Supplementary Table VIII - Lst of transcription factors with enriched binding sites in the promoter region of hormone receptor genes

Affymetrix ID	**Gene name**	**Symbol**	**TRANSFAC Matrix**	**over-representation Pvalue**
1382372_at	aryl hydrocarbon receptor	Ahr	V$AHR_Q5; V$AHRHIF_Q6	0.013; 0.041
1369244_at	aryl hydrocarbon receptor nuclear translocator	Arnt	V$AHRHIF_Q6	0,041
1375437_at	aryl hydrocarbon receptor nuclear translocator	Arnt	V$AHRHIF_Q6	0,041
1387076_at	hypoxia-inducible factor 1, alpha subunit	Hif1a	V$AHRHIF_Q6	0,041
1386641_at	hepatic leukemia factor	Hlf	V$HLF_01	0,036
1370917_at	heat shock transcription factor 1	Hsf1	V$HSF_Q6; V$HSF1_Q6	0.015; 0.026
1398561_at	interferon regulatory factor 2	Irf2	V$IRF2_01	0,025
1369242_at	paired box 6	Pax6	V$PAX6_Q2	0,048
1379397_at	RAR-related orphan receptor alpha	Rora	V$RORA1_01	0,041
1392180_at	Sp1 transcription factor	Sp1	V$SP1_Q6; V$SP1_Q4_01; V$SF1_Q6; V$SP1_Q2_01	0.003; 0.009; 0.011; 0.047

The 1 kb upstream sequences, starting from the transcription start site (TSS), of 6 hormone receptor genes (GLP-1R, Prlr, Gipr, Ghr, Vipr2 and Cckar) were retrieved from the ENSEMBL database together with a large set of background sequences (2 kb upstream sequences of the whole rat genome) and analyzed by the Clover program. The p-value indicates the probability that the motif's presence in the target sequences is explained just by chance. Motifs were declared as significantly over-represented in the promoter sequences of the hormone receptor genes if their p-value was $\leq$ 0.05