

### Transcription factor binding sites

The statistical testing of the predicted and conserved transcription factor (TF) binding sites among the upregulated genes revealed that binding sites for Arnt-Ahr, NHLH1, TCF11-MafG, RELA, SP1, CREB1, deltaEF1, ZNF42\_1-4, and Pax5 were enriched among this list of genes, with p-values from 0.01 to 0.05 (data not shown). The function of these sites was not empirically verified.

Based on the statistics, the most highly enriched transcription factor binding site among the upregulated genes was Arnt-Ahr, which can be activated through hypoxia. Hypoxia has previously been shown to induce expression of leptin and glucose transporter 1 [1], and glucose transporter 4 (Slc2a4) [2], which was also upregulated in the present microarray data. The data suggest that the diet has effect of the oxidative processes in the adipose tissue, and may require further study. CREB1 was among the statistically enriched transcription factor binding sites, which may help to understand how beta-3 adrenergic receptor could be one of the factors driving leptin transcription as observed in the present data.

1. Grosfeld A, Zilberfarb V, Turban S, Andre J, Guerre-Millo M, Issad T: Hypoxia increases leptin expression in human PAZ6 adipose cells. *Diabetologia* 2002; 45: 527-530.
2. Chou SW, Chiu LL, Cho YM, Ho HY, Ivy JL, Ho CF, Kuo CH: Effect of systemic hypoxia on GLUT4 protein expression in exercised rat heart. *Jpn J Physiol* 2004; 54: 357-363.