Supplementary figures

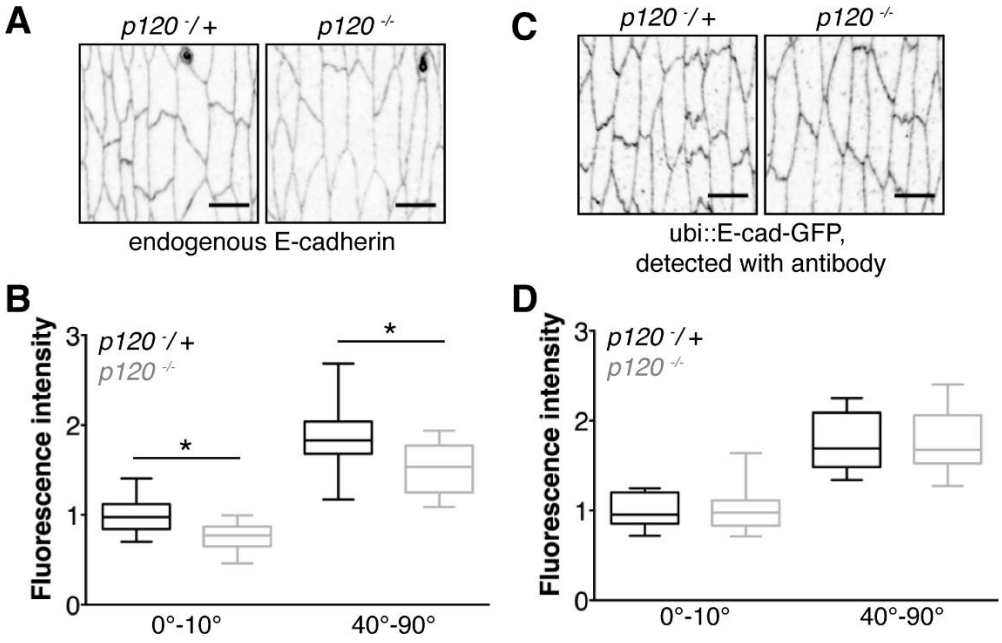

Figure S1. p120catenin increases endogenous E-cad levels in stage 15 embryos. (A-D) Endogenous E-cad and ubi::E-cad-GFP amounts in stage 15 embryos visualized by antibody staining. The latter was used as a control for non-specific effects of p120catenin loss on antibody sensitivity. Examples of endogenous E-cad (A) and ubi::E-cad-GFP (C) visualized with antibody staining are shown. Bar, 5μm. The quantifications are shown in B and D. * - $p<0.01$.

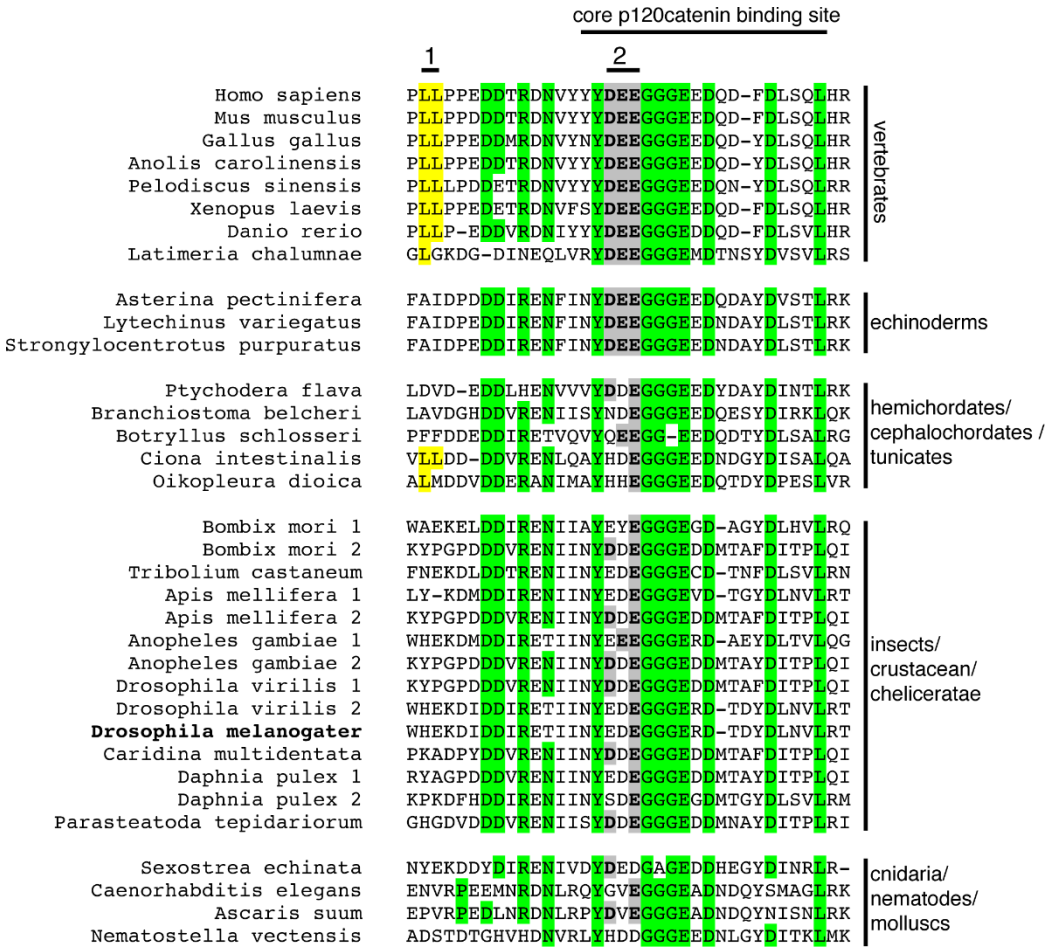

Figure S2. Multiple sequence alignment of Cadherin-1/E-cadherin.

The core p120catenin binding site is indicated with the conserved residues marked in green. Two endocytic motifs, LL (1, yellow) and DEE (2, grey) that are inhibited by p120catenin binding are marked.

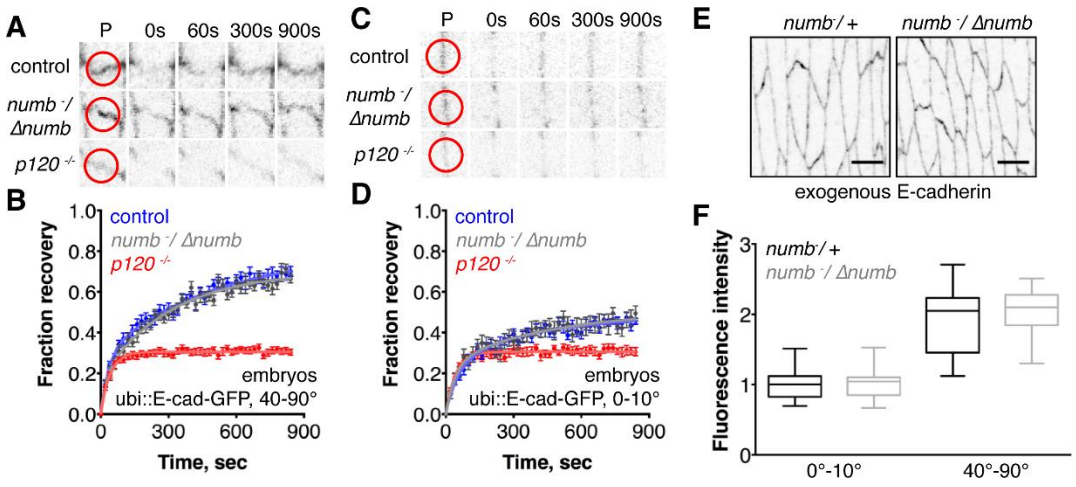

Figure S3. Numb is not required for ubi::E-cad-GFP junctional levels and recovery in FRAP experiments.

(A-D) ubi::E-cad-GFP FRAP in the absence of Numb at 40-90° (A, B) and 0-10° cell-cell borders (C, D) in embryonic epidermal cells. Examples of recovery are shown in A and C with red circles on the prebleached frame (P) showing the bleach spots. Average recovery curves (dots with error bars showing mean ± SEM) and the best fit curves (solid lines) are shown in B and D. ubi::E-cad-GFP FRAP in embryos in the absence of p120catenin are shown for comparison. (E-F) Quantification of ubi::E-cad-GFP levels in absence of Numb in stage 15 embryos. Examples of direct fluorescence of ubi::E-cad-GFP are shown in E. Scale bar 5μm. The quantification of fluorescence intensities is shown in F.

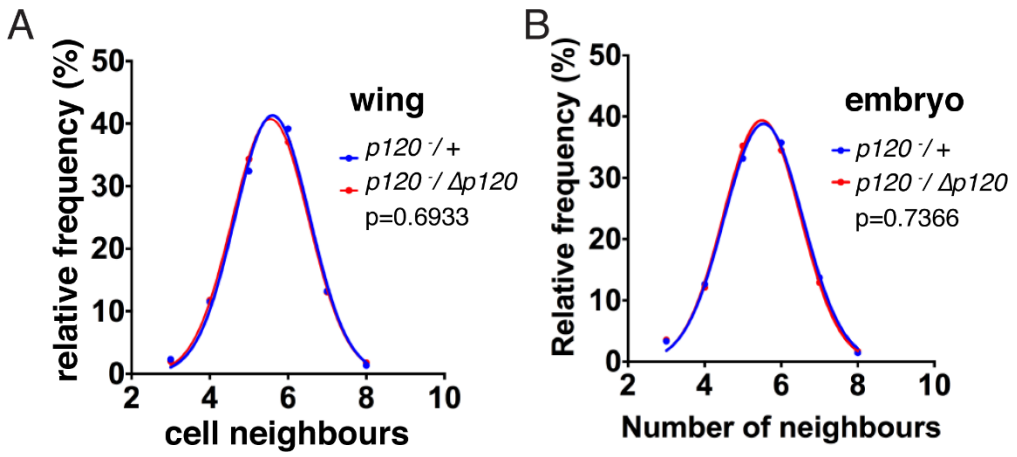

Figure S4. The number of cell neighbours does not require p120catenin.
The numbers of cell neighbours in wing discs (A) and stage 15 epidermis (B) in control (blue) and in the absence of p120catenin (red). The percentages of cells at each value are depicted with dots, and the best fit normal distributions are shown with lines. p values show the probabilities of the distributions being the same.

Table S1

Genotype	Type of borders	FRAP (maximum of recovery)	Number of FRAP experiment s (curves/ embryos)	Halftime 1 (sec)	Halftime 2 (sec)	Goodness of fit (R square)*	Replicates test for lack of fit (p-value)	p-value**
embryo cadherin								
wt	40-90°	0.79 ± 0.06	24/7	24 ± 6	342 ± 100	0.5865	0.9997	< 0.0001
	0-10°	0.49 ± 0.03	20/7	38 ± 12	256 ± 120	0.4829	0.9813	0.0013
p120 $^{-/-}$	40-90°	0.31 ± 0.01	19/5	29 ± 3	n.i.	0.4028	1.0000	0.1857
	0-10°	0.31 ± 0.01	16/5	30 ± 3	n.i.	0.3649	0.9999	0.2323
p120 $^{-}$ / Δ*p120*	40-90°	0.31 ± 0.01	16/4	40 ± 5	n.i.	0.2773	0.9131	n.i.***
	0-10°	0.32 ± 0.01	13/4	29 ± 5	n.i.	0.2215	1.0000	n.i.***
numb $^{-}$ / Δ*numb*	40-90°	0.70 ± 0.02	13/4	15 ± 8	212 ± 33	0.7143	0.8426	0.0001
	0-10°	0.50 ± 0.07	13/4	28 ± 9	304 ± 150	0.3782	0.9994	0.0019
Bazooka								
wt	40-90°	1.00 ± 0.10	20/6	59 ± 15	394 ± 128	0.8832	0.9949	< 0.0001
	0-10°	1.00 ± 0.08	20/5	52 ± 10	389 ± 157	0.8678	0.9339	< 0.0001
p120 $^{-/-}$	40-90°	0.47 ± 0.01	19/6	65 ± 5	n.a.	0.5177	1.0000	0.9452
	0-10°	0.51 ± 0.01	16/6	54 ± 4	n.a.	0.5462	1.0000	0.6566
wing cadherin								
wt	n.i.	0.89 ± 0.21	22/3	38 ± 6	734 ± 468	0.9877	0.0636	< 0.0001
p120 $^{-/-}$	n.i.	0.41 ± 0.01	18/3	31 ± 3	n.i.	0.9043	0.5028	0.0551
p120 $^{-/-}$ (1)	n.i.	0.89 (fixed)	18/3	16 ± 4	2610 ± 266	0.1522	0.9940	n.i.

n.i. - not identified

* - Goodness of fit was calculated by considering each replicate as an individual point.

** - p-value of comparison between null hypothesis (single exponential recovery) and alternative hypothesis (bi-exponential recovery)

*** - bi-exponential fit is ambiguous

(1) The recovery fitted by a bi-exponentia model with the parameters except for halftimes fixed as in control

Table S2

Genotype	Vesicles number (vesicles/µm^3 ± S.E.M) 0 min	10 min	30 min	60 min	Best fit model	Goodness of fit (R square)*	Replicates test for lack of fit (p-value)	p-value**	Half time (min ± S.E.M)***	Maximum (vesicles/ µm^3 ± S.E.M)***	Slope (vesicles/ µm^3 ± S.E.M)****
p120 $^{-}$ / +	0.0010 ± 0.0006	0.0064 ± 0.0028	0.0266 ± 0.0010	0.0293 ± 0.0010	Exponential	0.8675	0.3427	0.0108	18 ± 7	0.0353 ± 0.0054	
p120 $^{-}$ / + (0-30 min)					Linear	0.9083	0.7879	Other fit is ambigous			0.00088 ± 0.00009
p120 $^{-/-}$	0.0015 ± 0.0005	0.0074 ± 0.0021	0.0062 ± 0.0018	0.0132 ± 0.0026	Linear	0.4366	0.2966	Other fit is ambigous			0.00016 ± 0.00004
p120 $^{-}$ / + (CQ)°	0.0009 ± 0.0005	0.0041 ± 0.0020	0.0281 ± 0.0029	0.0380 ± 0.0036	Linear	0.8449	0.3186	0.0777	36 ± 22	0.0595 ± 0.0203	0.00067 ± 0.00007
p120 $^{-/-}$ (CQ)	0.0013 ± 0.0011	0.0035 ± 0.0025	0.0103 ± 0.0034	0.0222 ± 0.0024	Linear	0.7394	0.8618	Other fit is ambigous			0.00035 ± 0.00005

n.i. - not identified

* - Goodness of fit was calculated by considering each replicate as an individual point.

** - p-value of comparison between null hypothesis (exponential increase) and alternative hypothesis (linear increase)

*** - when best fit is exponential model

**** - when best fit is linear model

° - though the linear fit is slightly better, the best fit values are shown for both models