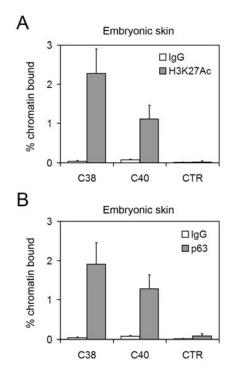
Supplementary data

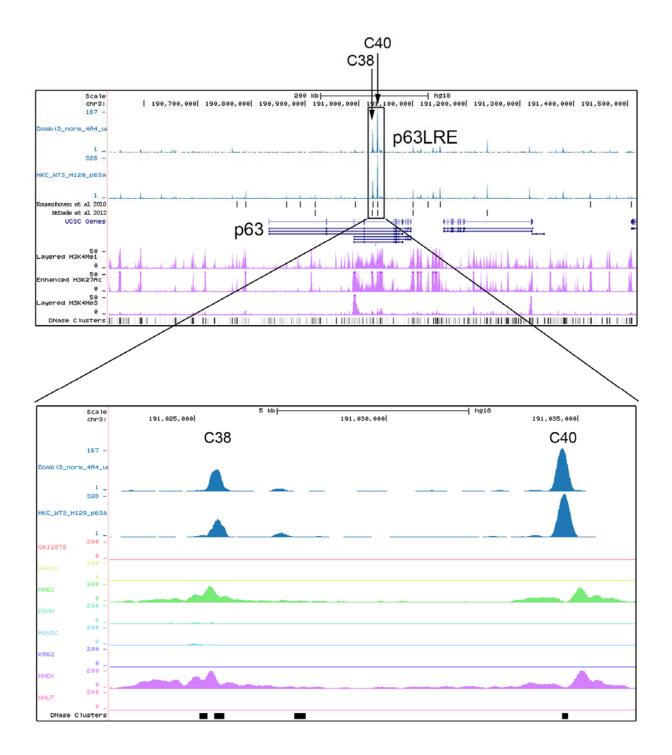
A composite enhancer regulates *p63* gene expression in epidermal morphogenesis and in keratinocyte differentiation by multiple mechanisms

Antonini et al.

## **Supplementary Figures**



**Supplementary Figure S1.** (A,B) ChIP-qPCR was performed on mouse embryonic skin at E14.5 using anti-H3K27Ac (A), anti-p63 (B) (grey bars), or rabbit IgG (white bars) as negative control. Error bars denote SD.



**Supplementary Figure S2.** The position of the p63-binding regions in the *p63* genomic loci was obtained from previously published ChIP-seq analyses in human primary keratinocytes using 4A4 and H129 antibodies, as indicated with the blue peaks and black bars (Kouwenhoven et al. 2010), and with black bars (McDade et al. 2012). C38, C40 elements and p63LRE enhancer regions corresponding to the mouse genomic regions are indicated. Genomic regions enriched for DNAse clusters and H3K27ac in

the indicated cell lines were obtained from the ENCODE project (Sabo et al. 2006; Ernst et al. 2011). The following human cells were used: B-lymphoblastoid cells (GM12878), hepatocellular carcinoma cells (HepG2), mammary epithelial cells (HMEC), skeletal muscle myoblasts (HSMM), umbilical vein endothelial cells (HUVEC), erythrocytic leukaemia cells (K562), normal epidermal keratinocytes (NHEK) and normal lung fibroblasts (NHLF).

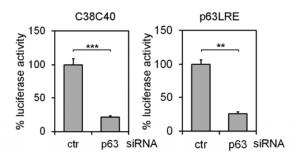


А

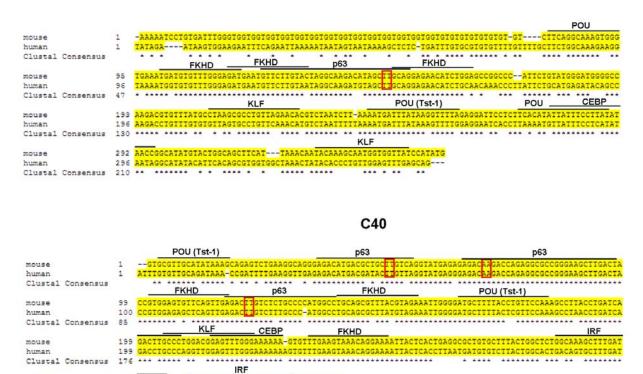
В

WT p63LRE-LacZ

**Supplementary Figure S3.** (A) E13.5 wild type (WT) and transgenic embryos containing either four copies of C40 (C40x4-LacZ) or p63LRE-LacZ were tested for  $\beta$ -galactosidase activity. (B) Histological sections of skin at P2 of wild type (WT) and p63LRE-LacZ transgenic mice were stained for  $\beta$ -galactosidase activity, and subsequently immunostained with anti-p63 antibodies (H137; Santa Cruz Biotechnology).



Supplementary Figure S4. C38C40-Luc and p63LRE-Luc luciferase activity were tested in mouse keratinocytes transfected with p63 siRNA. Data are expressed relative to luciferase activity in keratinocytes transfected with control siRNA (ctr). (\*\*  $P \le 0.005$ ; \*\*\*  $P \le 0.0005$ ; n=3). Error bars denote SD.



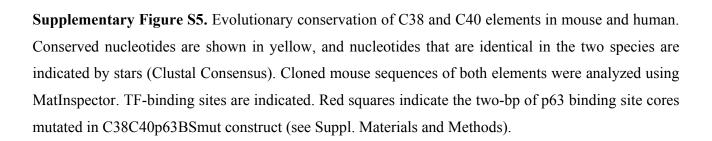
298 1

299

mouse

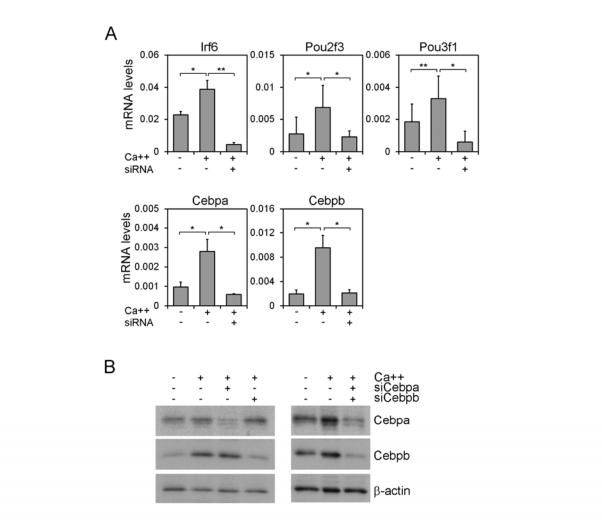
human

Clustal Consensus

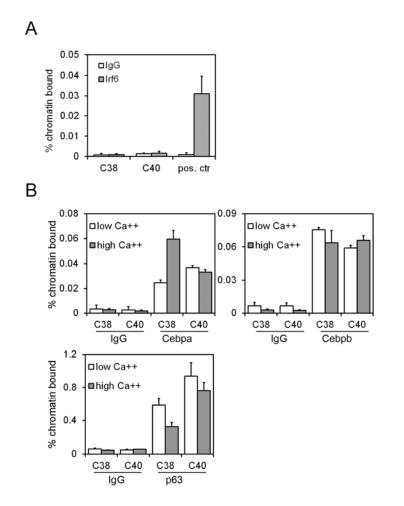


TITTTTTTAAGTTTTGGGAGGAAA

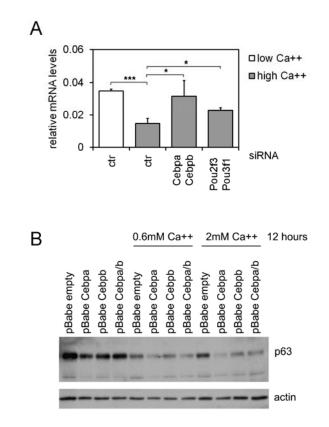
#### C38



**Supplementary Figure S6.** (A) mRNA expression levels of the indicated genes was measured by real time RT-PCR on RNA isolated from proliferating (-) or differentiated (+) keratinocytes treated with calcium (Ca++), and transfected with the siRNA corresponding to the indicated genes or negative control (-). (\*  $P \le 0.05$ ; \*\*  $P \le 0.005$ ; n=4). Error bars denote SD. (B) Immunoblotting of total cell extracts from primary mouse keratinocytes transfected with the indicated siRNAs using antibodies against the indicated proteins. Keratinocytes were cultured in undifferentiated or in undifferentiated conditions (0.6mM Ca<sup>++</sup> for 24 hours).



**Supplementary Figure S7.** (A) ChIP-qPCR was performed on human keratinocytes using rabbit anti-Irf6 antibodies (kindly provided by Dr. Mike Dixon, University of Manchester) (grey bars), or rabbit IgG (white bars) as negative control. Error bars denote SD. (B) ChIP-qPCR was performed on undifferentiating (white bars) and differentiating (grey bars) mouse primary keratinocytes using antibodies specific for Cebpa, Cebpb, p63 or rabbit IgG as negative control. Error bars denote SD.



Supplementary Figure S8. (A) p63 mRNA expression levels in differentiated (grey bars) and proliferating (white bars) keratinocytes upon transfection of the indicated siRNAs. (\*  $P \le 0.05$ ; \*\*\*  $P \le 0.0005$ ; n=3). Error bars denote SD. (B) Immunoblotting of total cell extracts from primary mouse keratinocytes infected with the indicated retroviruses using antibodies against p63 and  $\beta$ -actin proteins. Keratinocytes were cultured in proliferating or in differentiated conditions with 0.6 or 2mM calcium for 12 hours as indicated.

	Matrix				Core	Matrix	Human	Chicken
Element	Family	Matrix	Position	Strand	sim.	sim.	cons.	cons.
C38	V\$OCT1	V\$OCT1.02	80	+	0.75	0.816	Y	
C38	V\$FKHD	V\$HNF3.01	100	-	1	0.971	Y	Y
C38	V\$FKHD	V\$FOXP1_ES.01	114	-	1	0.959		
C38	V\$P53F	V\$P53.07	130	+	0.858	0.779	Y	Y
C38	V\$FKHD	V\$FOXP1_ES.01	148	+	1	0.959	Y	Y
C38	V\$P53F	V\$P53.05	188	+	1	0.745		
C38	V\$FKHD	V\$FOXP1_ES.01	193	-	1	0.981	Y	
C38	V\$OCT1	V\$POU3F3.01	198	-	1	0.849	Y	Y
C38	V\$KLFS	V\$GKLF.02	208	-	0.897	0.916		
C38	V\$P53F	V\$P53.03	210	+	0.859	0.896	Y	
C38	V\$FKHD	V\$FOXP1_ES.01	216	+	1	0.959	Y	Y
C38	V\$BRNF	V\$TST1.01	240	+	0.9	0.888	Y	
C38	V\$KLFS	V\$GKLF.02	251	+	0.862	0.936		
C38	V\$FKHD	V\$XFD3.01	263	-	0.783	0.774	Y	
C38	V\$OCT1	V\$OCT1.04	265	-	1	0.771		
C38	V\$BRNF	V\$TST1.01	269	-	0.9	0.924		
C38	V\$FKHD	V\$FHXB.01	271	-	1	0.872	Y	
C38	V\$OCT1	V\$OCT1.05	272	+	0.85	0.921	Y	
C38	V\$FKHD	V\$HNF3.01	274	-	0.971	0.959	Y	Y
C38	V\$CEBP	V\$CEBPB.01	278	-	1	0.916	Y	Y
C38	V\$OCT1	V\$OCT1.03	309	+	1	0.853		
C38	V\$FKHD	V\$FOXP1 ES.01	314	+	1	0.981		
C38	V\$OCT1	V\$OCT1.02	322	+	0.75	0.828		
C38	V\$KLFS	V\$GKLF.01	326	+	0.78	0.833	Y	
C38	V\$OCT1	V\$POU3F3.01	338	-	0.761	0.859		
C40	V\$OCT1	V\$POU3F3.01	3	+	1	0.821		
C40	V\$P53F	V\$P53.03	24	+	1	0.9	Y	Y
C40	V\$P53F	V\$P53.07	34	+	1	0.853	Y	Y
C40	V\$P53F	V\$P53.03	54	+	0.922	0.872	Y	Y
C40	V\$P53F	V\$P53.02	63	_	0.885	0.894	Ý	Ý
C40	V\$FKHD	V\$HFH1.01	102	_	0.75	0.798		
C40	V\$P53F	V\$P53.03	105	+	0.828	0.912	Y	Y
C40	V\$P53F	V\$P53.03	114	-	0.922	0.975	Ý	Ý
C40	V\$FKHD	V\$FREAC2.01	140	-	1	0.825		
C40	V\$P53F	V\$P53.02	186	+	0.885	0.92	Y	Y
C40	V\$P53F	V\$P53.01	196	+	0.844	0.701	Ý	-
C40	V\$KLFS	V\$BTFB3.01	204	+	1	0.906	•	
C40	V\$CEBP	V\$CEBPA.01	214	+	0.972	0.944	Y	
C40	V\$RBPF	V\$RBPJK.02	215	+	1	0.945	Y	
C40	V\$FKHD	V\$HNF3.01	213	+	0.857	0.931	Y	Y
C40	V\$FKHD	V\$HNF3.01	225	_	1	0.962	Y	•
C40	V\$CEBP	V\$CEBP.02	230	+	0.971	0.898	Y	
C40 C40	V\$CEBF	V\$CEBF.02 V\$TST1.01	230	+	0.971	0.898	Y	Y
C40 C40	V\$FKHD	V\$FOXP2.01	232	+	1	0.995	Y	Y
C40 C40	V\$PKID V\$OCT1	V\$POXF2.01 V\$OCT1.06	233	+	1	0.995	Y	Y
C40 C40	V\$UCT1 V\$IRFF		284	Ŧ	1	0.763	T	T
		V\$IRF7.01 V\$IRF4.01		-	1			
C40		1 -	290	-		0.912		
C40			294	-	0.886	0.94		
C40		V\$GKLF.02	302	-	1	0.931		
C40	V\$IRFF	V\$IRF1.01	305	-	1	0.887		

Supplementary Table S1. Predicted transcription factor binding sites using MatInspector

Note. Sim: similarity; cons.: conservation

### SUPPLEMENTARY MATERIAL AND METHODS

### **Retroviral preparation and infection.**

High titer retrovirus production was obtained in HEK-293T cells by transient transfection of the pBabepuro, pBabe-Cebpa and pBabe-Cebpb constructs with pEco vector using Lipofectamine 2000 as previously described (Antonini et al. 2006). Primary keratinocytes were infected twice with the retrovirus 24 and 48 h after plating in the presence of 8  $\mu$ g/ml polybrene. Cells were cultured for 4 additional days in the presence of 2 $\mu$ g/ml puromycin.

### **Immunostaining for p63**

For immunohistochemistry, 7-µm thick sections were deparaffinized and stained with the Vectastain kit according to the manufacturer's instructions (Vector Laboratories) using the p63 (H137; Santa Cruz Biotechnology) primary antibodies.

## Recombineering

Miniarms were amplified by PCR from the BAC RP23-239F8 containing mouse *p63* genomic region using the following oligonucleotides containing NotI and XbaI (region 1 at the 5' of C38; 540bp), XbaI and SpeI (region 2 at the 3' of C40; 440bp), KpnI and SacI (region1 $\Delta$ C38 at the 3' of C38; 530bp) and SacI and NheI (region2 $\Delta$ C40 at the 5' of C40; 510bp): region1 Forward CATAAGCGGCCGCGCACACTGCTTGAATCTCTCTCTC; region1 Reverse GTCATCTCTAGACCAGGTGTGGGTCTAACTTAGGTGTTGG; region2 Forward GTCATCTCTAGACCACGTCTCTGATTCTAGCTGATG; region1 $\Delta$ C38 Forward CATAAGGTACCGTCTGGAATGTCCTTCTTGCCACT; region1 $\Delta$ C38 Reverse GTCAAGAGGTCCAGGCTTGCAAGATGGAGGCTTAGT; region2 $\Delta$ C40 Forward GTCAAGAGGCTCAGGCTGAGGTAGGTGTCTCCTCATGC; region2 $\Delta$ C40 Reverse GTCTGAAGCTAGCACCTGAGGCTGAGGCTGACTATGC; region2 $\Delta$ C40 Reverse GTCTGAGCTAGCACCTGAGGCTGGCTCACTATAACT Miniarms were cloned in the  $\beta$ -globin-lacZ vector p1229 or in pGL3 basic Luc (Promega). After cloning the vector was linearized and was electroporated together with BAC RP23-239F8 in the modified DH10B

bacterial strain SW102 using a Biorad GenePulser. Prior electroporation, SW102 were grown at 32°C

and induced to express RED recombination proteins at 42°C for 15', as previously described (Liu et al. 2003).

# Cloning C38 and C40 elements

The following sequence of mouse C38 element was clone in TK-pGL3-luc (Ohno et al. 1999) in SacI/NheI:

The following sequence of mouse C40 element was clone in TK-pGL3-luc (Ohno et al. 1999) in SmaI: GTGCGTTGCATATAAAGCAGAGTCTGAAAGGCAGGGAGACATGACGCTGCTTGTCAGGTAT GAGAGAGACAAGACCAGAGGCGCCGGGGAAGCTTGACTACCGTGGAGTGTTCAGTTGAGA CTTGTCTCTGCCCCATGGCCTGCAGCGTTTACGTAGAAATTGGGGAAGCTTTTACCTGTTCC AAAGCCTTACCTGATCAGACTTGCCCTGGACGGAGTTTGGGAAAAAAGTGTTTGAAGTAA ACAGGAAAATTACTCACTGAGGCGCTGTGCTTTACTGGCTCTGGCAAAGCTTTGATTTCTT TTCCCCCCTTTTCAGTTTTGGGACAAGAGACT

# Oligonucleotide primers for Real Time RT-PCR on mouse samples.

β-actin CTAAGGCCAACCGTGAAAAGAT GCCTGGATGGCTACGTACATG p63 CATGAGCTGAGCCGTGAGTTC GGCTGTTCCCTTCTACTCGAA Irf6 CAGCTCTCTCCCCATGACTGA CCCATACTCCTTCCCACGATAC Cebpa GCGAGCACGAGACGTCTATAGA GCCAGGAACTCGTCGTTGAA Cebpb ACAAGGTGCTGGAGCTGAC CTGCTCCACCTTCTTCTGC Pou3f1 TGGGCACCCTCTACGGTAAC GGCCTCGAAACGGCAGAT Pou2f3 CCTGAGCCAAGGACCTACCA GAAGCCATGTCCCCAGACA

## Oligonucleotide primers for ChIP analysis on mouse genomic DNA

-20kb from p63 P1 promoter ATAAGAAAGAGAGCAGGGCATGA TGCTTGGTCAAATTAGGATCCA p63 P1 promoter GGGCTCTAAAACTGTGGCAGA CTGGGCACCCCTGTAAAG p63 intron 1 TGCTGCCGAAGAGAGCATTTA AGCATTGATAACCACTCCAAGGA p63 P2 promoter AGCCCAGGTGGAAGTTGATG GGGCGGGACTCTTCACTTTAC C38 ACATAGCTTGCAGGAGAACATCTG TCTTGGCCCCATCCCATAC C40 TGTTCCAAAGCCTTACCTGATCA TTTTCCCAAACTCCGTCCAG

### Oligonucleotide primers for ChIP analysis on human genomic DNA

C38 CAACAAACCCTTATTCTGCATGAG CATGTTTGAACAGGCACTAACACA C40 CGTTCCAAAGCCTAACCTGATCA TTTTCCCAAACTCCAACCTG Irf6 positive control GACGCGCTCTTGCACAGA TTGGAATCGGGAGATTTTTCC

## Oligonucleotide primers for site-directed mutagenesis (mutant bps are underlined)

C38p63BS\_1 AGGCAAGACATAGC<u>CC</u>GCAGGAGAACATCT C40p63BS\_1 GAGACATGACGCTGC<u>CC</u>GTCAGGTATGAGAG C40p63BS\_2 GGTATGAGAGAGAGAC<u>CC</u>GACCAGAGGCGCCG C40p63BS\_3 TGTTCAGTTGAGAC<u>CC</u>GTCTCTGCCCCATG

## siRNA sequences

p63 UCACAACAGUCCUGUACAAUUUCAU (Stealth RNAi, Invitrogen) Cebpa CCUGAGAGCUCCUUGGUCAUU (siRNA, Qiagen) Cebpb GAAAAGAGGCGUAUGUAUAUU (siRNA, Qiagen) Pou2f3 GGAAAUGAUCGAAAUGGCCUAGAUU (Stealth RNAi, Invitrogen) Pou3f1 GAGAGCCACUUUCUCAAGUGUCCA (Stealth RNAi, Invitrogen)

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