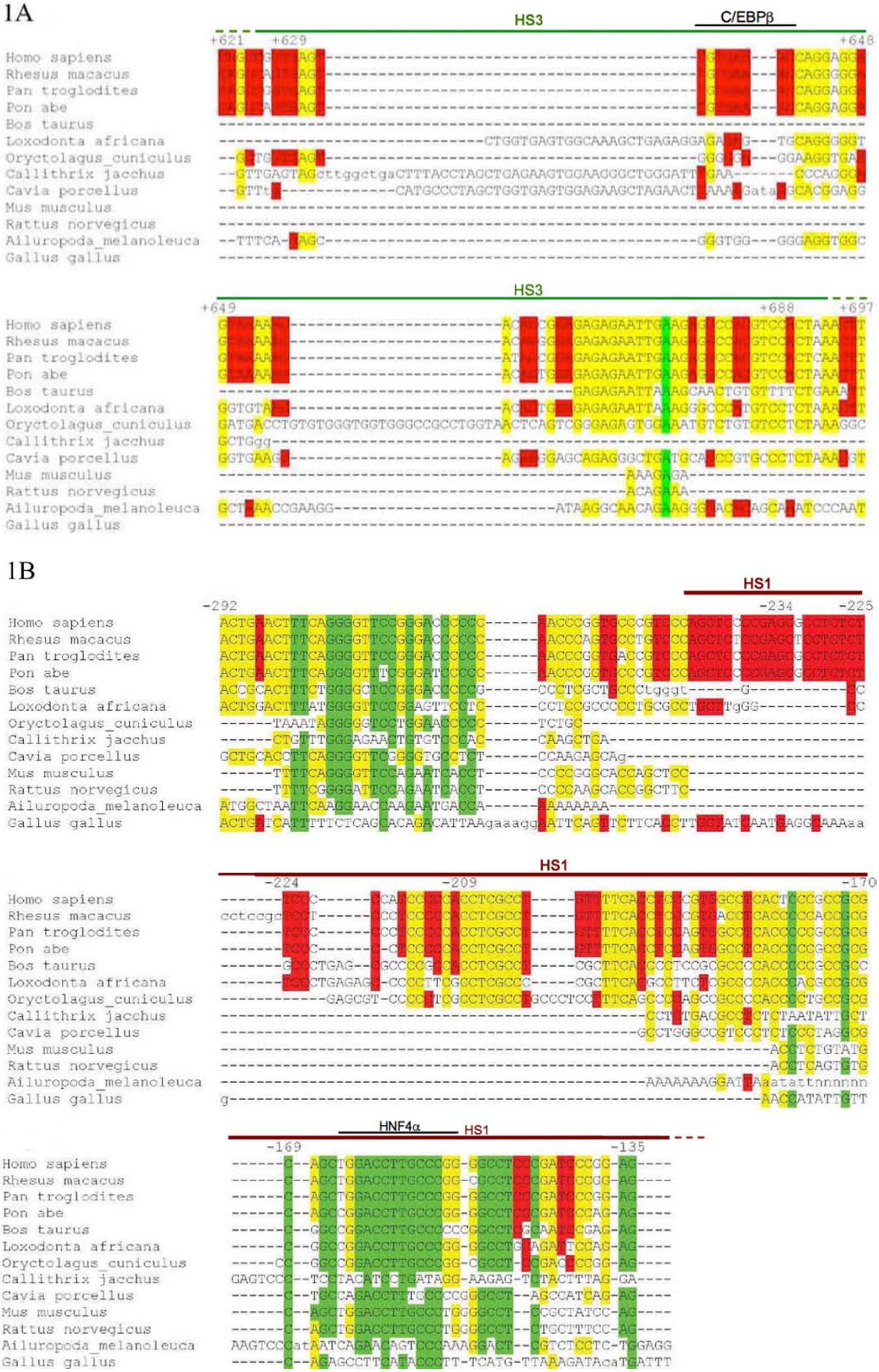
1A
HS3
C/EBPβ
+621
+629
+648
Homo sapiens
Rhesus macacus
Pan troglodites
Pon abe
Bos taurus
Loxodonta africana
Oryctolagus_cuniculus
Callithrix jacchus
Cavia porcellus
Mus musculus
Rattus norvegicus
Ailuropoda_melanoleuca
Gallus gallus
HS3
+649
+688
+697
1B
HS1
-292
-234
-225
HS1
-224
-209
-170
HNF4α
HS1
-169
-135

Supplementary Figure 1 : Results of the alignment of different regions of the human *ABCC6* gene and the orthologs in 13 vertebrate species. Colors indicate nucleotide conservation: green: 10 species or more, yellow: 7 species or more, red: in all primates. 500 nucleotides upstream and 2kb downstream of the annotated TSS were considered. A) Alignment of the human +629/+688 intronic region. B) alignment of proximal promoter regions. Regions located in HS1 or HS3 are indicated by horizontal bars. C/EBPß and HNF4α binding sites are indicated. Consensus C/EBPß binding site present in primates is located between +632/+640 and is either completely absent or interrupted by insertions/mutations in the other species.

	Forward (numbering relative to ATG)	Reverse (numbering relative to ATG)
ABCC6 primers for Southern blot probe	+1435 GGGTTAATGTCAGGATGAAAGG	+1735 CATCTACCTCCTCTTCATCCAC
ABCC6 primers for luciferase constructs	-332 TCGGTACCGATTCTTGTTGCAGGGGG	+72 ACCAAGCTTGGAAAAGGAGAGTGGGGC
	-234 CTCGGTACCCGCCTCTCTTCCCCCAT	+513 CAAAAGCTTTAGCAGCATGGCACAAGG
	-209 CCGGTACCTCGCCTGTTTTCACCTCC	+629 TCAAGCTTCACCGGCTGTGCAAACTT
	-145 CGGGTACCGAGCTCGAATCCCAGCCG	+652 TGGAAGCTTACTCCTCCTGGTTTCACA
		+688 AGAAGCTTGGACGTGGCCTCTTCAAT
		+817 TCAAGCTTAATCCTCCTGCCTCAGCC
		+960 CAAAAGCTTTCAAGCAATCCTCCCACC
ABCC6 primers for mutated luciferase constructs	mut1f TATTAATCCATTTAATTCCCCTCATAGAGGTAGA	mut1r TCTACCTCTATGAGGGGAATTAAATGGATTAATA
	mut2f TTCCCCCTTTTACAGGGAAGTACCCTGAGATACA	mut2r TGTATCTCAGGGTACTTCCCTGTAAAAGGGGGAA
	mut3f CAGCCGGTGAGTTGTTACCCCAGGAGGAGTAAA	mut3r TTTACTCCTCCTGGGGTAACAACTCACCGGCTG
	delf GCCCCACTCTCCTTTTCCGAGTTGTGAAACCAGGAGG	delr CCTCCTGGTTTCACAACTCGGAAAAGGAGAGTGGGGC
ABCC6 primers for ChIP	+503 CCATGCTGCTATGAACTTTGC	+700 TTGAAGTTTAGTGGACGTGGC

Supplementary table I: Primers used in this study.