

# Divergent roles of HDAC1 and HDAC2 in the regulation of epidermal development and tumorigenesis

Winter M. *et al.*, The EMBO Journal (2013) 32, 3176–3191

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# Histone modifications

## **Histone acetylation by histone acetyltransferases (HATs)**

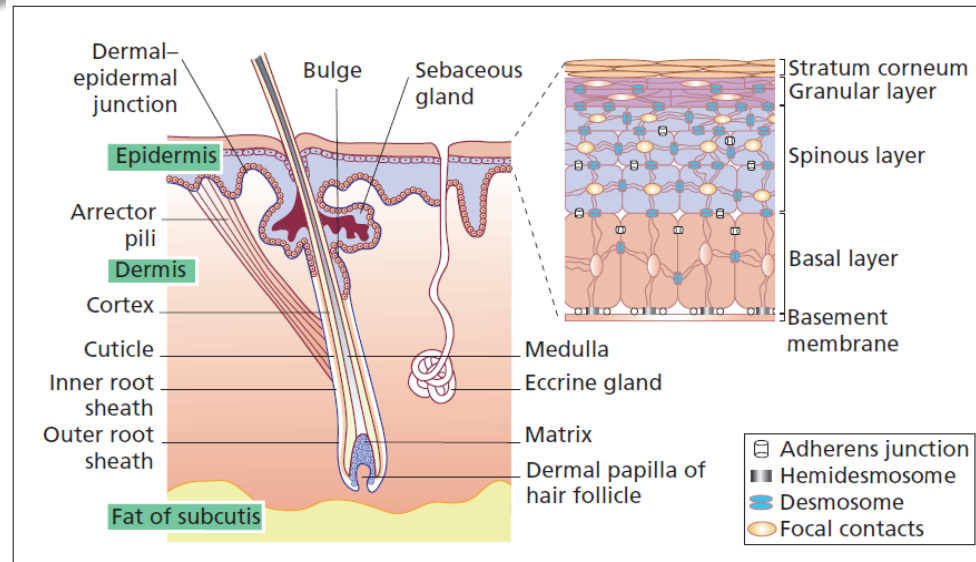
- Opening of local chromatin structures
- Transcriptional activation

## **Histon deacetylation by histone deacetyltransferases (HDACs)**

- Repression
- HDAC1 and HDAC2: components of the Sin3, NuRD, CoREST and NODE co-repressor complexes

➔ Potential regulatory functions of HDAC1 and HDAC2 in epidermal development?

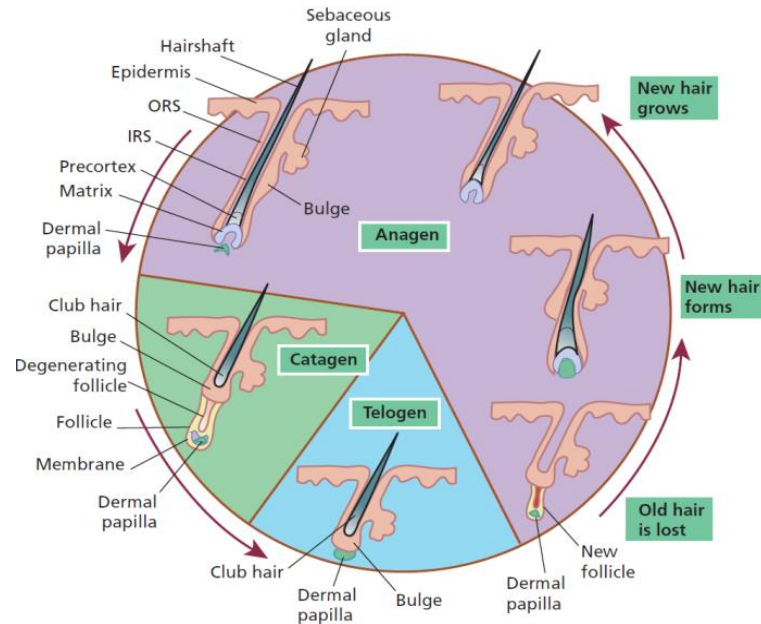
# Skin



Burns *et al.*, 2004

- physical barrier against the environment
- differentiation of multipotent stem cells (SCs) into
  - Interfollicular epidermis (IFE) lineage
  - Sebaceous gland (SG) lineage
  - Hair follicle (HF) lineage

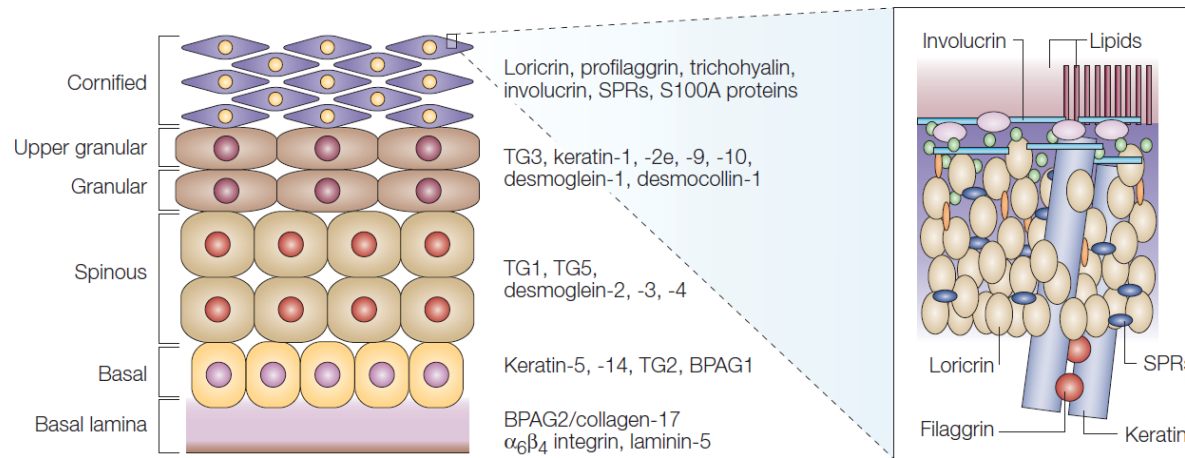
# Hair cycle



(Burns *et al.*, 2004)

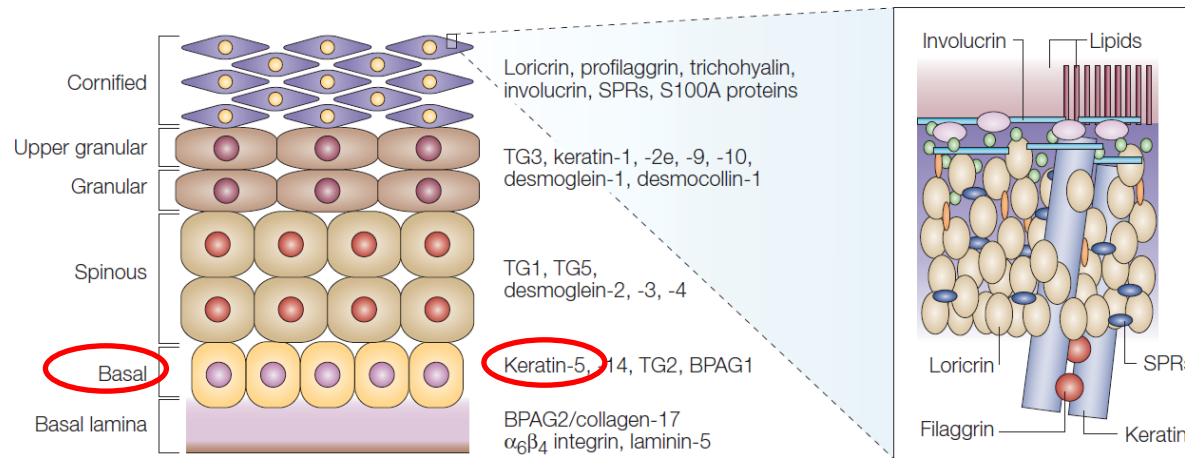
- **Anagen:** hair growth
- **Catagen:** hair regression
- **Telogen:** resting phase

# Keratinocyte differentiation



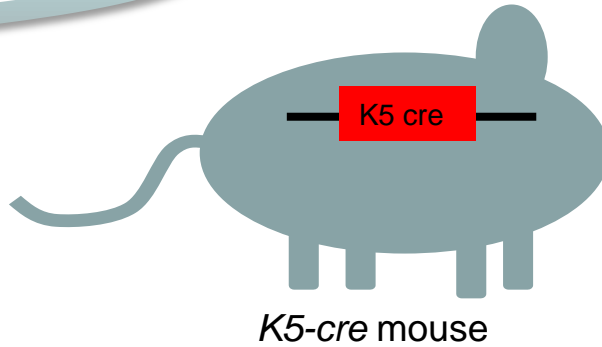
Candi *et al.*, 2005

# Keratinocyte differentiation

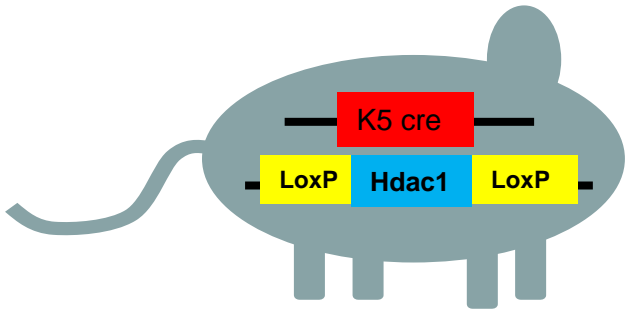
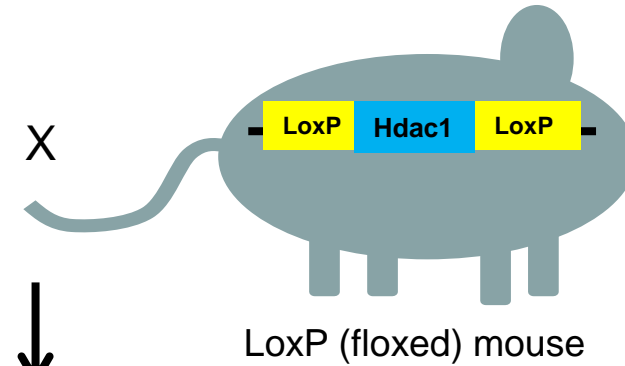


Candi *et al.*, 2005

# Tissue specific knock out (epidermis)



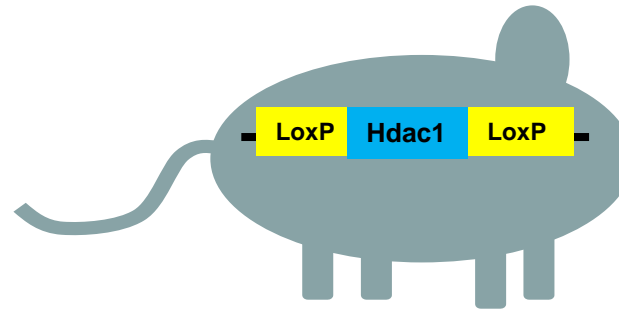
X



active *K5 -Cre* → gene deletion of *Hdac1*

= *Hdac1<sup>f/f</sup> K5-Cre mouse*

= *Hdac1<sup>Δ/Δep</sup>*



no active *K5 -Cre*

→ original gene function of *Hdac1*

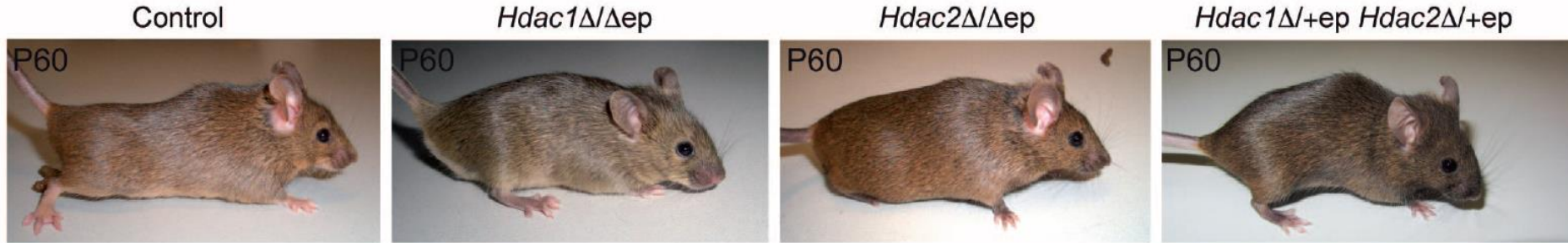
= *Hdac1<sup>f/f</sup>*

# Results

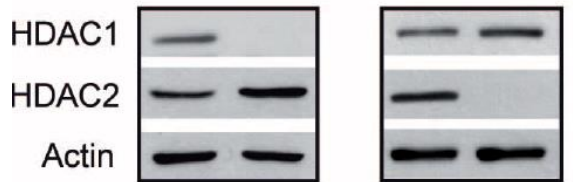
## Epidermal development



# Single knock out of HDAC1 and HDAC2

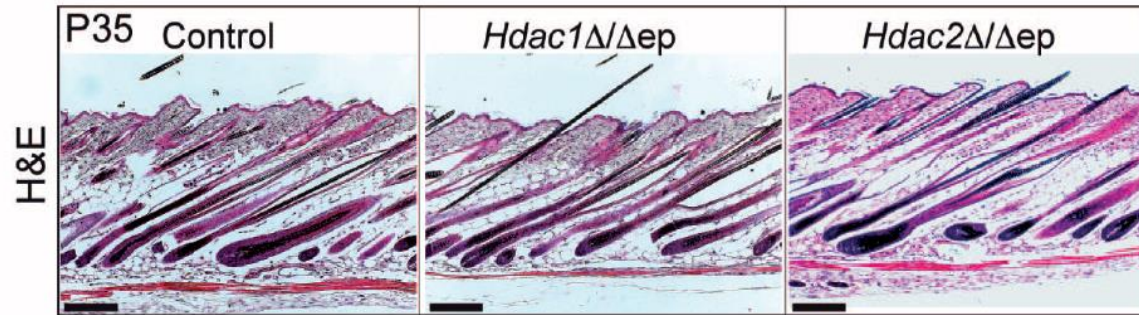
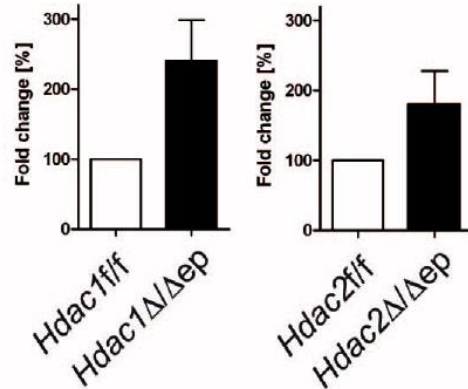


**Protein**



HDAC2 / Actin

HDAC1 / Actin

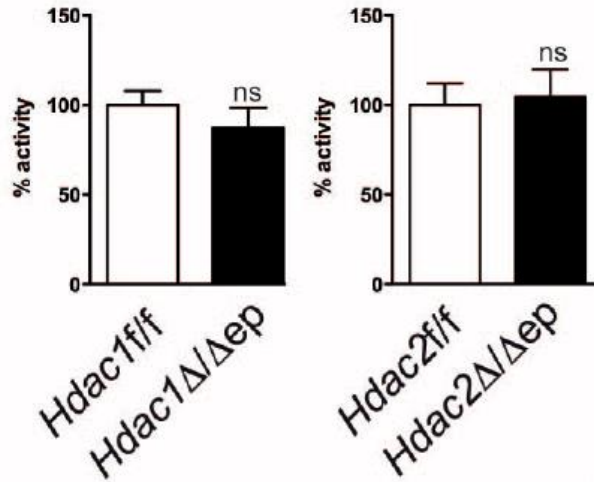


→ Normal epidermal development in the absence of either HDAC1 or HDAC2

# Double knock out of HDAC1 and HDAC2

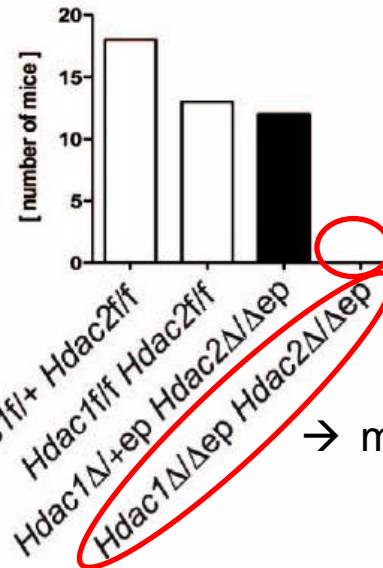
**K**

**total HDAC activity**



**L**

**Distribution of  
genotypes**



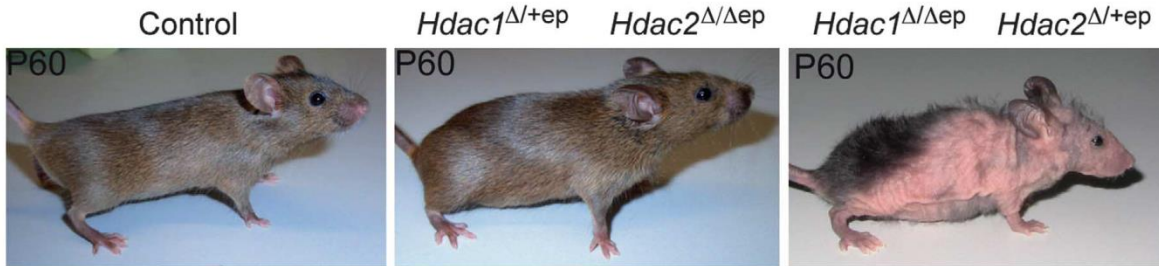
→ mice were not viable

→ No altered  
HDAC activity

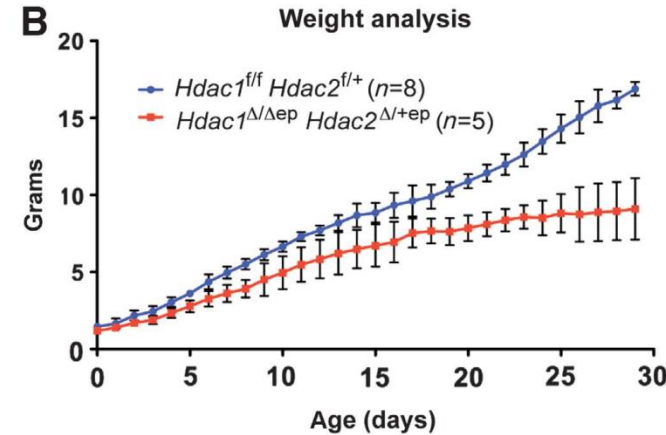
→ Indispensable role of HDAC1 and HDAC2 for  
epidermal development

# Developmental abnormalities in *Hdac1 $\Delta/\Delta$ <sup>ep</sup> Hdac2 $\Delta/+$ <sup>ep</sup>*

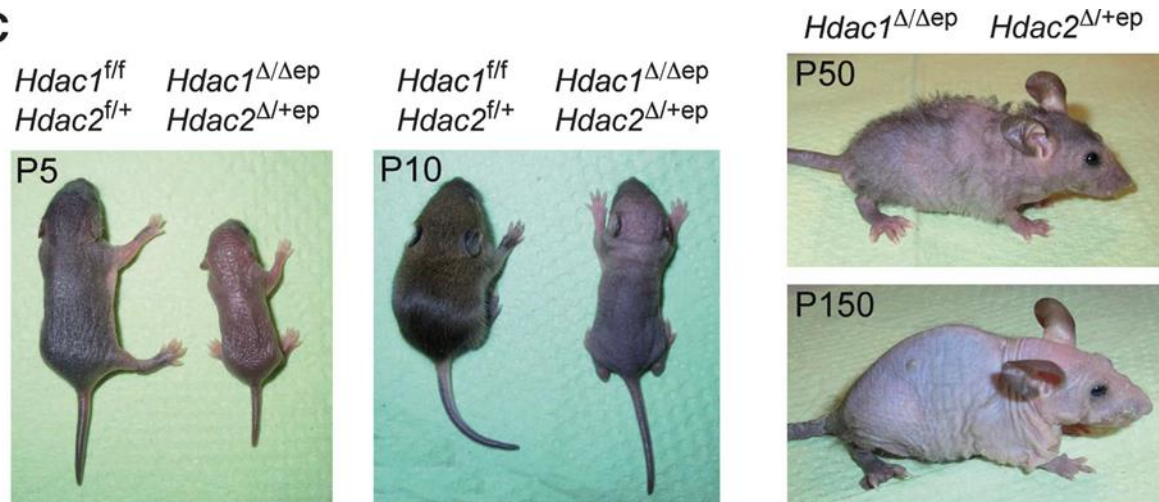
**A**



**B**

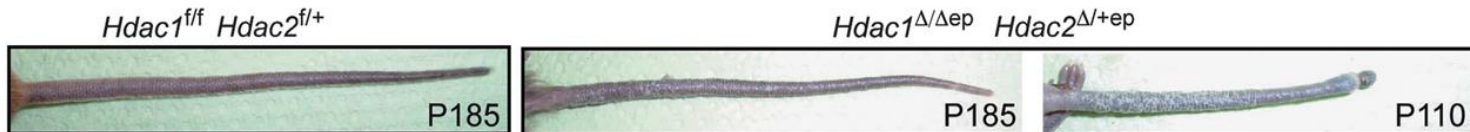


**C**

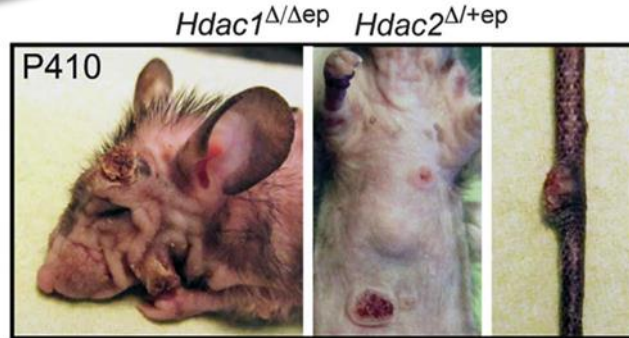


- Progressive alopecia
- Smaller after birth
- Reduced body weight
- Scaly tail regions

**E**



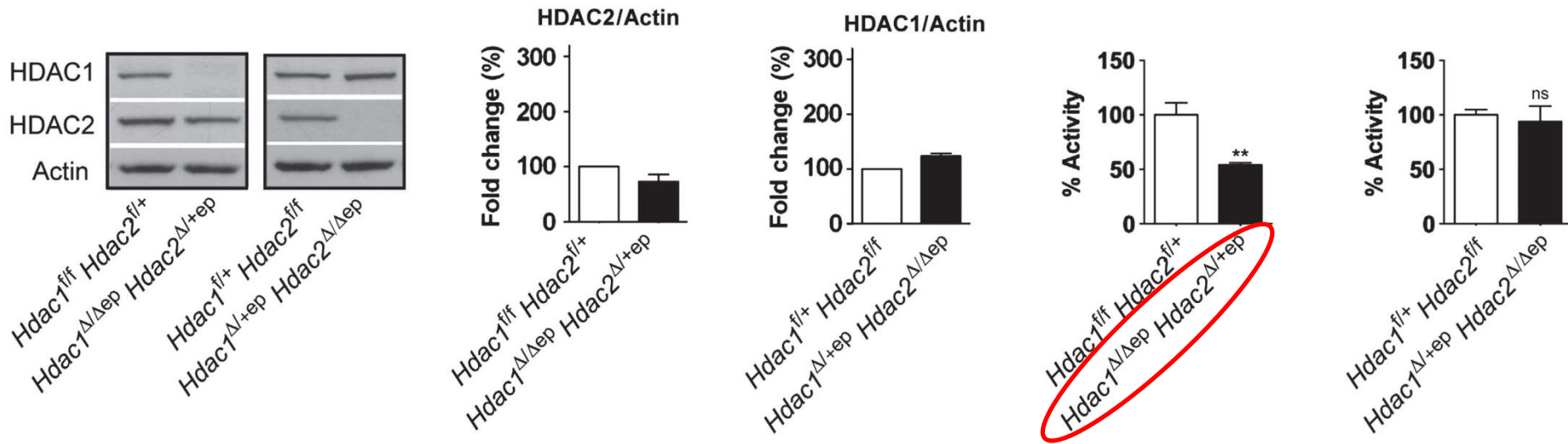
# Severe phenotype of *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>



→ Papilloma like lesions

**F Protein quantification**

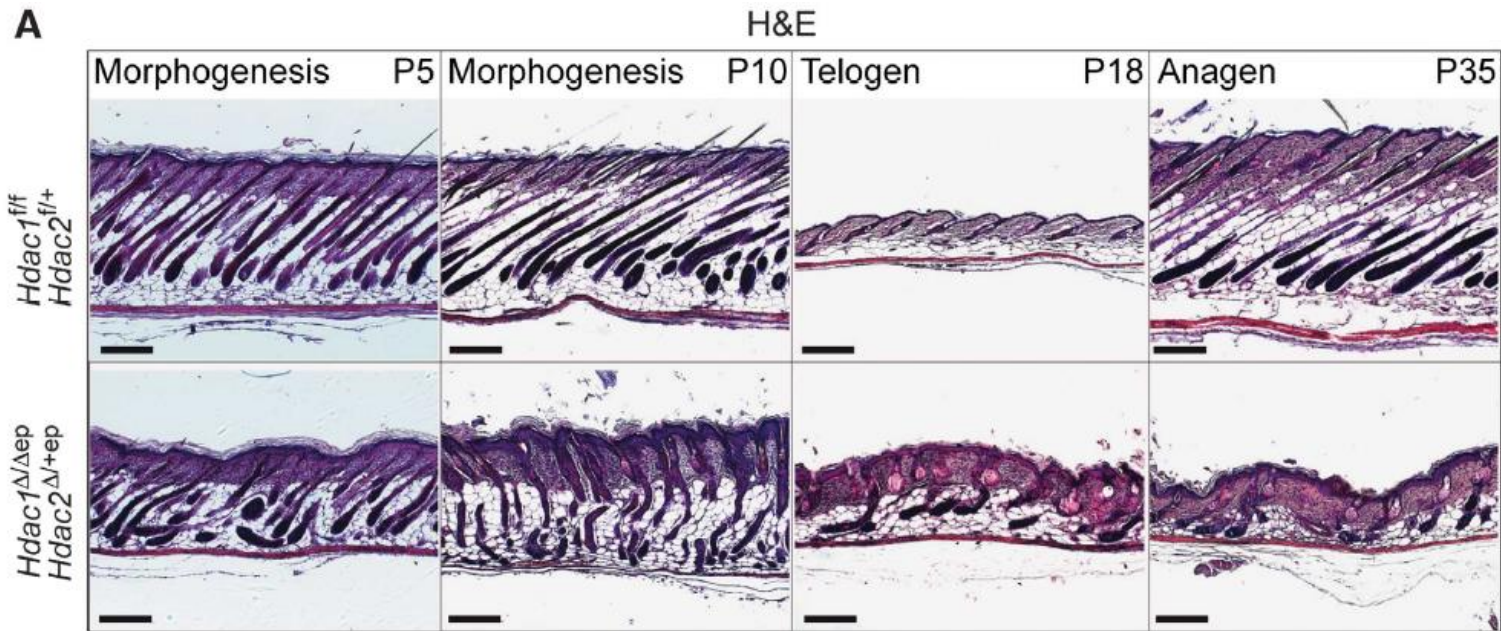
**G Total HDAC activity**



→ Single *Hdac1* allele can compensate for HDAC2 deficiency  
but not the other way around

# Disturbed hair follicle development

*Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>



**Mutant hair follicles:** → mostly shorter and disordered

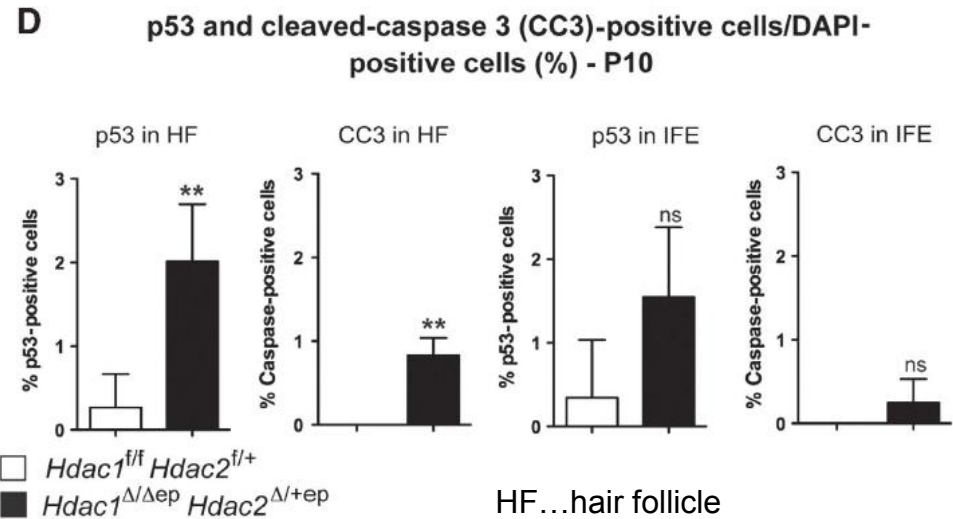
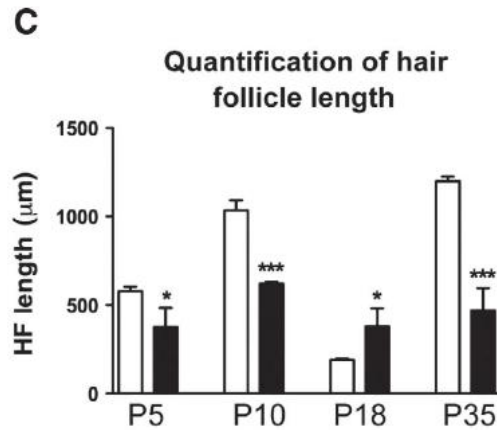
→ failed to enter the telogen phase in a synchronized manner

→ became atrophied

→ failed to enter the anagen phase

# Disturbed hair follicle development

*Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>



HF...hair follicle

IFE...interfollicular epidermis

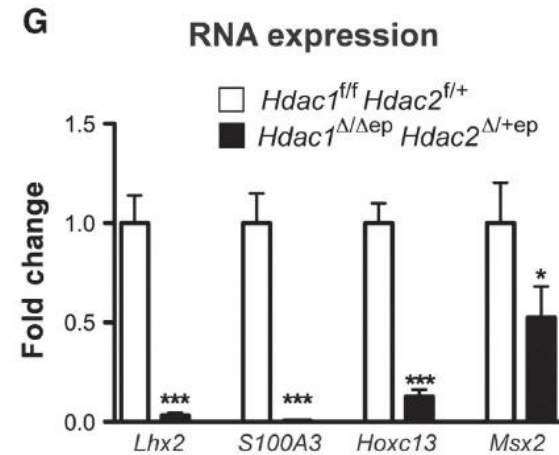
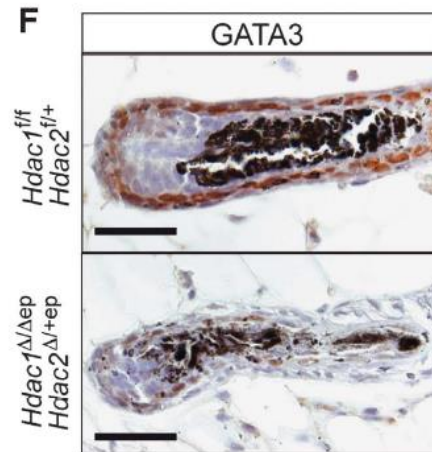
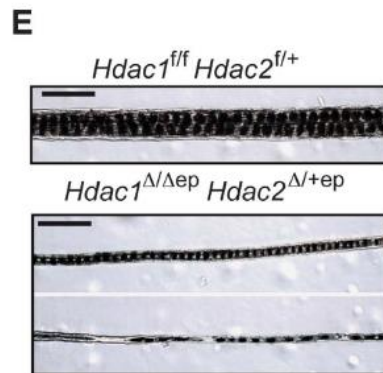
*Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> HF

→ Increased p53 expression and apoptosis (cleaved caspase-3)

# Disturbed hair follicle development

*Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>

TF GATA3: epidermal lineage determination and  
differentiation of the inner root sheath

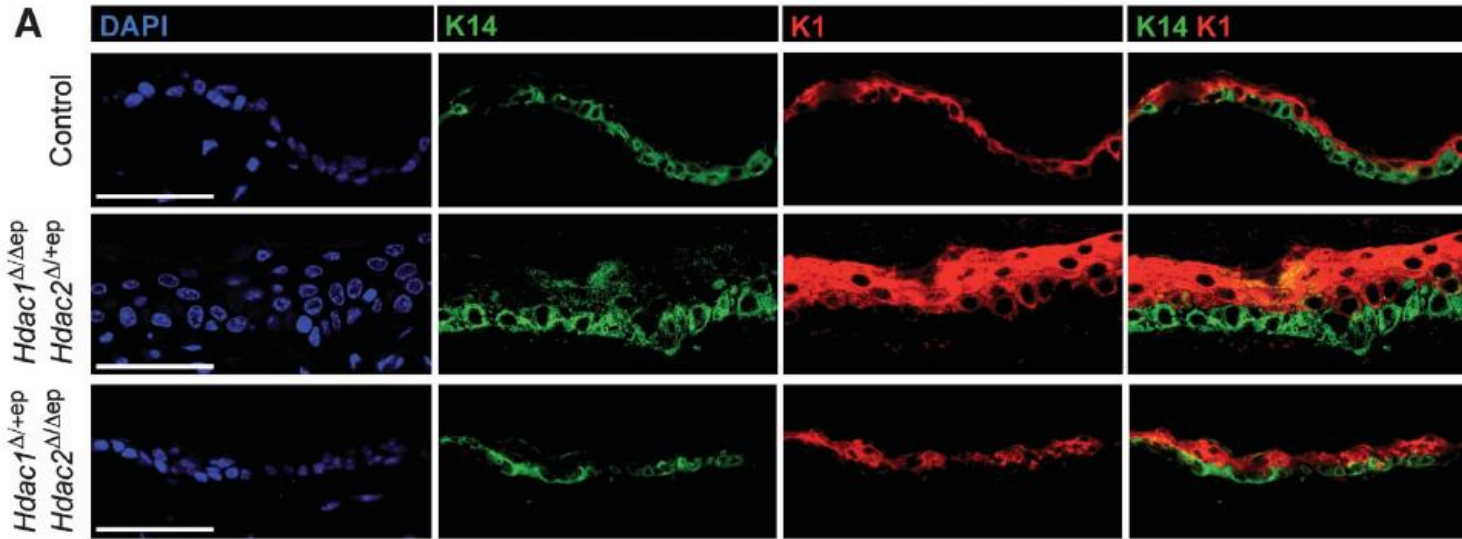


*Lhx2*, *S100A3*, *Hoxc13*, *Msx2* genes important for hair development

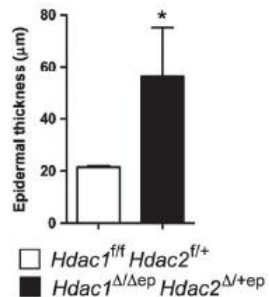
→ Reduced in *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>

# Hyperkeratosis in *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> mice

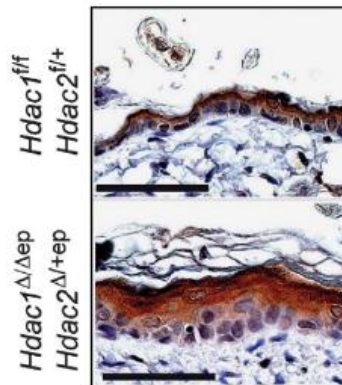
back skin



**B** Quantification of epidermal thickness



**D** Involucrin



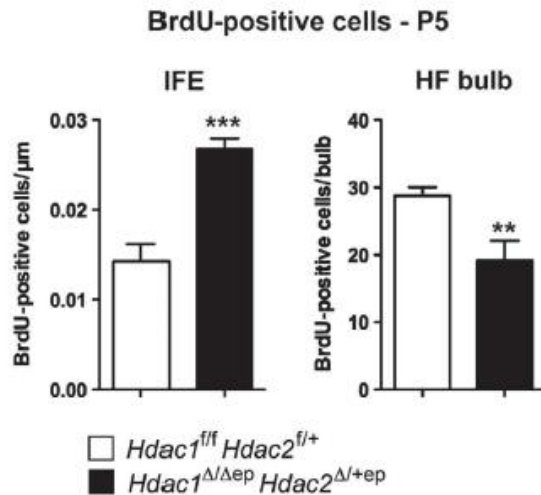
→ thickening of the epidermis



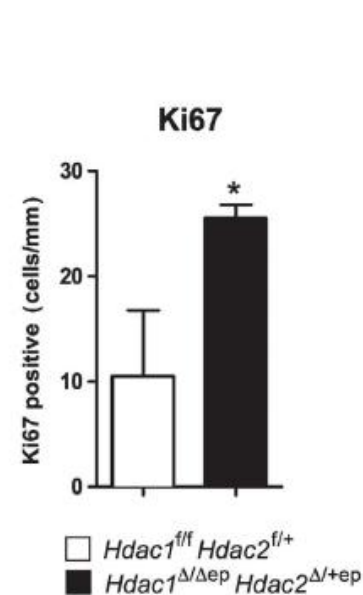
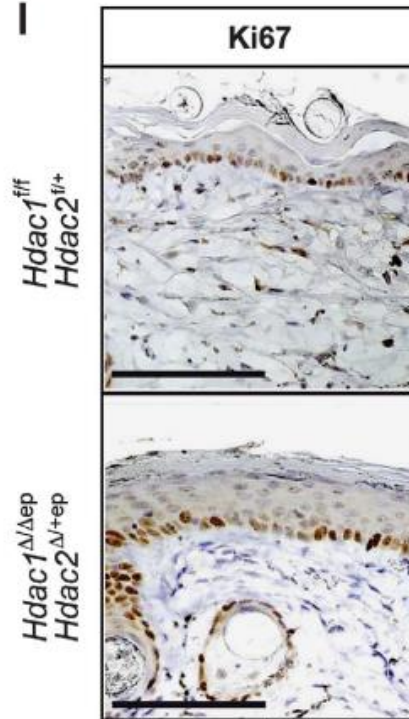
# Hyperkeratosis in *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> mice

## Quantification of proliferating cells

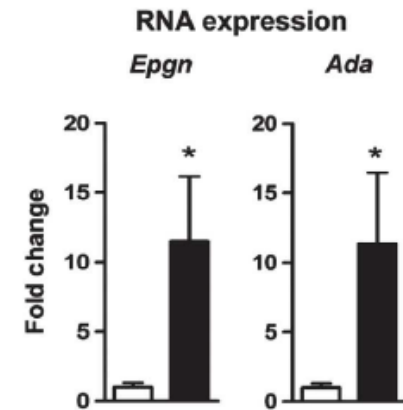
**H**



**I**



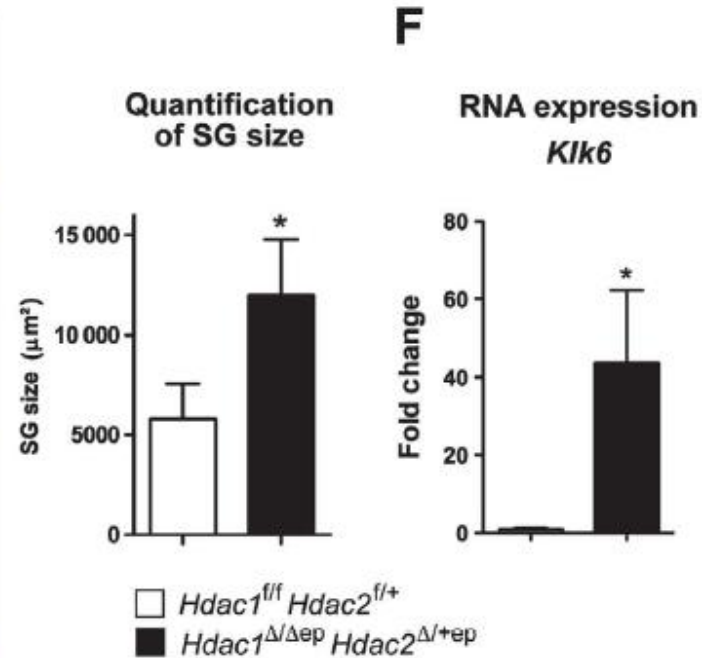
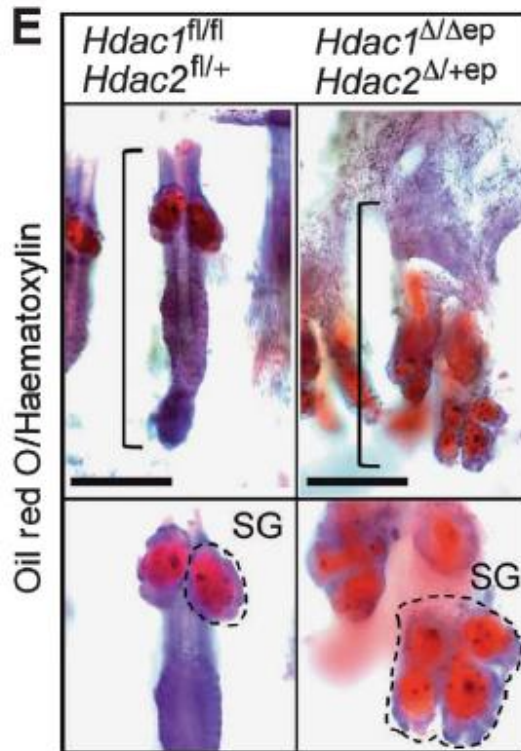
**G**



*Epgn* and *Ada*... genes crucial for epithelial morphogenesis and proliferation

→ Hyperproliferation of the IFE in *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> mice

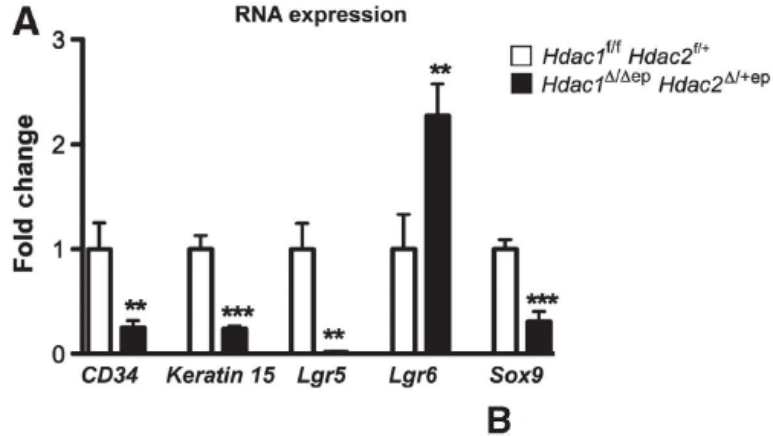
# Enlarged sebaceous gland in *Hdac1<sup>Δ/Δep</sup> Hdac2<sup>Δ/+ep</sup>* mice



Klk6...serine protease predominatly expressed in SGs

# Changes in lineage determination

## *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> epidermis



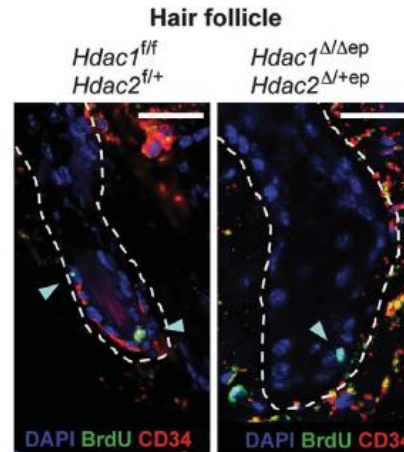
→ Downregulation of SC markers in the HF bulge (*CD34*, *Keratin 15*) and hair sheath (*Lgr5* and *Sox9*)

→ Upregulation *Lgr6* (SC marker for SG and IFE growth)

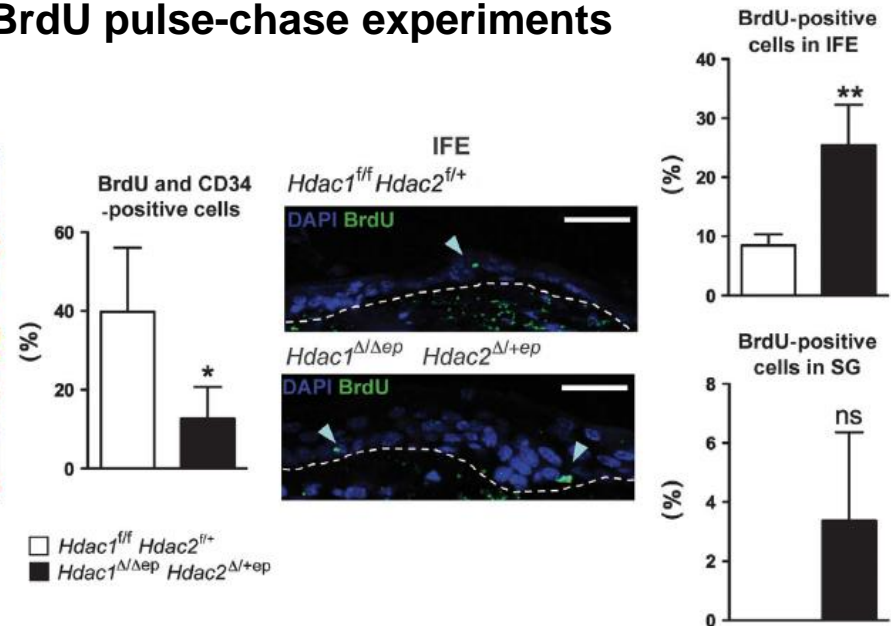
→ Reduction of BrdU+/ CD34+ in HF

→ Increase of BrdU+ cells in the IFE

**B**



### BrdU pulse-chase experiments

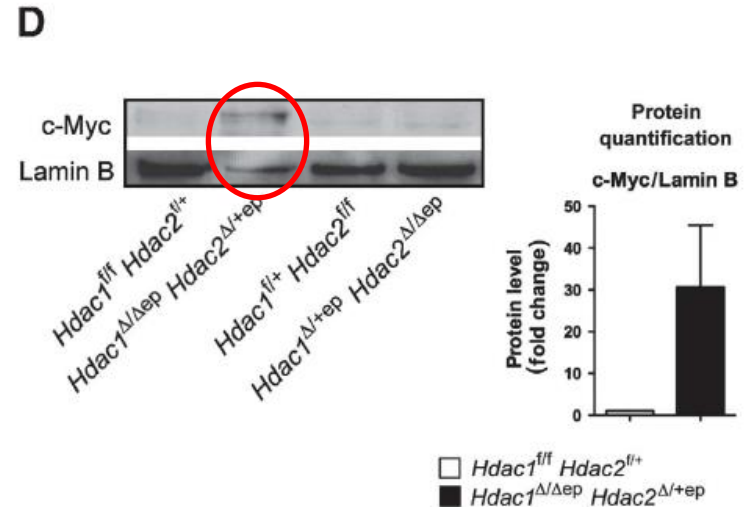
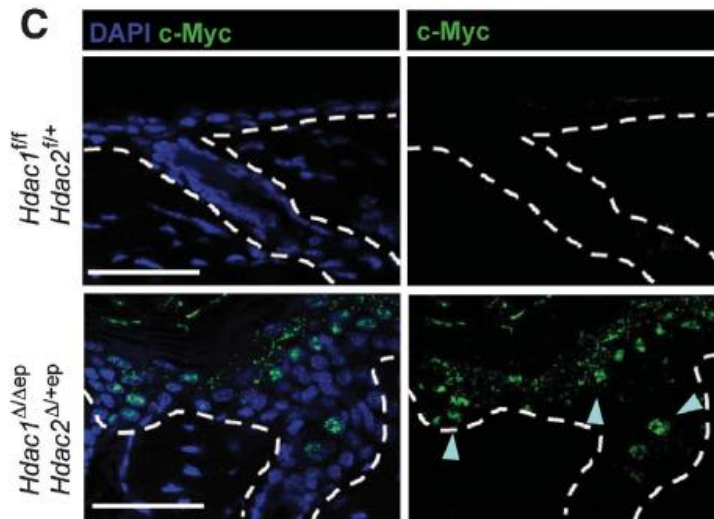


# c-Myc activation in *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> epidermis

c-Myc overexpressing mice:

Epidermal hyperproliferation along the SG and IFE lineages  
at the expense of HF differentiation

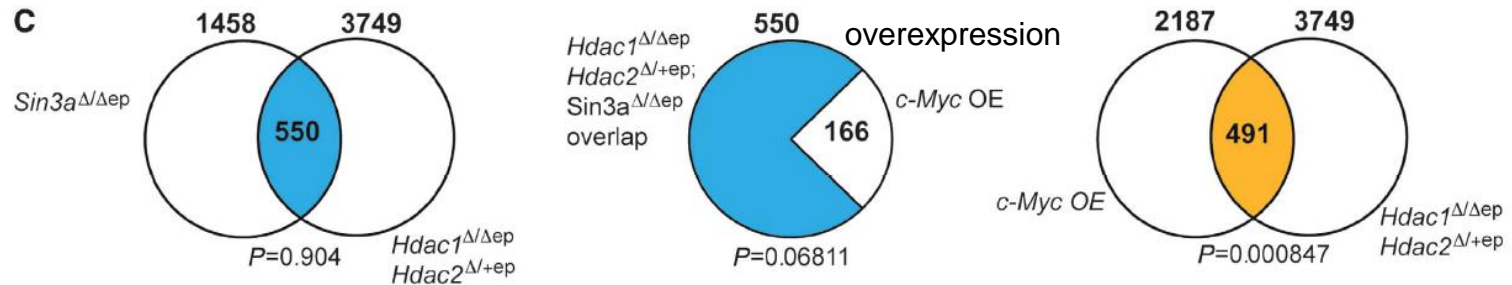
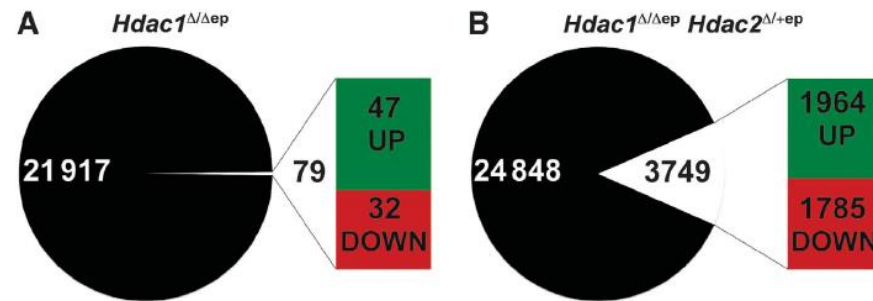
back skin



# Gene expression changes in

## *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup> epidermis

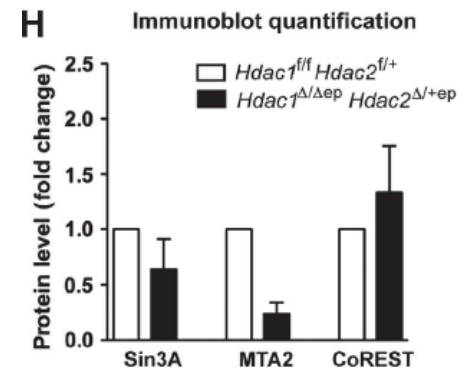
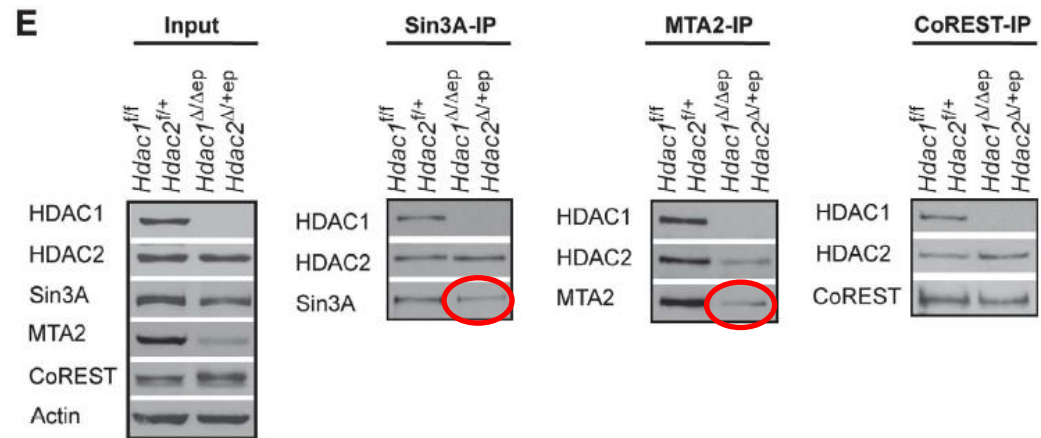
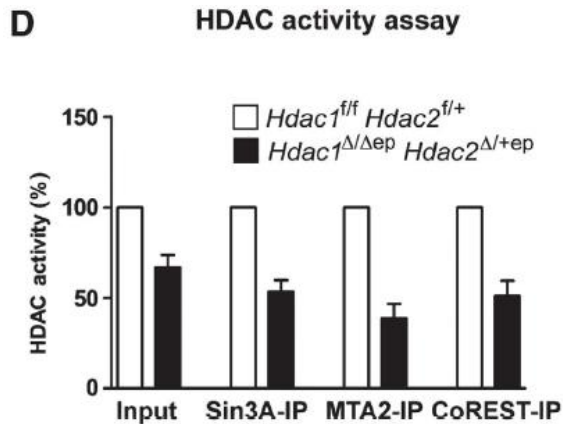
Global gene  
expression profiling



*Sin3a*<sup>Δ/Δep</sup> displayed *c-Myc* upregulation similar to the phenotype of *Hdac1*<sup>Δ/Δep</sup> *Hdac2*<sup>Δ/+ep</sup>

# Alteration in repressor complex function

*Hdac1 $\Delta/\Delta$ <sup>ep</sup> Hdac2 $\Delta/+$ <sup>ep</sup>*



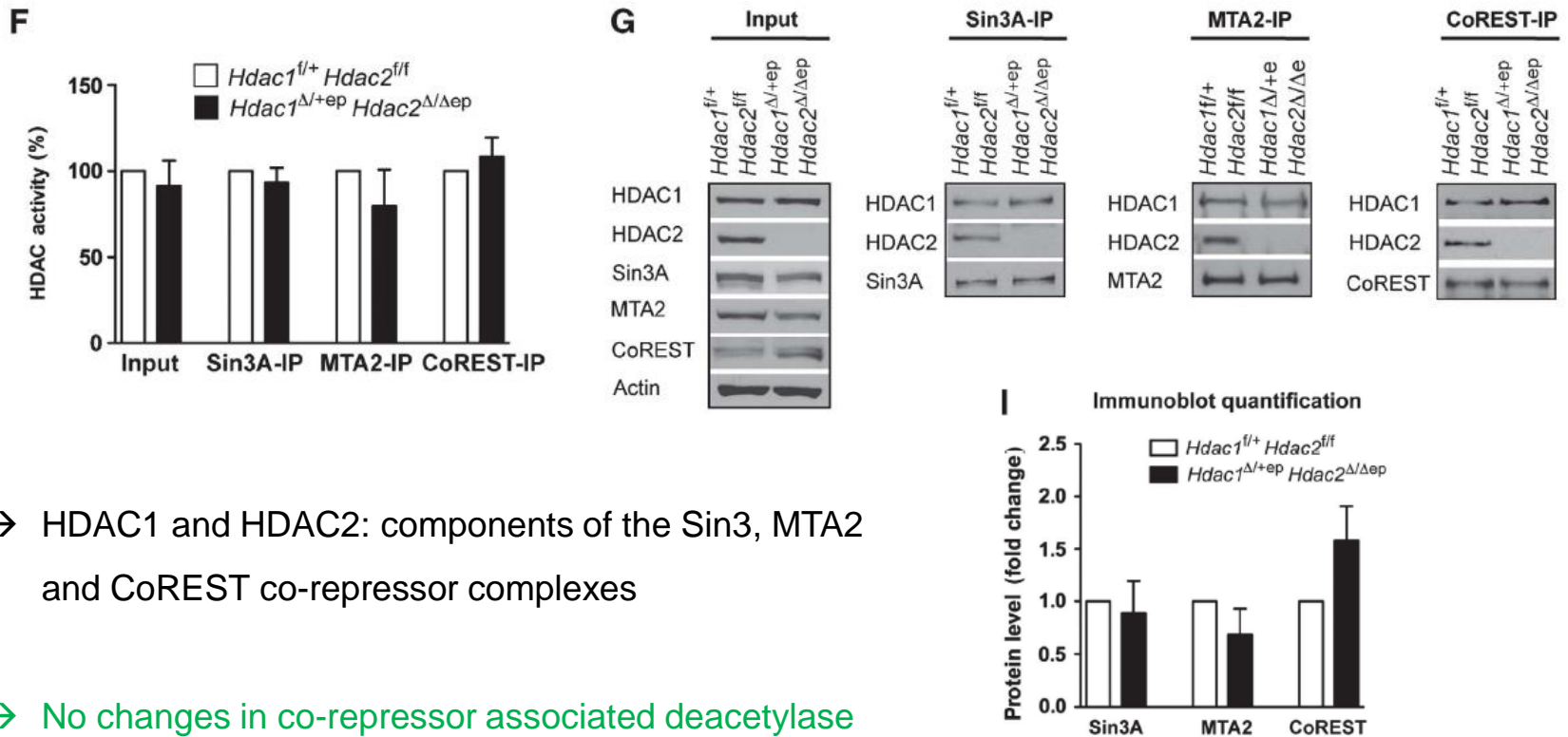
→ HDAC1 and HDAC2: components of the Sin3, MTA2 and CoREST co-repressor complexes

→ Reduced deacetylase activities

→ Reduced protein levels of Sin3A and MTA2

# Repressor complex function in

*Hdac1*<sup>Δ/+ep</sup> *Hdac2*<sup>Δ/Δep</sup> mice



→ HDAC1 and HDAC2: components of the Sin3, MTA2 and CoREST co-repressor complexes

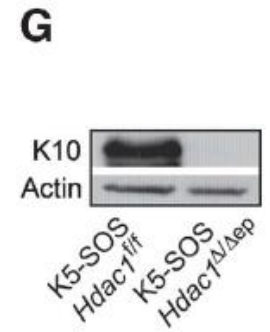
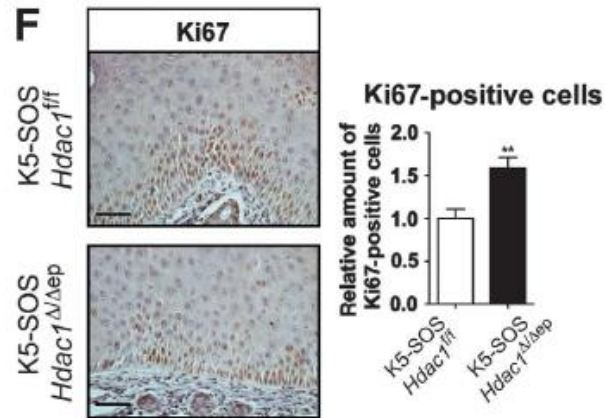
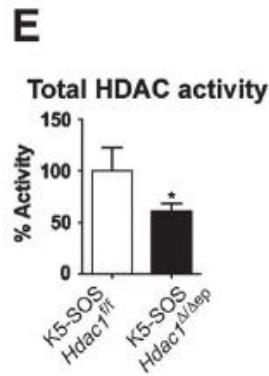
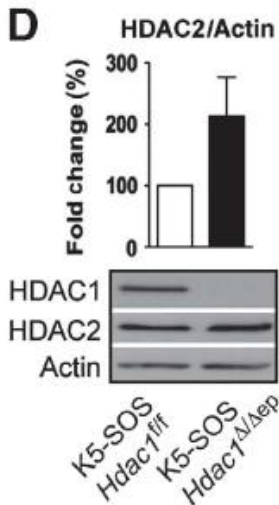
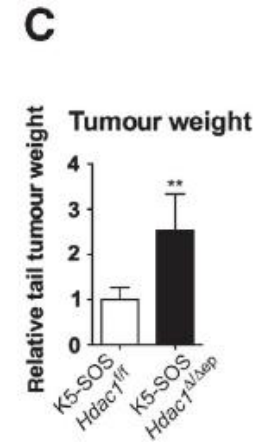
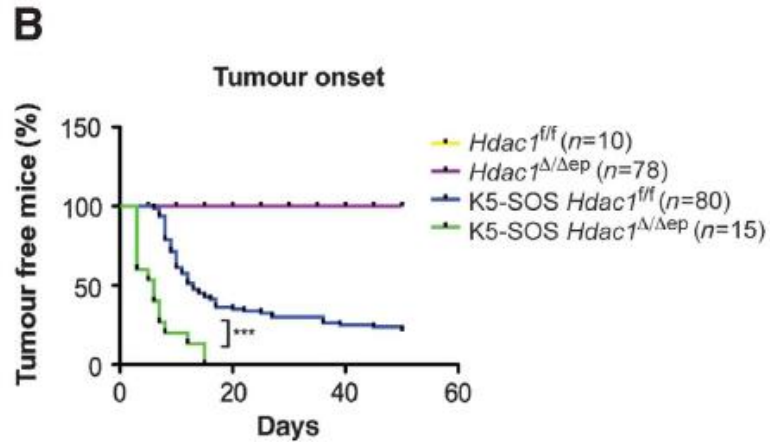
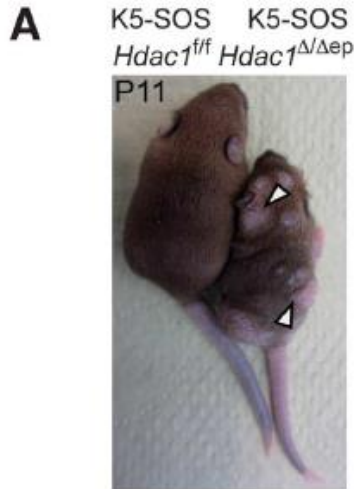
→ No changes in co-repressor associated deacetylase activities

# Results

## Tumour development

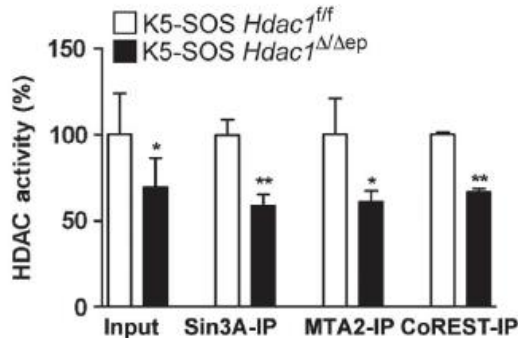


# Tumor development in *K5-SOS Hdac1 $\Delta/\Delta$ ep* mice

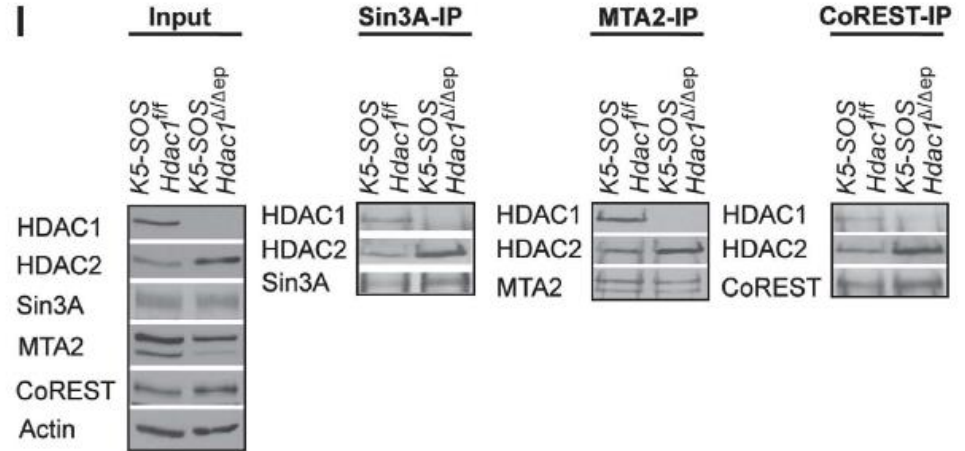


# Tumor development in *K5-SOS Hdac1 $\Delta/\Delta$ ep* mice

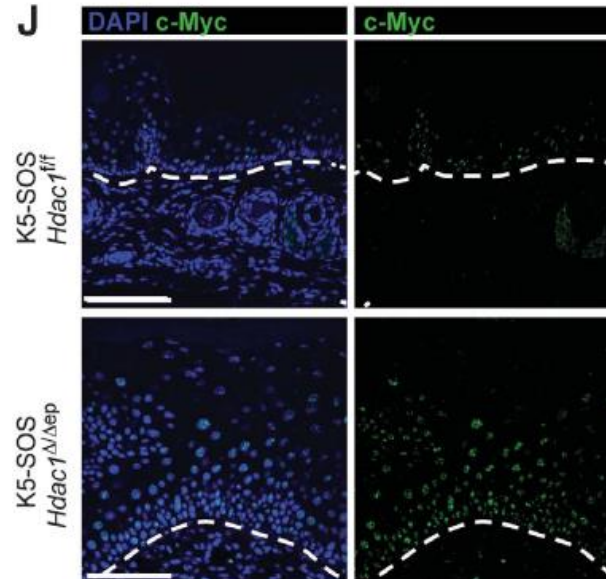
**H**



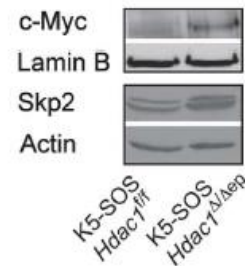
**I**



**J**



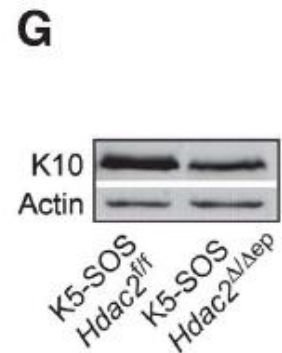
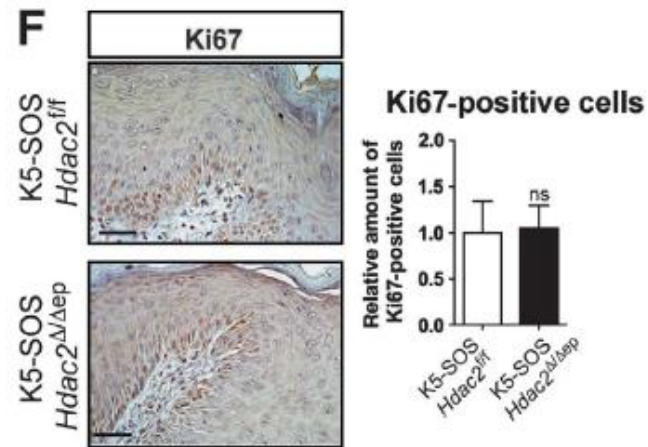
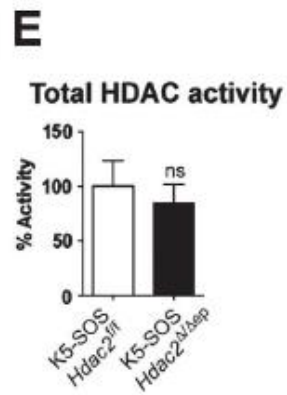
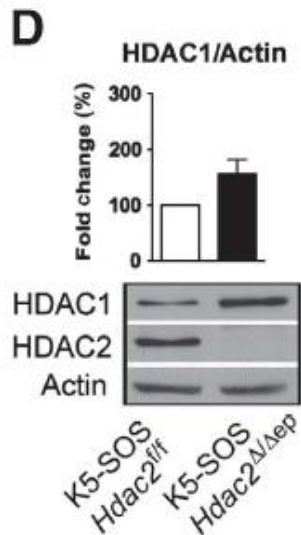
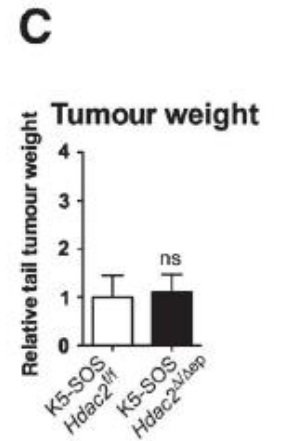
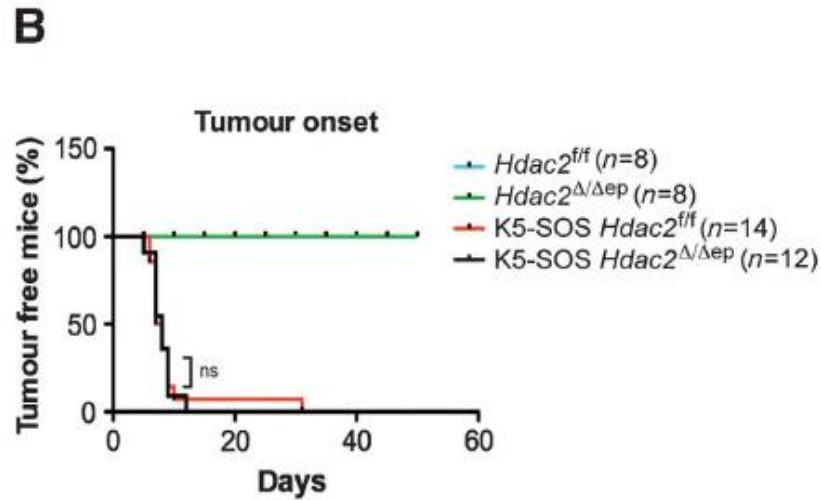
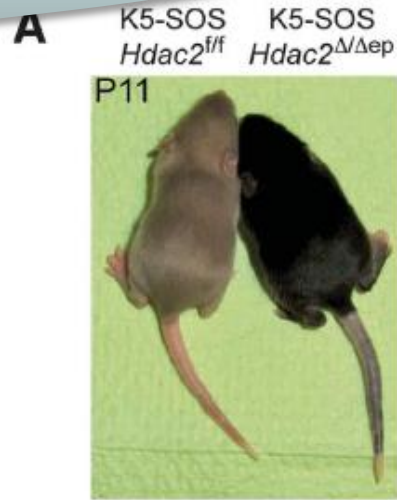
**K**



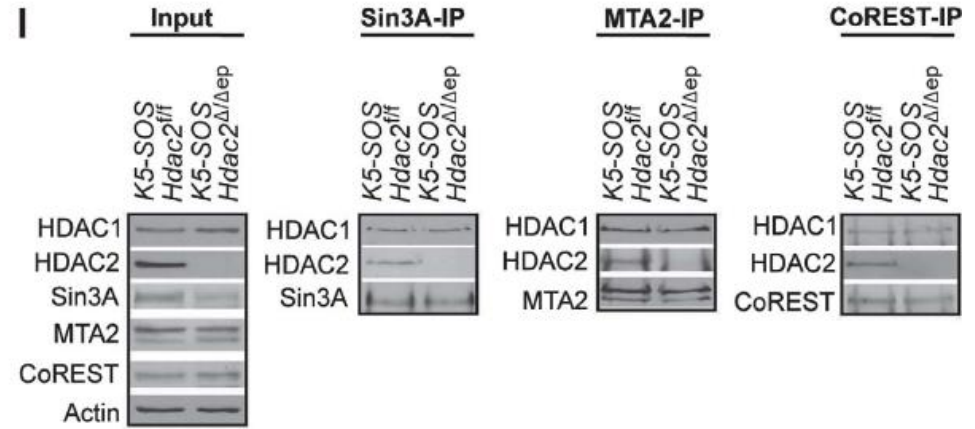
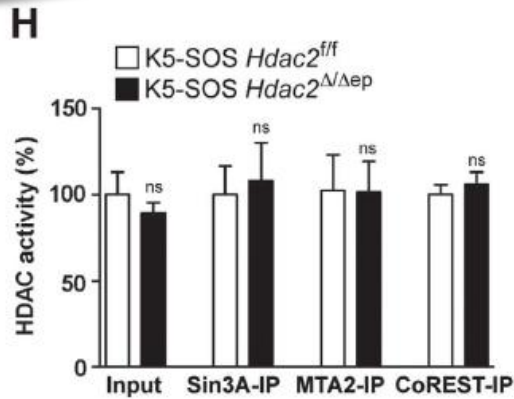
→ Reduced co-repressor associated deacetylase activity

→ Increased levels of c-Myc protein

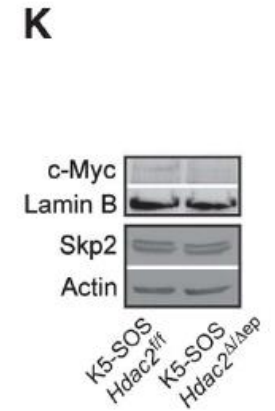
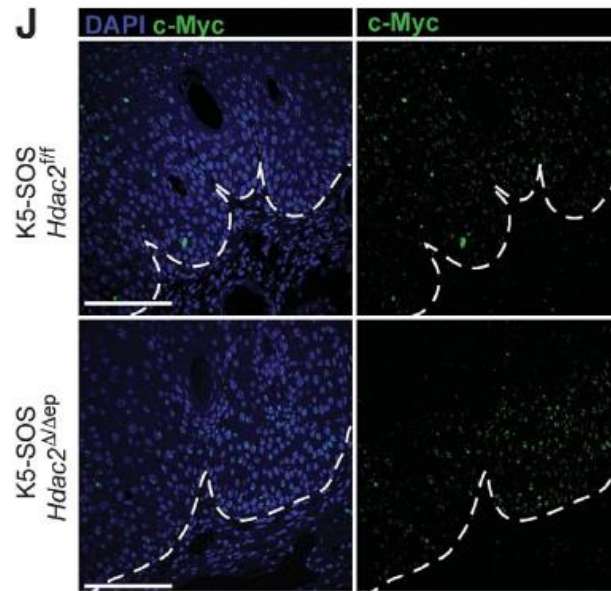
# K5-SOS *Hdac2*<sup>Δ/Δep</sup> mice



# K5-SOS *Hdac2*<sup>Δ/Δep</sup> mice



→ No effects on HDAC activity  
and c-Myc expression



# Discussion

# Divergent roles of HDAC1 and HDAC2

- Single *Hdac1* allele sufficient to maintain proper epidermal development
- But a single *Hdac2* allele displayed a severe developmental phenotype in the epidermis (hyperkeratosis, hair loss and sebaceous gland enlargement)
- HDAC1 play a role in embryonic development (Lagger *et al.*, 2002), in B cells (Reichert *et al.*, 2012) and T cells (Grausenburger *et al.*, 2010; Dovey *et al.*, 2013; Heideman *et al.*, 2013)
- Contrary, single *Hdac2* allele sufficient for normal oocyte (Ma *et al.*, 2012) and brain development (Hagelkruys, Lagger *et al.*, manuscript in revision)

→HDAC1 and HDAC2 specific functions in differentiation and development

# HDAC1 acts as a tumour suppressor in the epidermis

- Under mechanical or oncogenic stress conditions HDAC2 cannot fully compensate for the loss of HDAC1 in the epidermis
- Sin3A and HDAC1 as negative regulators of the proto-oncogene c-Myc
- *Lck-Cre Hdac1<sup>Δ/Δep</sup> Hdac2<sup>Δ/+</sup>* resulted in neoplastic transformation of immature T cells (Dovey *et al.*, 2013)



**Ankersmit  
Laboratory**

for Diagnosis & Regeneration  
in Thoracic Diseases  
& Applied Immunology



**MEDIZINISCHE  
UNIVERSITÄT  
WIEN**