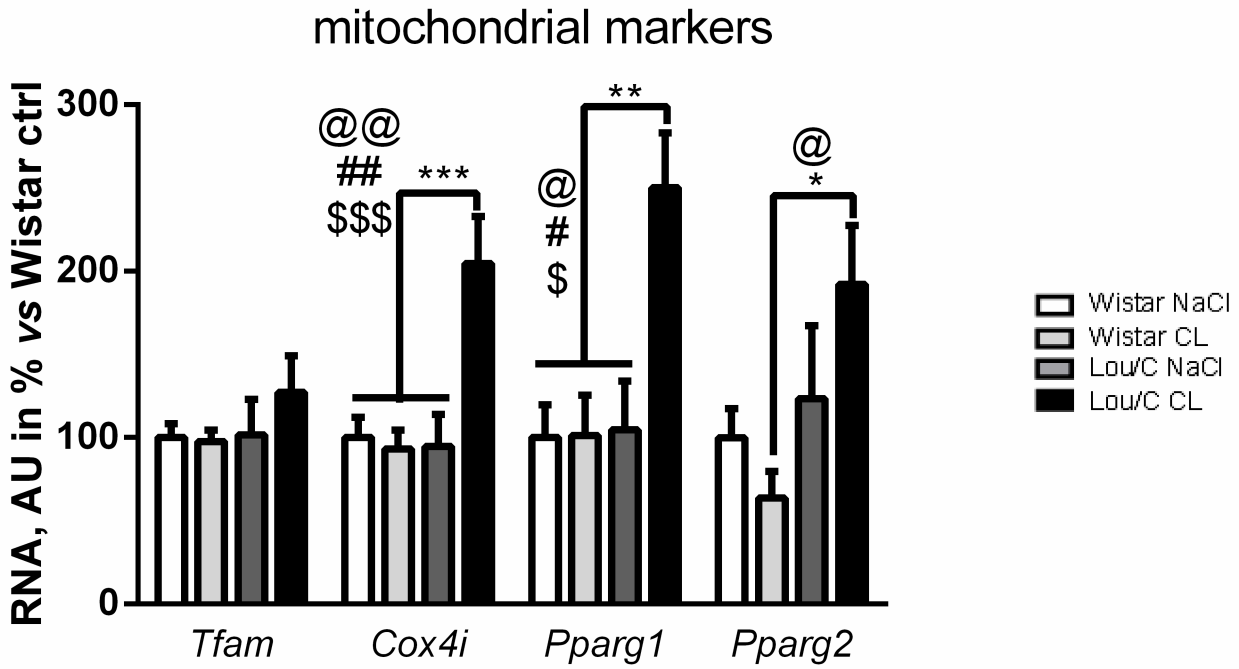
SUPPLEMENTARY DATA

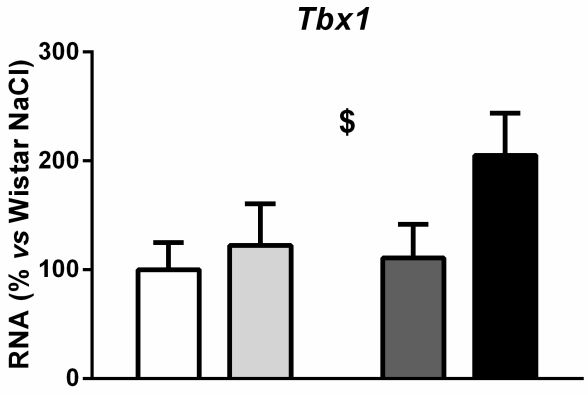
**Supplementary Table 2.** Glycemia and insulinemia values before and at the end of euglycemic-hyperinsulinemic clamps

| | Wistar | | Lou/C | |
|---|---|---|---|---|
| | **NaCl** | **CL** | **NaCl** | **CL** |
| **Basal glycemia (mmol/L)** | **4.8±0.3** | **4.1±0.2** | **4.4±0.3** | **4.2±0.1** |
| **Steady state glycemia (mmol/L)** | **5.7±0.2** | **5.4±0.1** | **5.7±0.1** | **5.7±0.1** |
| **Basal insulin (ng/mL)** | **3.62±0.70** | **2.94±1.28** | **2.66±0.75** | **1.57±0.16** |
| **Steady state insulin (ng/mL)** | **34.31±2.14** | **26.74±2.48** | **28.21±1.20** | **24.41±2.21** |

SUPPLEMENTARY DATA

**Supplementary Figure 1.** The expression of mitochondrial and beiging markers is increased by the CL-316243 treatment in Lou/C rats.
Expression of *Tfam*, *Cox4i*, *Pparg1* and *Pparg2* for mitochondrial markers in iWAT.
Expression of *Tbx1* as a beiging marker in iWAT. Statistical significance assessed by two-way ANOVA: # strain effect, @ treatment effect, $ interaction between strain and treatment. *significant difference by post hoc pairwise comparison between different conditions. Single, double, and triple symbols imply $p<0.05$, $p<0.01$, and $p<0.001$, respectively.



SUPPLEMENTARY DATA

**Supplementary Figure 2.** UCP1 is overexpressed in eWAT of Lou/C rats by CL-316 2423.
(A) Representative H&E staining in eWAT (7µm), scale bars = 50 µm. (B) *Ucp1* and *Adrb3* mRNA expression in eWAT.
Results are means ± SEM of 8 experiments per group. Statistical significance assessed by two-way ANOVA: $ interaction between strain and treatment. *significant difference by post hoc pairwise comparison between different conditions. Single symbols imply $p<0.05$.