**S2 Table**: Linear regression analysis of the effect of the smaller (pre Shungin et al, 2015 publication) WHRadjBMI-increasing SNPscore on lipolysis phenotypes.

|  |  |  |
| --- | --- | --- |
|   | pre Shungin SNP score | pre Shungin SNP score no pleiotropy |
|   | N | adjR2 | Beta | Se | L95 | U95 | Pmain | Pinter | N | adjR2 | Beta | Se | L95 | U95 | Pmain | Pinter |
| Spontaneous lipolysis | 322 | 0.321 | 0.008 | 0.012 | -0.015 | 0.031 | 0.4850 | 0.3130 | 322 | 0.323 | 0.014 | 0.013 | -0.012 | 0.040 | 0.2960 | 0.5780 |
| Isoprenaline-stimulated lipolysis\* | 551 | 0.182 | 0.000 | 0.004 | -0.009 | 0.009 | 0.9920 | 0.3400 | 551 | 0.182 | -0.001 | 0.005 | -0.011 | 0.009 | 0.8230 | 0.5610 |
| dcAMP-stimulated lipolysis\* | 534 | 0.163 | -0.002 | 0.005 | -0.012 | 0.007 | 0.6450 | 0.8880 | 534 | 0.163 | -0.004 | 0.005 | -0.015 | 0.006 | 0.4380 | 0.6650 |
| Where: adjR2, adjusted R2 from regression models; L95, lower boundry of 95% confidence interval; U95, upper boundry of 95% confidence interval; Pmain, P value for main effect; Pinter, Pvalue for sex interaction; \* compared to basal lipolysis levels. The limited score based upon 14 lead SNPs reported by Randall et al and Heid et al (*TBX15-WARS2, DNM3, LYPLAL1, GRB14-COBBL1, PPARG, NISCH-STAB, ADAMTS9, MAP3K1, HSD17B4, VEGFA, RSPO3, NFE2L3, HOXC13, ZNRF3-KREMEN1* loci). |

**S1 Figure 1: Schematic demonstrating the different steps by which isoprenaline and dibutyryl cyclic AMP (dcAMP) stimulate activation of lipolysis to produce release of glycerol.** In blue, endogenous cellular components, in red the 2 stimuli used in this study. Isoprenaline-stimulated activation relies upon the efficient function of the β-adrenergic receptor signalling to activation of protein kinase A. In contrast, dcAMP directly activates Protein kinase A to initiate glycerol release.

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