Legends to Supplementary Figures

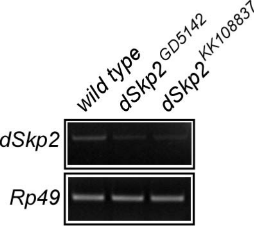
Figure S1. Semi-quantitative RT-PCR showing the knockdown efficiency in two RNAi lines. Salivary glands of the 3rd instar larvae of *wild type*, *dSkp2*^{KK108837} and *dSkp2*^{GD5142} in combination with *Sgs-Gal4*, respectively, were used for total RNA extraction. Rp49 represents the internal control.

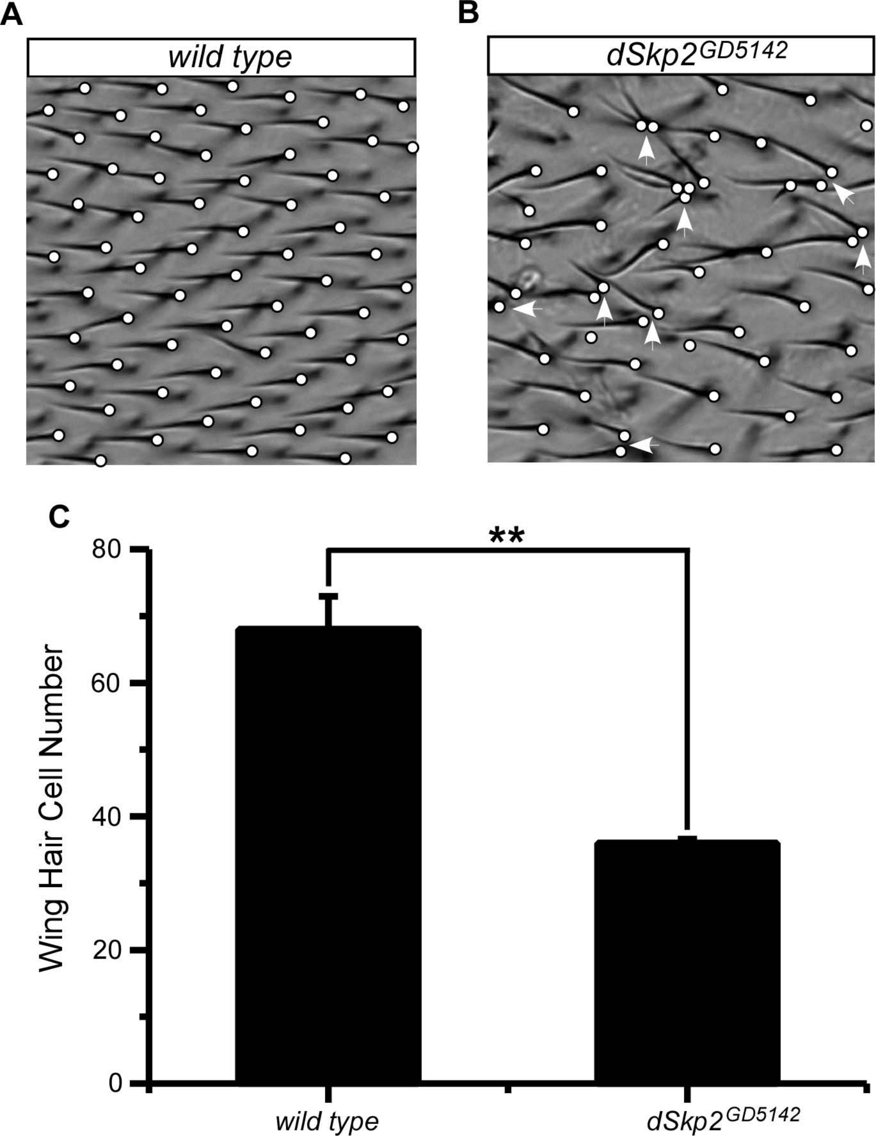
Figure S2. Quantitative presentation of the WHS phenotype caused by *dSkp2* RNAi. Wing hair cells are marked with blue filled black circles in a corresponding region in *wild type* (A) and *dSkp2* (B) knockdown region. White arrows indicate the multiple wing hairs in the wings with *dSkp2* knockdown. (C) is a bar graph showing the number of wing hair cells within six equal-sized areas of *wt* and *dSkp2* knockdown adult wings. **indicates $p<0.01$.

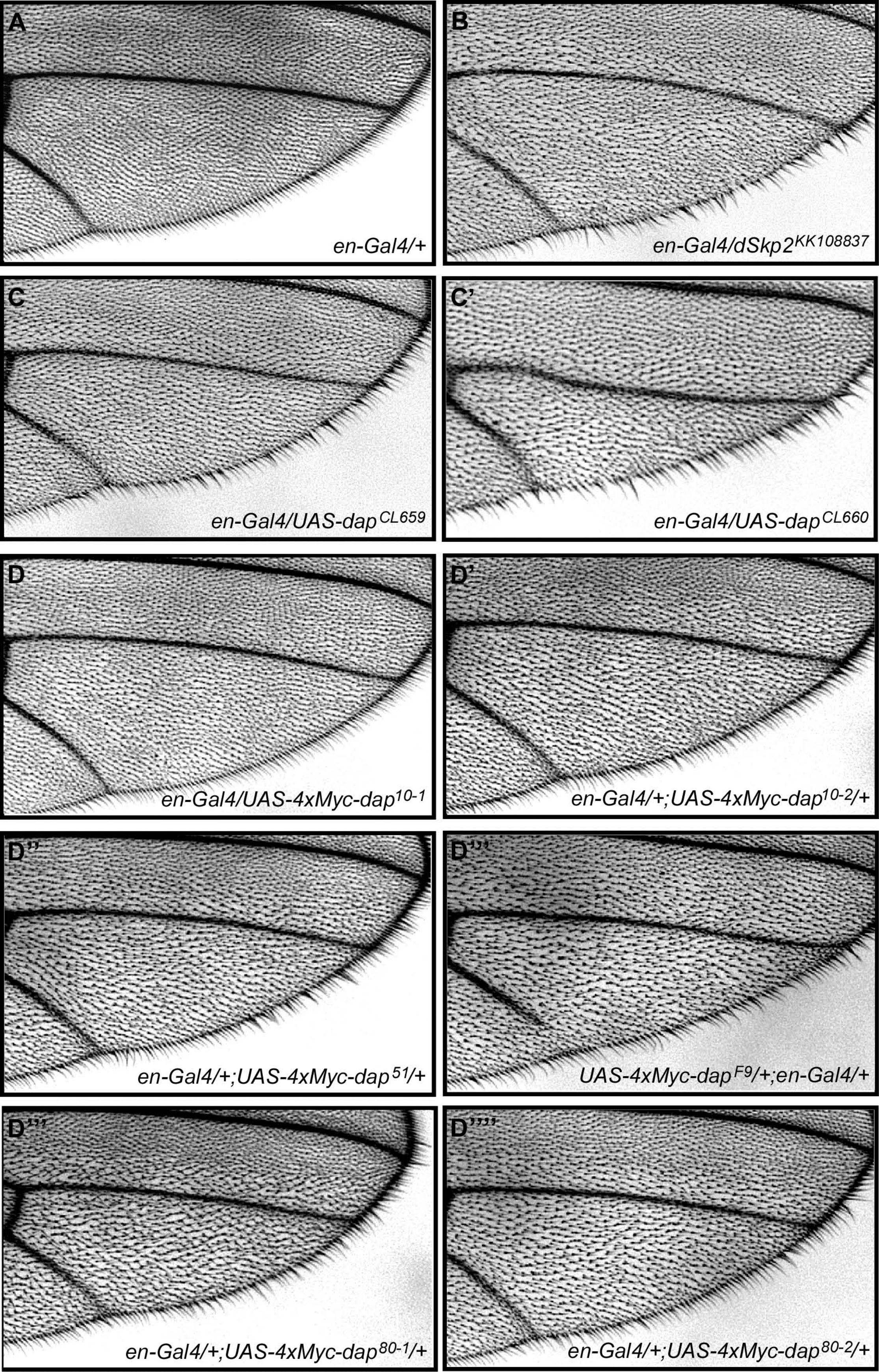
Figure S3. High magnification images showing the WHS phenotype of *dap* overexpression or *dSkp2* knockdown in the wing. (A) A control wing of *en-Gal4*. (B) *dSkp2* knockdown in the posterior region of the wing under the control of *en-Gal4* leads to a typical WHS phenotype. Overexpression of *dap* in independent transgenic lines (C-C’ and D-D’’’’) under the control of *en-Gal4* causes similar phenotypes.

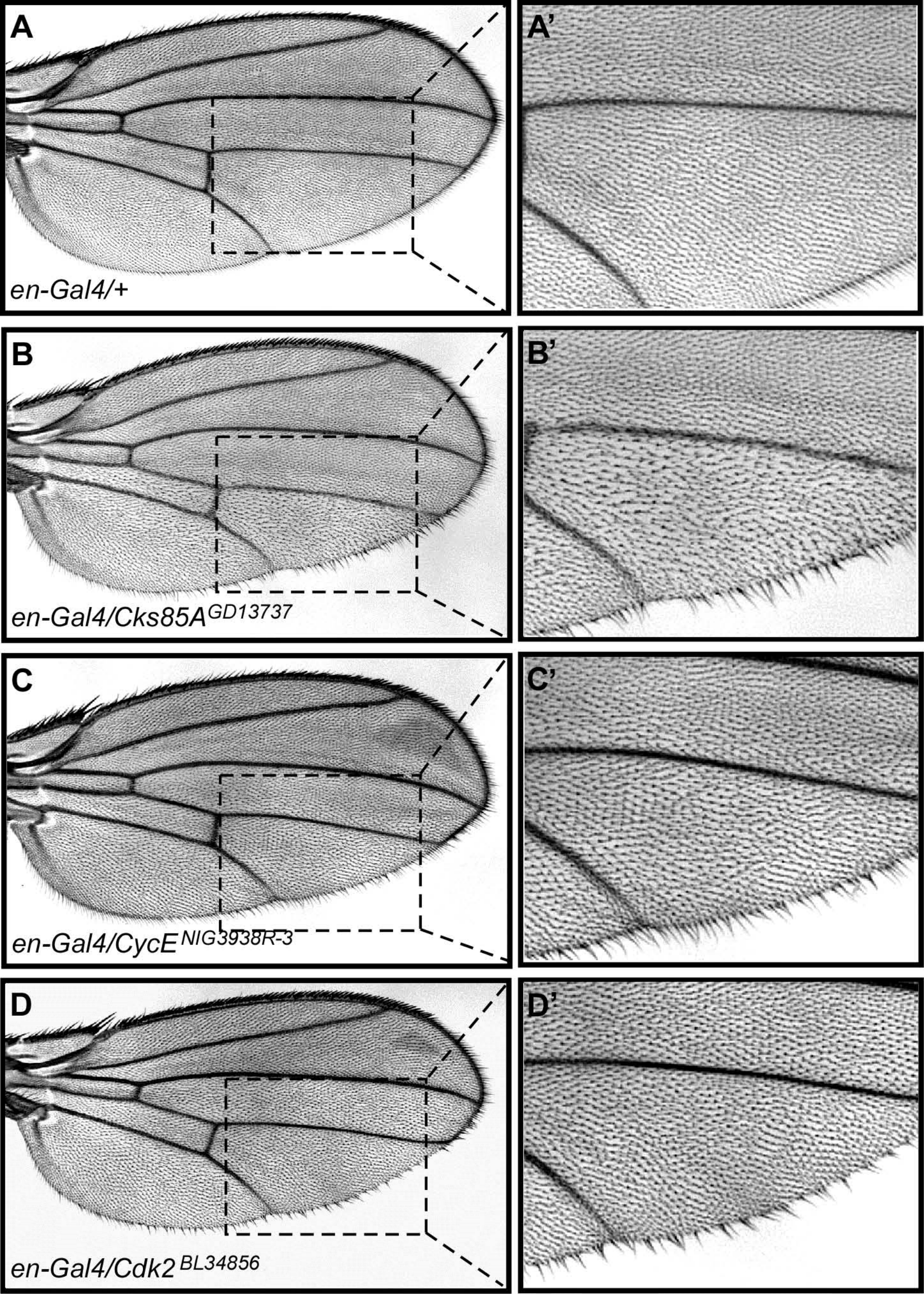
Figure S4. Wing hair spacing phenotype caused by overexpression of cell cycle regulator genes. Shown are wings with *en-Gal4*-driven overexpression of *Cks85A* (B), *CycE* (C) or *Cdk2* (D) in the posterior region of the wing. The detected WHS phenotype is similar to that of *dSkp2* knockdown.

Figure S5. *dSkp2* knockdown in the posterior region of the wing discs under the control of *en-Gal4* in combination with *UAS-dcr2* (marked by GFP, B and C) leads to an accumulation of endogenous Dap protein (B’). This effect is further enhanced by simultaneous knockdown of *Cks85A* (C’; see Discussion). In both cases, only a small fraction of disc cells exhibit increased accumulation of Dap signals (see Discussion). A and A’ are controls.


wild type
dSkp2 GD5142
dSkp2 KK108837
dSkp2
Rp49


A
wild type
B
dSkp2^GD5142
C
**
80
60
40
20
0
Wing Hair Cell Number
wild type
dSkp2^GD5142


A
en-Gal4/+
B
en-Gal4/dSkp2KK108837
C
en-Gal4/UAS-dapCL659
C'
en-Gal4/UAS-dapCL660
D
en-Gal4/UAS-4xMyc-dap10-1
D'
en-Gal4/+;UAS-4xMyc-dap10-2/+
D''
en-Gal4/+;UAS-4xMyc-dap51/+
D'''
UAS-4xMyc-dapF9/+;en-Gal4/+
D''''
en-Gal4/+;UAS-4xMyc-dap80-1/+
D'''''
en-Gal4/+;UAS-4xMyc-dap80-2/+


A
A’
en-Gal4/+
B
B’
en-Gal4/Cks85A^{GD13737}
C
C’
en-Gal4/CycE$^{NIG3938R-3}$
D
D’
en-Gal4/Cdk2^{BL34856}

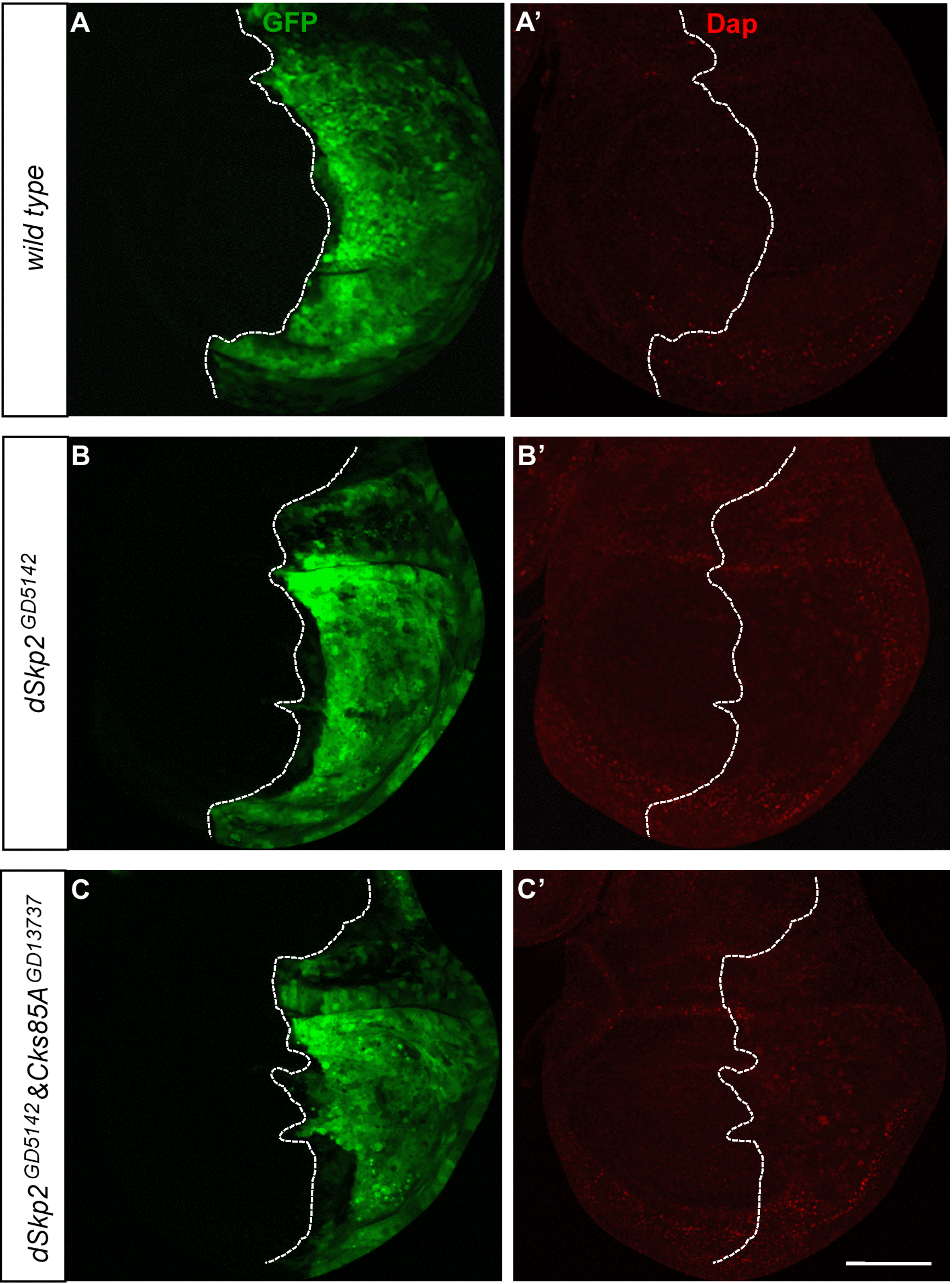

A
GFP
A’
Dap
wild type
B
B’
dSkp2 GD5142
C
C’
dSkp2 GD5142 &Cks85A GD13737

Table S1. Different RNAi lines of *dSkp2* lead to similar phenotype

	en-Gal4	*en-Gal4* in combination with *UAS-dcr2*
$dSkp2^{GD5142}$	WHS++	Die in pupae+++
$dSkp2^{KK108837}$	WHS+	WHS++
$dSkp2^{JF01326}$	Normal-	WHS+
$dSkp2^{HMS00116}$	WHS+	WHS++

WHS: Wing-Hair-Spacing