

SUPPLEMENTARY DATA

Supplementary Table 1. Ct-values for BMP antagonists in undifferentiated human preadipocytes, isolated mature adipocytes and *in vitro* differentiated human preadipocytes.

Gene	Undifferentiated preadipocytes mean deltaCt-value	Differentiated preadipocytes mean deltaCt-value	Isolated mature Adipocytes mean deltaCt-value
<i>CHRDLI</i>	19.8	13.7	10.9
<i>CHRD</i>	18.6	20.0	19.1
<i>NOG</i>	17.2	16.1	24.4
<i>FST</i>	14.2	14.7	20.2
<i>BAMBI</i>	13.2	14.7	16.3
<i>GREM1</i>	13.8	15.6	24.3

Analyses of mRNA were determined with quantitative real-time PCR (Q-PCR) and 18S was used as reference. A deltaCt-value >26 is considered as not expressed, between 22-26 as low expression and <15 is considered as high expression. Results are means of 34 individuals (isolated cells) and 24-38 individuals (*in vitro* differentiated cells) analyzed in duplicates.

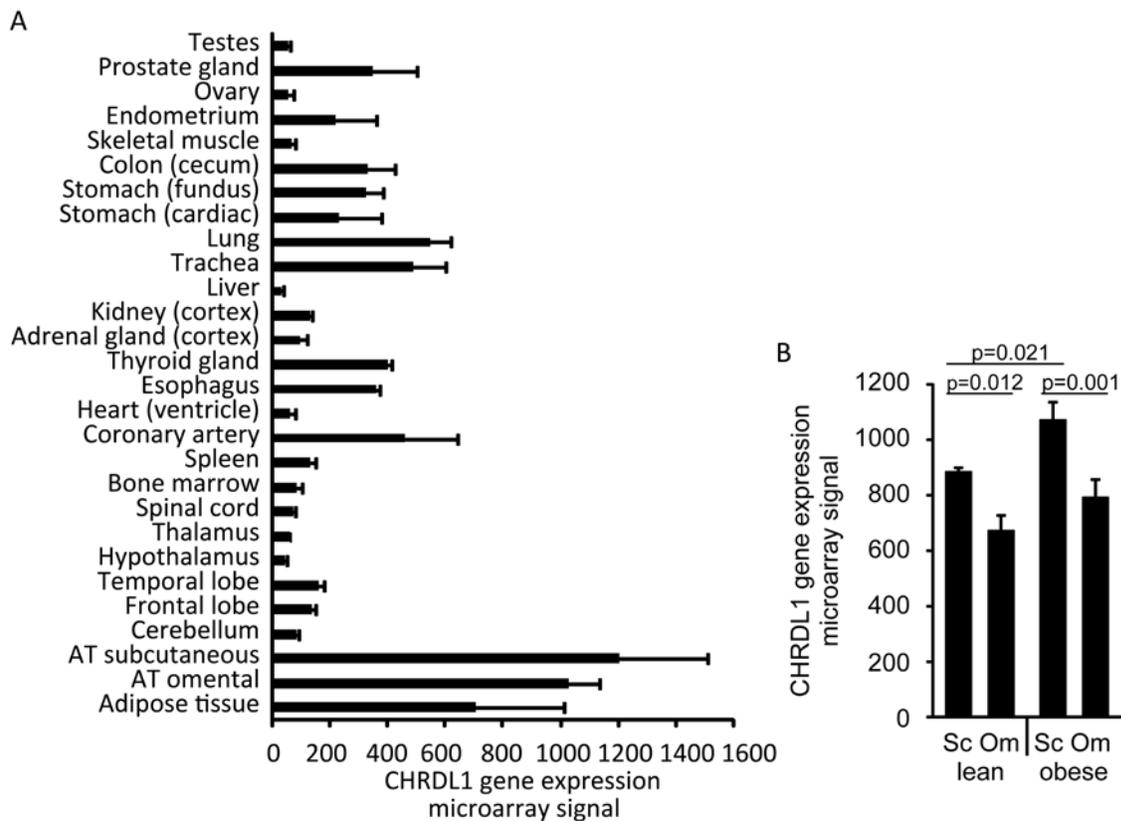
Supplementary Table 2. Correlations between mRNA levels for BMP4 and BMP inhibitors in isolated adipocytes and adipose tissue biopsies.

Gene	Isolated R	adipocytes <i>P</i> -value	Adipose tissue R	biopsies <i>P</i> -value
<i>CHRD</i>	0.34	0.047	0.26	0.17
<i>FST</i>	0.04	0.82	-0.26	0.17
<i>NOG</i>	0.37	0.03	0.20	0.29
<i>CHRDLI</i>	0.69	<0.001	0.50	0.005
<i>GREM1</i>	0.38	0.044	0.38	0.02

Results are means of 34 individuals analyzed in duplicates. mRNA levels were analyzed with Q-PCR and related to one individual (RQ=1). Spearman's rank correlation was used to analyze data, which were not normally distributed. A *P*-value <0.05 was considered as significant.

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Supplementary Figure 1. *CHRDL1* is highly expressed in human adipose tissues. (A) *CHRDL1* expression in human tissues analyzed by DNA microarrays. Data from the GSE3526 data set in the GEO database and is presented as mean expression \pm SEM. (B) *CHRDL1* gene expression in adipose tissue from lean vs. obese individuals. Paired abdominal subcutaneous (Sc) and omental (Om) adipose tissue. Surgical biopsies were obtained from ten women undergoing elective surgery (liposuction and elective gynecological procedures). These procedures were in accordance with guidelines of the South Birmingham Ethics Committee. The subjects were divided into two cohorts according to BMI (lean, BMI 23.0 ± 1.2 kg/m², n=5; obese, BMI 33.2 ± 3.1 kg/m², n=5). Gene expression was analyzed using the Human Genome U133 plus 2.0 DNA microarrays (Affymetrix). *CHRDL1* gene expression was analyzed using the 209763_at probe set.



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Supplementary Figure 2. Expression of *GREM1* in different human tissues. *GREM1* expression was analyzed by DNA microarrays. Data is from the GSE3526 data set in the GEO database and is presented as mean expression +/- SEM.

