

Supplementary Information

A Palindromic Motif in the -2084 to -2078 Upstream Region is Essential for ABCA12 Promoter Function in Cultured Human Keratinocytes

Yoshitaka Shimizu¹, Yasushi Ogawa¹, Kazumitsu Sugiura¹, Jun-ichi Takeda², Kaori Sakai-Sawada³, Teruki Yanagi³, Atsushi Kon⁴, Daisuke Sawamura⁵, Hiroshi Shimizu³, Masashi Akiyama^{1*}

¹Department of Dermatology, and ²Division of Neurogenetics, Nagoya University Graduate School of Medicine, Nagoya, Japan

³Department of Dermatology, Hokkaido University Graduate School of Medicine, Sapporo, Japan

⁴Department of Nutrition, Aomori University of Health and Welfare, Aomori, Japan

⁵Department of Dermatology, Hirosaki University Graduate School of Medicine, Hirosaki, Japan

*Correspondence:

Masashi Akiyama, M.D., Ph.D.

Department of Dermatology

Nagoya University Graduate School of Medicine

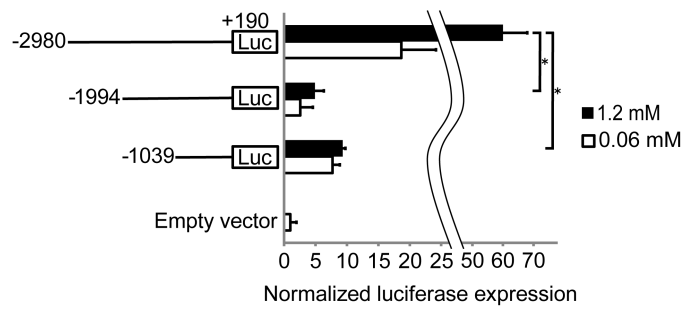
65 Tsurumai-cho, Showa-ku, Nagoya 466-8550, Japan

Telephone: +81-52-744-2314

Fax: +81-52-744-2318

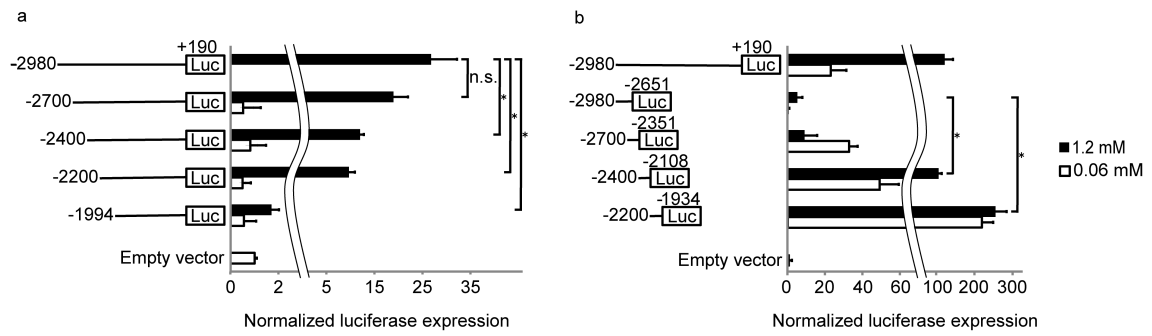
E-mail: makiyama@med.nagoya-u.ac.jp

Supplementary Figures



Supplementary Figure S1. Detailed presentation of promoter activities of less potent reporters used in Figure 1

Figure 1 is differently represented with a magnified Y-scale to show the promoter activities of less potent reporters.



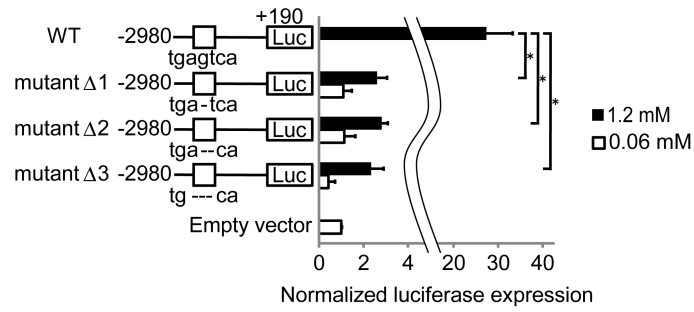
Supplementary Figure S2. Detailed presentation of promoter activities of less potent reporters used in Figure 3

Figure 3 is differently represented with a magnified Y-scale to show the promoter activities of less potent reporters.



Supplementary Figure S3. Diagram of putative transcription factor binding elements

The -2980 to -1934 region of the *ABCA12* gene is depicted. The predicted AP1 element and the predicted Sp1 element within the -2200/-1934 fragment are shown. The TSS is indicated by the bent arrow. Downward bars represent 398 putative transcription factor binding sites predicted by the *in silico* analysis.



Supplementary Figure S4. Detailed presentation of promoter activities of less potent reporters used in Figure 4

Figure 4 is differently represented with a magnified Y-scale to show the promoter activities of less potent reporters.

Human	ACACTTGAGTCAAGTCAT
Chimp	ACACTTGAGTCAAGTCAT
Gorilla	ACACTTGAGTCAAGTCAT
Orangutan	ACACTTGAGTCAAGTCGT
Gibbon	ACACTTGAGTCAAGTCAT
Rhesus	ACACTTGAGTCAAGTCGT
Crab-eating_macaque	ACACTTGAGTCAAGTCGT
Baboon	ACACTTGAGTCAAGTCGT
Green_monkey	ACACTTGAGTCAAGTCAT
Marmoset	ACACTTGAGTCAAGTCAT
Squirrel_monkey	ACACTTGAGTCAAGTCAT
Bushbaby	ACACTTGAGTCAAGTCAT
Squirrel	ACACTTGAGTCAAGTCAT
Guinea_pig	ACGCATGAGTCAAGTCAT
Pig	GCATTTGAGTCAAGTCAT
Tibetan_antelope	ACAGTTGAGTCAAGTCAT
Cow	ACAGTTGAGTCAAGTCAT
Sheep	ACAAGTCAAGTCAT
Domestic_goat	ACAATGAGTCAAGTCAT
White_rhinoceros	ACACTTGAGTCAAGTCAT
Cat	ACACTTGAGTCAAGTTGT
Dog	ACACTTGAGTCAAGTTGC
Ferret	ACACTTGAGTCAAGTTAT
Panda	ACACTTGAGTCAAGTTGT
Pacific_walrus	ACACTTGAGTCAAGTTGC
Weddell_seal	ACACTTGAGTCAAGTTGT
Star-nosed_mole	ACACTTGAGTCAAGTCAT
Elephant	ACACTTGAGTCAAGTCAT
Cape_golden_mole	ACACTTGAGTCAAGTCAT
Armadillo	AAACTTGAGTCAAGTCAT
Alpaca	ACAGCTGAGTCAAGTCGT
Bactrian_camel	ACATCTGAGTCAAGTCGT
Naked_mole-rat	AGTAAAGAGTCAAGTCAT
Brush-tailed_rat	ACTCATGAGCCAGTCAT
Horse	GCACTTTGATTTAGTTGT
Chinese_tree_shrew	ACACCTGAGTCAATCAT
Lesser_Egyptian_jerboa	ATGCTTGAATCAGCCAT
Mouse	ACACTTGAATCAGCCCC
Prairie_vole	ACACTTGAATCAGTACC
Chinese_hamster	CCGCTTGAATCAGTCCT
Rat	ACGCTTGAATCAGTCCT
Chinchilla	ACACATGAGTCAATTAT
Rabbit	ACACTTGAGTCAAGTCCT
Pika	ACACTTGTGTAAGTCCT
Dolphin	GCACTTTTGTCAAGTCCT
Killer_whale	GCACTTTTGTCAAGTCCT
Black_flying-fox	ACATTTGAGTCAATTTGT
David's_myotis_(bat)	ATATTTGAGTCAATTCAT
Big_brown_bat	ACATTTGAGTCAATTCAT
Microbat	ACATTTGG-GTCAATTCAT
Hedgehog	ACATTTGAGTCTATCAT
Aardvark	ACGTTTGAATCAGTCCT
Megabat	ACCTTTGAATCAGTTGT
Golden_hamster	CCAATCGAATCAGTCCT
Cape_elephant_shrew	ATCCTTGCAGTCAG----
Consensus	ACACTTGAGTCAAGTCAT

ACACTTGAGTCAAGTCAT

Supplementary Figure S5. The -2084/-2078 AP1 binding element is highly conserved among vertebrate species.

The multiple alignments of the -2048 to -2078 region of the ABCA12 among 55 vertebrate species are shown. The -2084/2078 motif is boxed. The consensus sequence is shown as a sequence logo at the bottom.