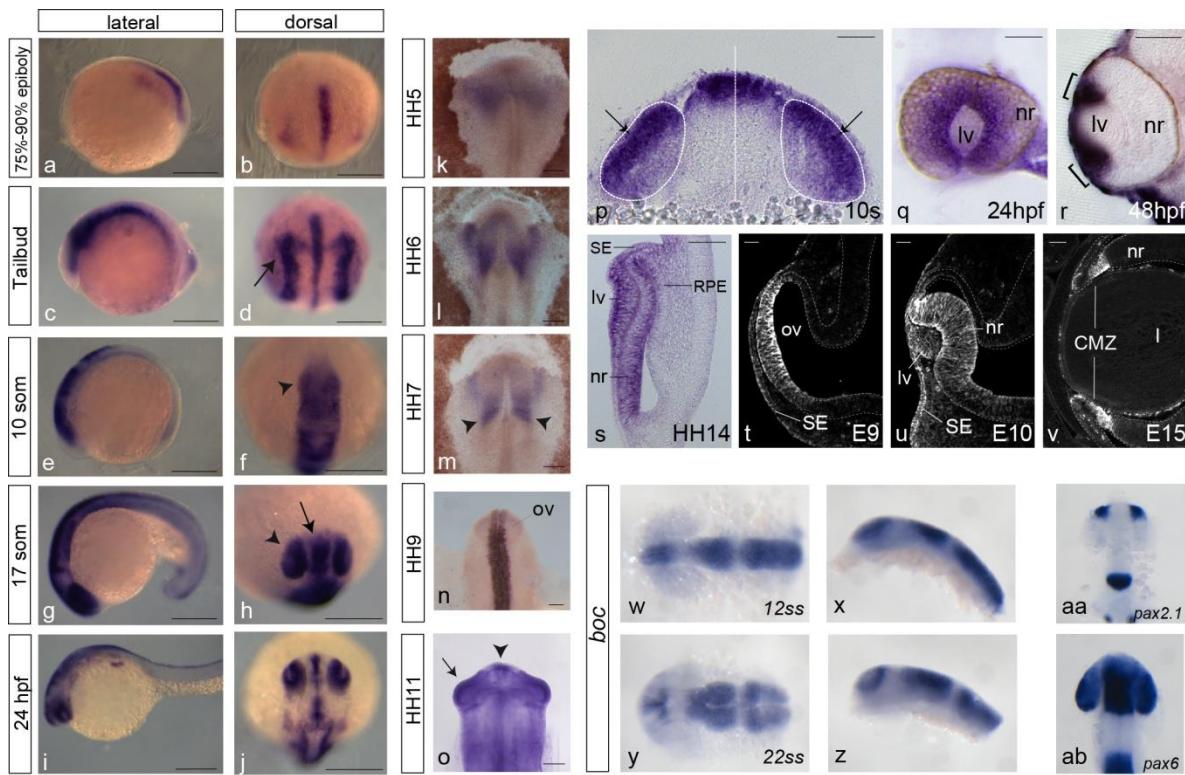
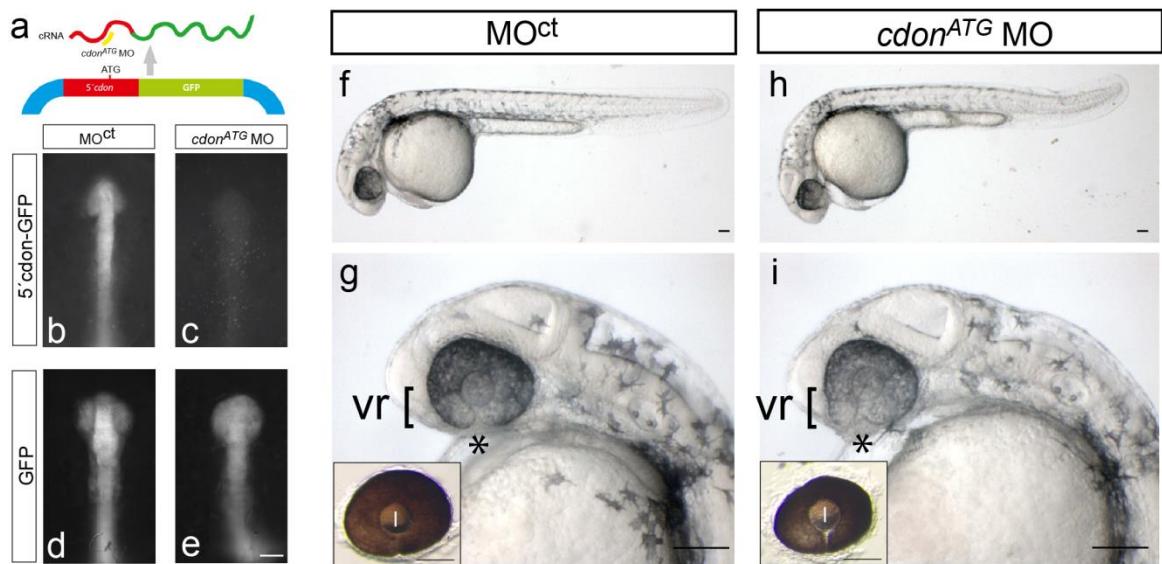


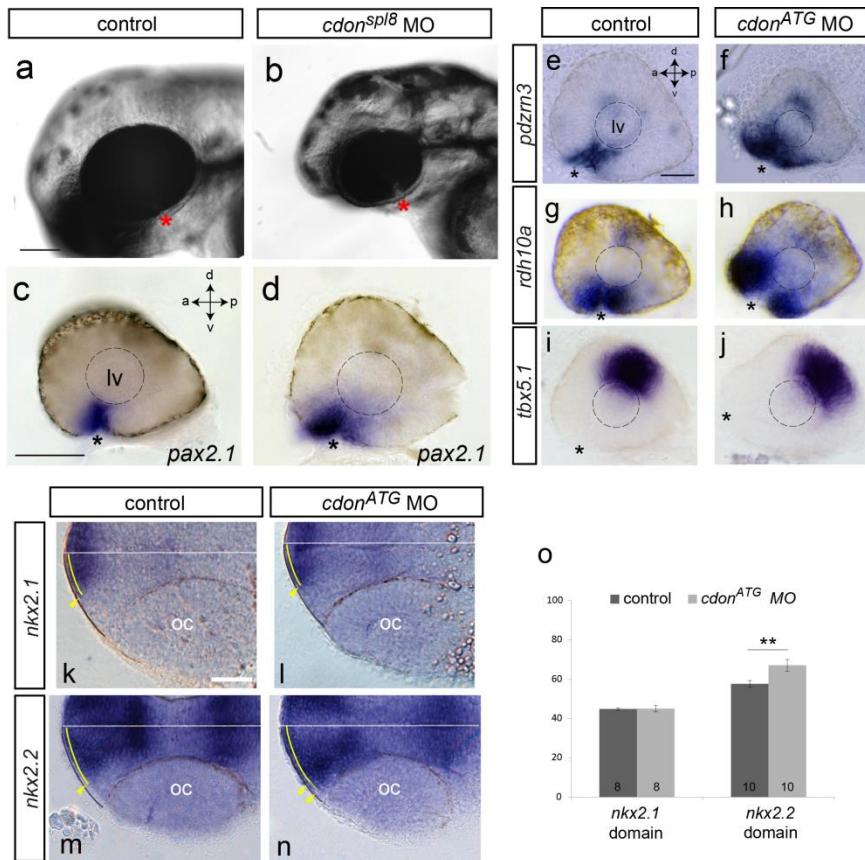
SUPPLEMENTARY INFORMATION



Supplementary Figure 1. *Cdon* expression in vertebrate embryos. Lateral (a-i) and dorsal (b-j) views of zebrafish and ventral (k-m) and dorsal (n, o) views of chick embryos at different developmental stages hybridized *in toto* with a *Cdon* specific probe and immunohistochemistry of *Cdon* distribution in the developing mouse embryonic eye (t-v). The zebrafish distribution of *boc* (w-z), *pax2.1* (aa) and *pax6* (ab) is shown for comparison with embryos hybridized *in toto* with probes specific for *cdon* at different stages of development. Images in (p, r) are coronal cryostat sections of zebrafish embryos hybridized *in toto*. In zebrafish at 75-90% epiboly *cdon* transcripts are detected in the ventral midline (a, b). At tailbud stage *cdon* mRNA localizes to the presumptive neural crest (c, d arrow) and at 10-17 somite stages in the optic vesicles (f, h arrowhead), prechordal plate, telencephalon (h, arrow) and dorsal neural tube (e-h). At 24 hpf *cdon* expression becomes restricted to the retina and the dorsal neural tube (i, j). In chick embryos, *Cdon* expression is first detected at the Hensen's node (k), and later in the presumptive neural crest (l-n), somites (m arrowheads) and CNS (n). At HH11 *Cdon* mRNA localizes to the optic vesicles and dorsal CNS (o, arrow and arrowhead respectively). *Cdon* expression is restricted to regions of the telencephalon and the presumptive retinal domain of the optic vesicle at 10ss stage (p) to finally restricting to the ciliary margin zone (CMZ) (see brackets in q, r). *Cdon* expression in the developing eye is conserved in chick (s) and mouse embryos (t-v). Note that *boc* is not expressed in the optic vesicle (w, x) or the optic cup (y, z). The white dashed lines in p indicate the midline and the optic vesicles. The white dashed line in t-v delineates the neural epithelium. CMZ, ciliary marginal zone; l, lens; Iv, lens vesicle; nr, neural retina; ov, optic vesicle; RPE, retinal pigmented epithelium; SE, surface ectoderm. Scale bars: 200 μ m.



Supplementary Figure 2. *cdon^{ATG}* MO efficiently interferes with *cdon* expression inducing morphants that present defects in the ventral region of the eye. **a)** Schematic diagram of the strategy used to test the specificity of an antisense morpholino (MO) designed against the translation start site sequence of *cdon* (*cdon^{ATG}*). This MO or a standard control MO (*MO^{ct}*) were co-injected into medaka fish embryos with the cRNA of a reporter construct (5'cdon-GFP) carrying the zebrafish *cdon* 5' sequence upstream of the *gfp* sequence. Translation of this construct (evident by expression of GFP) was efficiently knocked down by *cdon^{ATG}* MO (**c**) (25/25 embryos) but not by the *MO^{ct}* (**b**) (20/20 embryos). None of the two MO interfered with the translation of the GFP alone (**d, e**) (23/23 embryos). Bright field lateral (**f-i**) views of embryos injected with *MO^{ct}* (**f, g**) or *cdon^{ATG}* MO (**h, i**). *cdon^{ATG}* MO (**h, i**) but not *MO^{ct}* (**f, g**) injected embryos are characterized by alteration of the ventral retina (vr) at 28 hpf. The asterisks indicate the optic fissure in *cdon^{ATG}* morphant (**i**), which remains open at 36 hpf (compare insets in **g, i**). l, lens; vr, ventral retina. Scale bars: 40 μ m (**b-e**). Scale bars: 100 μ m (**f-i**).



Supplementary Figure 3. *cdon^{spl8}* splicing MO reproduces the phenotype observed in *cdon^{ATG}* morphants, which display an expansion of ventral markers. Bright field, lateral images of 48 hpf control (a) and *cdon^{spl8}* morphant characterized by the presence of coloboma (b). Lateral views of the eyes of control and *cdon^{spl8}* morphants hybridized *in toto* with probes for *pax2.1* (c, d) (17/40 embryos). Note that in *cdon^{spl8}* morphants *pax2.1* expression is expanded in comparison to controls (c, d). Lateral views of the eyes of control and *cdon^{ATG}* morphants hybridized *in toto* with probes for the ventral retinal markers *pdzrn3* (e, f) and *rdh10a* (g, h) or the dorsal retinal marker *tbx5.1* (i, j). In *cdon^{ATG}* morphants the ventral retina markers *pdzrn3* (28/54 embryos) and *rdh10a* (32/44 embryos) are also expanded in comparison to controls (e-h) whereas *tbx5.1* (62/62 embryos) shows no evident changes in comparison to controls (i, j). The dashed lines mark the lens, and the asterisks indicate the position of the optic fissure. (k-n) Horizontal cryostat sections of control and *cdon^{ATG}* morphant embryos hybridized with probes for *nkh2.1* and *nkh2.2* at 26hpf. The dotted black lines indicate the distance from the midline to the optic cup. The yellow lines depict the extent of gene expression in the medio-lateral direction and the yellow arrowheads indicate the most distal/lateral position of the positive signal. The dotted yellow line in n depicts the expansion of *nkh2.2* expression observed in *cdon^{ATG}* embryos. o) Quantitative analysis of the *nkh2.1* and *nkh2.2* anterior expression domains. Note that *nkh2.2* expression in morphants is significantly different from that of controls (**p< 0.01; Student's t-test). The number of embryos analysed in each case is as follow: *nkh2.1*, n=8 for both control and MO injected embryos; *nkh2.2*, n=10 for both control and MO injected embryos). This information is also indicated in each column. Error bars in o represent s.e.m. a, anterior; d, dorsal; lv, lens vesicle; oc, optic cup; p, posterior; v, ventral. Scale bars: 100 μ m.

a)

MHPDGLPCTLLYVLTILCSSVSSDLAPYFSEPLSAVQKLGPVVLHCSAQPVTRISWLHNGKTLGQNLEHKVHQGTLTILSLNSLLGYYQCLANNSIGAIVSGPATVSAVLGDGF
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ISGVTVEDVGMYQCVADNGIGFMHSTGRLEIENDGGFKPVIITAPVSAVADGDFVTLCNASGLPVPVIRWYDSSHGLITSHPSQVLRSKRSKSQLRPEGLNLEPVYFVLSQAGASSLHIQ
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YFVKYRKLDGCVMLGSWHTVRVPGSENELHAELEPSSLYEVLMVARSAAGECQPAMITFRTSKEKTASSKNTQASSPPVGIPKYPVVAEANNNFCVVLTDSRHSGVPEAPDRPTISTA
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PDHLQIAKSCVWEGLDSCARSETEINIVSWNALLPVPEGCAEKTMSPPGIPLDSPTEVLOQPRET

b)

MHPDGLPWLTLVYLICSSVSSDLAPYFISEPLSAVQKLGRPVVLHCSAKPVTARIWLNHGKRLDRNTEQIKIHRGTLTILSLNPLSGCYQCVANNSVGA VSGPATVSAALGDFDS
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VVVTWIPRANGGSPITAFKVEYKMRNSTDWLVAEDIPPSKLSVEVRSLEPGSTYKFRVIAINHYGESFRSSASRPYQVAGFPNRFSRPI TGHIA YTEAVSDTQIMLKWTYVPPSSNNNTP
IQGFYIYYRPTDSNDSDYKRDVVEGSKQWHMIGHIQPETSYDIKMQCFNEGGSEFSNVMICETKVKRPGASEYPVKEI STPPSSSGNAGNVGPATSPARSSDMYLIVGCVLGVMVIL
MVFIALCLWKSRSQSTI QYDPPGILYQGSEINGQMVEYTTLSGAARINGSVHGGFLSNCGSMLHHKGPSGVNGTSLGNINGLYSAHTNSLTRACFEHPHHLVNNSGGVYAVPQMDPLE
CINCRNCRNNRCFTKTNPLPVPPVVASYQPQGGLEMKPLNAMKPVCPASTVPDFHGQLPDCVKDSVAPIPTQHTCCQDNISDINSDSTEDTAEFSRGDSSGHSEAEDKVFSWNPLISPV
LEDCEGEKTA RSPGPPLDGLSVVILQQAET

Supplementary Figure 4. Sequences of the human and mouse Cdon protein. Cdon protein sequences from *Homo sapiens* (Q4KMG0; **a**) and *Mus musculus* (Q32MD9; **b**) as well as the position and sequence of the fibronectin type-III 2 (blue) and 3 (green) domains were obtained from Uniprot database¹.

Supplementary Figure 5. Alignment of the mouse and human Cdron FNIII 2 sequences with the Cdron zebrafish sequence (Uniprot, Q1L8D0) using Clustal Omega^{2,3}.

Cdon_Danio_rerio	MEDGGLRLLSAVLCVCHTLLNCPTVLSFSFRAEPLSAILKQGSSVHLHCTTHPATARIS
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	WLFQGQPLDPSHHGVELSQDSLSSLNLQPAUTGSYQCSARSETGSIISRHARVTIADIE
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	EFAETHRRSFTVNKGDTAVIECPLPRSNPPALPRFRIRGKWLEQSTDEYLILPSGNLQIV
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	SVSSEHQGMKYKCGAYNPLTRERTRVEAHGTKLVDSESSSPVRIVYPITPRSLTVDQSGS
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	LTLECVVSGSLSSKVKWMKNGAELSLSSKRLSHSNLVLNDIQPGDGHHYSCSVPTDRGA
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	VVSVNYTVNVLAHVSLRGLSDQAAVAGSSVRFTCAASGNPTPNITWLNAPLSSPRL
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	KISGTSLLISSTTLQDQGIYQCMFDNGISSAQSTGRLSIQSEFQSSSISAVPVKTQPSVH
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	PIQSDEGDELFLSMGEAALGETVGPPTERIGDRPTPEAPIIIISPQTHKPKNMYDLEWRAG
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	RDWGIAIIAYFVKYRKVDDMGNVVGWSHTVRVPGEKSLPLSELEPSSLYEVLMVARSA
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	GEGQPAMLTFRTGKERASPNKNSKAPIVSLPEKTPEDKTNTYYGVVIHDRVPEAPDRP
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	TISMATESSVYTWTIPRANGSPITAFRVEYRKQGRNGDWIIAADNISPLKLSVEVRNL
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	PGSTYRFRVIAMNNYGESPASATSRPYQVSMSSPVSNRPVTPGHISSTDQILLR
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
*:*****: *:*****:*	
Cdon_Danio_rerio	WTYTPSSNNNNTPIQGFYIYYRPTDSNDSDYKKDVVEGFKFWHMIGELQPETSYDIKMQC
FnIII_3_Mus_musculus	WTYVPSSNNNNTPIQGFYIYYRPTDSNDSDYKRDVVEGSKQWHTIGHLQPETSYDIKMQC
FnIII_3_Homo_sapiens	WTYIPSSNNNNTPIQGFYIYYRPTDSNDSDYKRDVVEGSKQWHMIGHLQPETSYDIKMQC
*** *****:*****:*****:*****:*****:*****:*****:*****:*****:	
Cdon_Danio_rerio	YNDGGESEYSNVMICETKARQPPGVPSLRFIPPPGFYPADTPSQPGGLLYLIVGCVLGV
FnIII_3_Mus_musculus	FNEGGESEFSNVMICET-----
FnIII_3_Homo_sapiens	FNEGGESEFSNVMICET-----
:*****:*****:*****	
Cdon_Danio_rerio	VLILLVFIVMCLWRNRQQNSMHKYDPPNYIYQSAEMNGHVLDYALPGSSHVNGSVHTGC
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	GHTAPMMMPOTCHHLHKLPNGLALLNNGGGLYPAGHPHAHDTSLHQNNEYEHPSPHLH
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	NGGGIYTALPQNDSSDCMSCQNFCCNNRCYTKTNGTFSGGTLPLMHRVAARQPDGLEMM
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	LNPILSRCHGRDSPQLNGCQDRDSVQQAEENVPPLSHNSPCLPVETKSSLEQQRGVQQV
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----
Cdon_Danio_rerio	QHEDSEGPPVCWERLGLLDCKEKTAWISTGSLTGDLIQPTVQEI
FnIII_3_Mus_musculus	-----
FnIII_3_Homo_sapiens	-----

Supplementary Figure 6. Alignment of the mouse and human Cdon FNIII 2 sequences with the Cdon zebrafish sequence (Uniprot, Q1L8D0) using Clustal Omega^{2,3}.

MEDGGGLRLLSAVLCVCHTLLNCPTVLSFSFRAEPLSAILKQGSSVHLHCTTHPATARIWLFQGQLDPSSHSGVELSQDSSLNLQPALTGSYQCSARSETGSIISRHARVTIADIEEF
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 CUVSGSLSSKVWMKNGAELSLSSKRMLSHSNLVLDIQPGDGHHYSCSVPDTDGAVVSVNYTVNLVLAHVSILRGLSDQAAGSVRFTCAASGNPTPNITWLNAAPLSSSPRLKISGTS
 LLISSTTLQDQGIYQCMFDNGISSAQSTGRLSIQSEPQSSSISAVPVKTQPSVHPIQSDEGDELFLSMGEAALGETVGPPTERIGDRPTPEAPIIIISPPQTHKPNMYDLEWRAGRDWGIAII
 AYFVKYRKVDDMGNVVGSWHTVRVPGEKSPLPLSELEPSSLYEVLVARSAAGEGQPAMLTFRTGKERASPNKNPSKAPIVSLPEKTPEDKTTNTYYGVVIHDRVPEAPDRPTISMATESSV
 YVTWIPRANGGSPITAFRVEYRKQGRNGDWIAADNISPLKLSVEVRNLEPGSYTYRFRVIAMNYGESPASATSRPYQVSMSSEPVSNRPVTGPHIISSTDQILRWTVTPSSNNNTP
 IQGFYIYYRPTIDSDNDSDYKKDVVEGFKFWHMIGELQPEETSYDIKMQCYNDGGESEYSNVMICETIKARQPPGPVPSLRITPPGYPADTPSQPGGLYLIVGCVLGVMVLILLVFIVMCLWR
 NRQQNSMHRKYDPPNYIYQSAEMNGHVLDYBALPGSSHVNNGSVHTGCCHTAPMMPQTCHLHHKLPGNLALLNGSGGLYPAGHPHAHDTSLHQNNMEYEHPSPHLHNNGGIYTALPQNDSSD
 CMSCCNFCNNRCYTKTNGTFSGGTLPMLHRVAARQPDGLEMMPLNIFLSRCHGRDSPQLNGCQDRDSVQQAEENVPLSHNSPCLPVETKSSLEQQRGVQQVQHEDSEGPVVCCWERLGLD
 LDCKEKTAWISTGSLTGDLIQPTVQEI

Supplementary Figure 7. Cdon *Danio rerio* sequence. Sequence of the zebrafish Cdon protein (Uniprot, Q1L8D0), in which the residues of the deduced fibronectin type-III(2) and fibronectin type-III(3) are indicated in blue and green, respectively. The homolog residues relevant for Ptch binding⁴ are highlighted in light blue, those relevant for Shh binding⁵ in red.

a) TATCCCATCTCGCAGGTTTGTCAAGATCAGGCTGCAGTTGGATTCTCTGTGAGATTACCTGTGCTGCCAGTGGCAATCCAACCCCCAACATCACATGGCTCTTAACGCTGCCCTT
 TATCTTCTCACCCCGCCTCAAATCTCTGCCACCTCCCTCACATCTCGCAACACCGCTCAAGATCAGGGAAATCTACCAAGTGCATGTTGATAATGGCATTAGCTCTGCACAATCCACA
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 AGTGGAGAGCAGGCCAGACTGGGCATCGTATCATGCATACTTGTCAAATATCGCAAGGTGGATGATGGGAAATGTGGTGGGAGCTGGCACACGGTGGGGTACCCGGCAGCGAG
 AAGTCTCTGCCCTGTCAGAGCTGGAGCCAGCGCTGTAGGGT

b) TATCCCATCTCGCAGGTTTGTCAAGATCAGGCTGCAGTTGGATTCTCTGTGAGATTACCTGTGCTGCCAGTGGCAATCCAACCCCCAACATCACATGACTCTTAACGCTGCCCTT
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 GGGAAATGTGGTGGGAGCTGGCACACGGTGCGGTACCCGGCAGCGAGAAGTCTGTGTCAGAGCTGGAGCCGCTTGTAGGGT

c) TATCCCATCTCGCAGGTTTGTCAAGATCAGGCTGCAGTTGGATTCTCTGTGAGATTACCTGTGCTGCCAGTGGCAATCCAACCCCCAACATCACATGGCTCTTAACGCTGCCCTT
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 GGAAAGACTCAGTATCCAATCAGAACCCACAGTCAGTTCCATATCTGCAGTTCCAGTGAAGACGCAACCTCTGTCACCCAACTCAGAGTGTGAGGGTGTGAACTGTTCTCTCCATGGG
 GGAGGGGGCGCTTGGAGAAAATGTGGATGATGGGAAATGTGGTGGGAGCTGGCACACGGTGGGGTACCCGGCAGCGAGAAGTCTCTGCCCTGTCAAGAGCTGGAGCCGTCAGCCTG
 ATGAGGTC

d) TATCCCATCTCGCAGGTTTGTCAAGATCAGGCTGCAGTTGGATTCTCTGTGAGATTACCTGTGCTGCCAGTGGCAATCCAACCCCCAACATCACATGGCTCTTAACGCTGCCCTT
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 GGAAAGACTCAGTATCCAATCAGGGATGATGGGAAATGTGGTGGGAGCTGGCACACGGTGGGGTACCCGGCAGCGAGAAGTCTCTGCCCTGTCAAGAGCTGGAGCCGTCAGCCTG
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e) ACACCTCCATCCAGCAATAACACACTCCCACCCAGGGCTCTACATCTACTATCGGCAACAGACAGCGACAATGACAGCAGTACAAGAAAGATGTGGTGGAGGCTCAAATTCTGC
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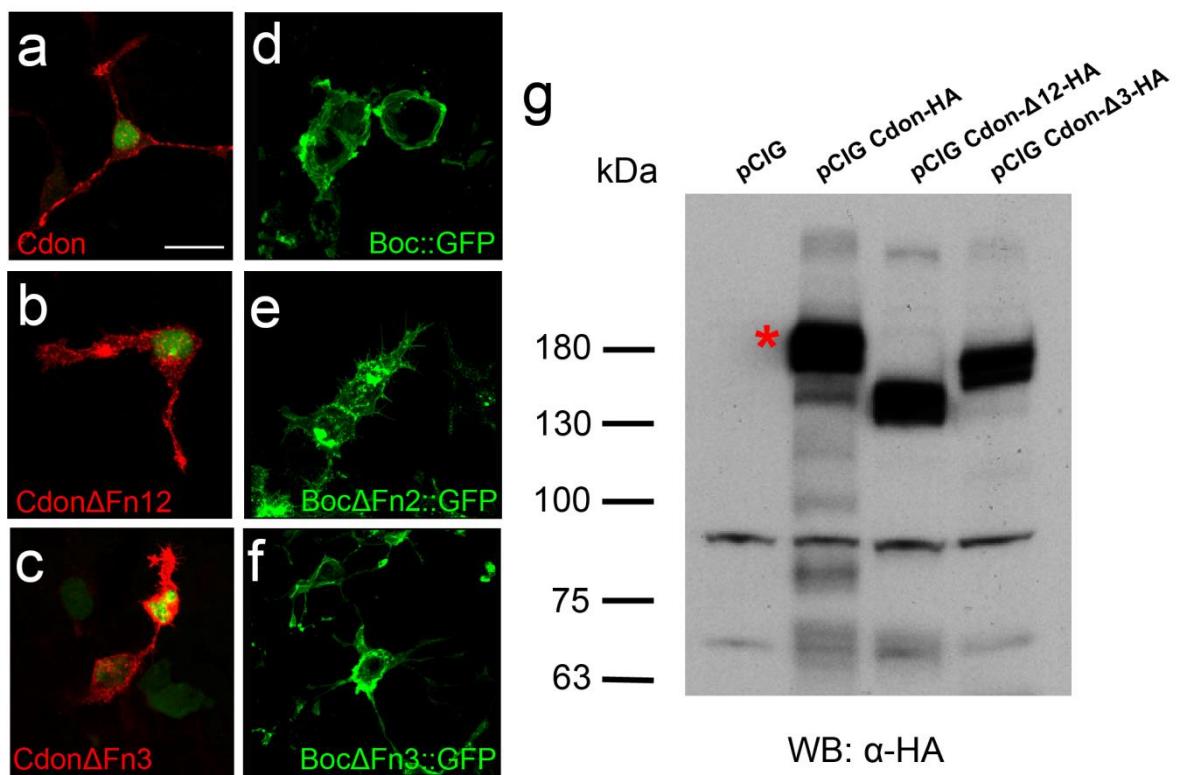
f) ACACCTCCATCCAGCAATAACACACTCCCACCCAGGGCTCTACATCTACTATCGGCAACAGACAGCGACAATGACAGCAGTACAAGAGAGATGTGGTGGAGCCGGCAGCCCTCAG
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 CTTGCTCTCATCGTCATGTGCTTATGGAGGA

g) CCAATAAGAATCCCTCAAAGCTCCAATTGTGCTCTACAGAGAAAATCCAGAAGATAAAACTACTAACACTTATTATGGAGTCGTACATGACAGAGTCCAGGGCTCAGACC
 GCCCCACAATCTCAATGGCGAGAAAATCTGTTAGTCACATGGGATACCTCGGGCAATGGTGGCTCCGATCACTGCAATTCCGTGGAGTACAGAAAACAGGGCGTAATGGAGAC
 TGGATCATTGCGAGCTGATAACATCTCACCGCTAAACTGTCAGTGGAGTGCACACCTTGAGCCAGGTTCCACTTACCGTTCCGTGCAATTGCGATGAAATAACTATGGTAAAGCCAGC
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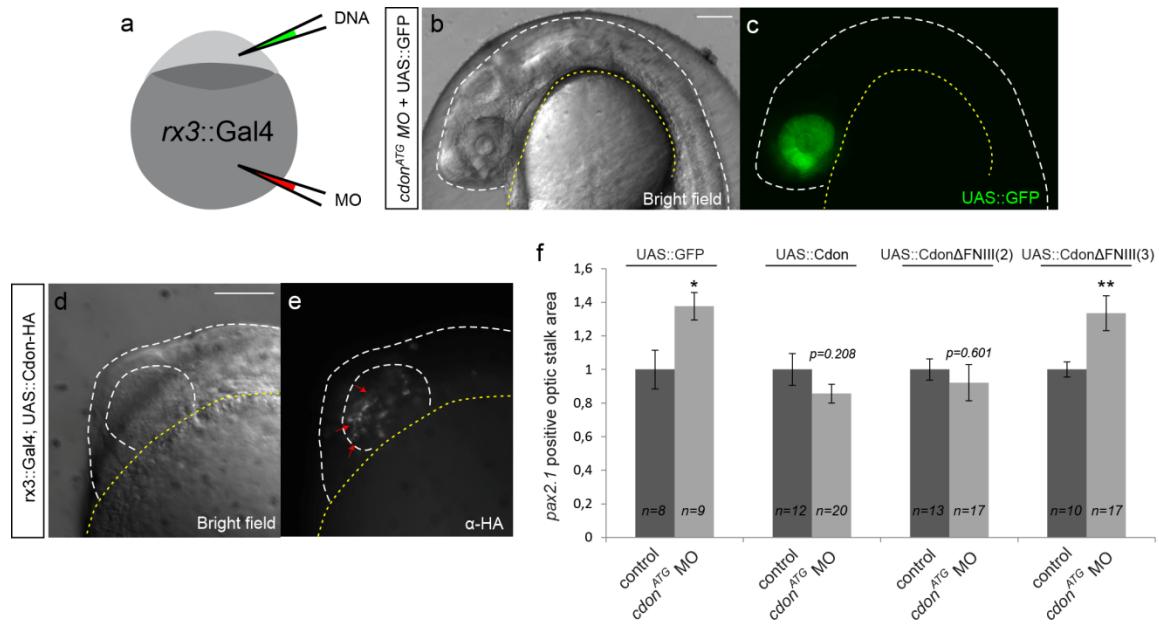
h) CCAATAAGAATCCCTCAAAGCTCCAATTGTGCTCTACAGAGAAAATCCAGAAGATAAAACTACTAACACTTATTATGGAGTCGTACATGACAGAGTCCAGGGCTCAGACC
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 CCATGTCAGTTACCTGTCGAACCGTCCAGTCAGTGGGCTCACATCTCTCCACTGATGCTGTTAGTGTACACTCAGATTCTGTAACGCTGG

i) CCAATAAGAATCCCTCAAAGCTCCAATTGTGCTCTACAGAGAAAATCCAGAAGATAAAACTACTAACACTTATTATGGAGTCGTACATGACAGAGGTTCCACTACCGTTCC
 GTGTGCTATTGCCATGAACTGACTATGGTGAAGCCCGACTAGCGCCACCTCCAGGCCATACCGGTCTCCAGTCAGTTCACCTGTCGAACCGTCCAGTCAGTGGGCTCACATCTCTTCC
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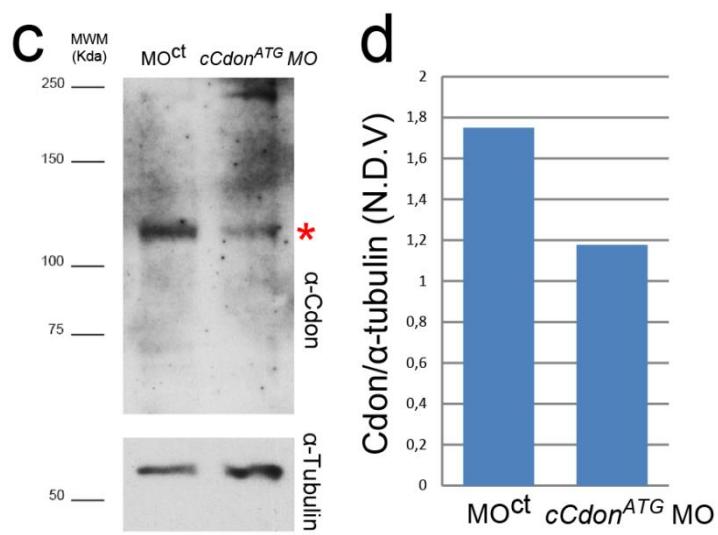
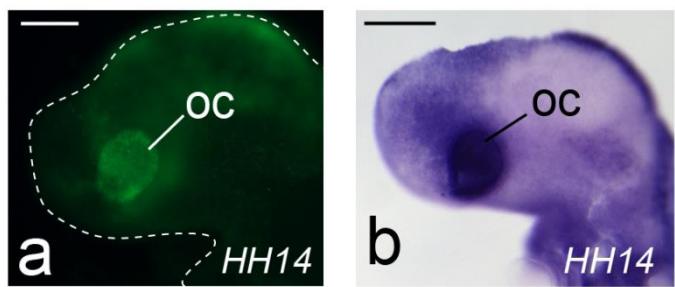
Supplementary Figure 8. Sequences of the *cdon* products generated by injection of splicing MOs. After splicing MO injections embryos were collected and the generated Cdon products were amplified by RT-PCR. The obtained amplicons are shown in figure 4. The corresponding sequences are illustrated in (a-i) as follow: **(a-d)** sequences of bands 1-4 in Fig.4c; **(e, f)** sequences of bands 5 and 6 in Fig.4f; **(g-i)** sequences of bands 7-9 in Fig.4i. **a)** Wild type band. **b)** Cryptic splice site activation generated a deletion of 73pb, producing a frame-shift mutation. **c)** Cryptic splice site activation generates a deletion of 162pb that does not produce a frame-shift mutation. **d)** Deletion of Cdon exon 8 (284pb) produces a frame-shift mutation. **e)** Wild type band. **f)** Deletion of Cdon exon 14 (123pb) does not produce a frame-shift mutation. **g)** Wild type band. **h)** Cryptic splice site activation generates a deletion of 29pb, producing a frame-shift mutation. **i)** Deletion of Cdon exon 11 (207pb) does not produce a frame-shift mutation.



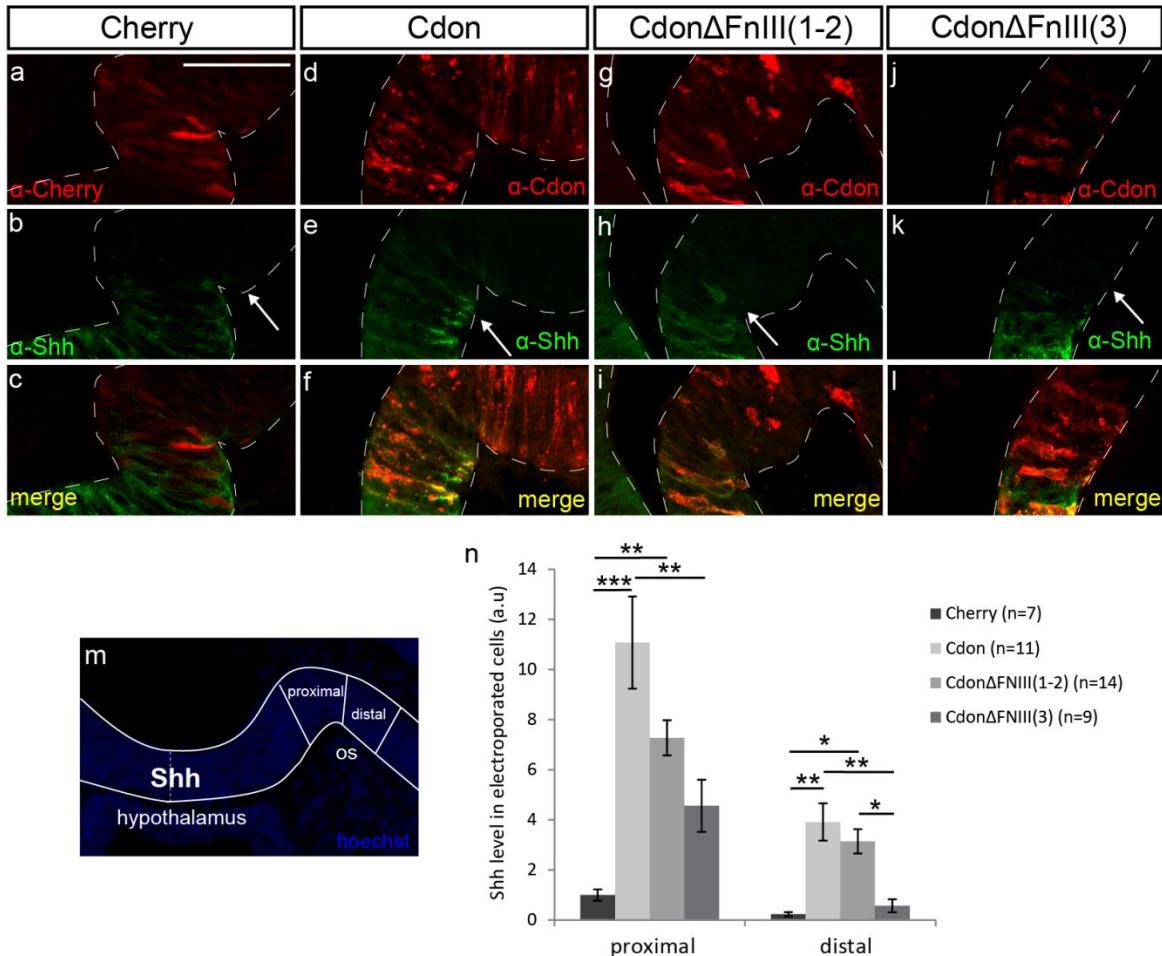
Supplementary Figure 9. Deletion of the fibronectin domains in Cdon and Boc does not affect protein stability or membrane localization. Fluorescent images of HEK cells transfected with Cdon, Boc-EGFP or their deleted versions as indicated in the panels (a-f). Cdon localization was determined by IHC. In all cases the fluorescent signal is detected at the plasma membrane. g) Western Blot analysis of lysates from cells transfected with Cdon or its derivatives shows that Cdon and deleted constructs are translated properly. The green signal in a-c corresponds to a nuclear GFP carried by pCIG vectors. The asterisk indicates the position of the band corresponding to full-length Cdon. Scale bar: 2 μ m.



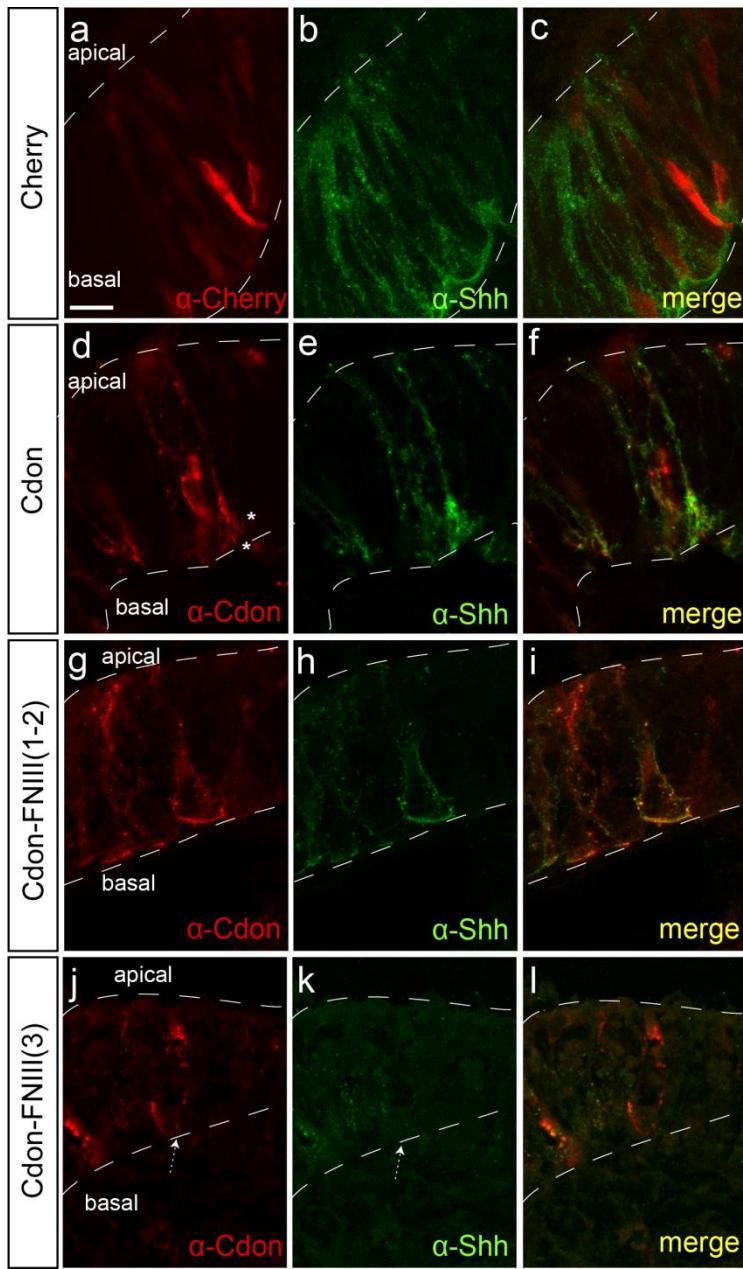
Supplementary Figure 10. Overexpression of *Cdon* or *CdonΔFnIII(2)* in the eye rescues the optic stalk phenotype of *cdon* morphants. **a)** The schema depicts the injection method used in rescue experiments. Embryos expressing Gal4 protein in the *rx3* positive domain (*rx3::Gal4*) were injected at 1-cell stage into the cell with UAS::GFP, UAS::Cdon, UAS::CdonΔFnIII(2) or UAS::CdonΔFnIII(3) DNA. After DNA injection, the eggs were injected with *Cdon*^{ATG} MO into the yolk and the embryos were let develop until 26hpf **(b)**. **c)** GFP expression was detected in the retinal and hypothalamic domains of the injected embryos. α -HA immunostaining in *rx3::Gal4* embryos injected with UAS::Cdon DNA confirmed localized expression of Cdon in the retina of injected embryos **(d, e)**. Note the membrane localization of the HA-signal (red arrows in **e**). **f)** Quantification of optic stalk *pax2.1*-positive domain in embryos co-injected with different UAS DNAs and *cdon*^{ATG} MO at 26–28hpf (* $p<0.05$, ** $p<0.01$; Student's *t*-test). The number of embryos analysed in each case is indicated in each column and are as follow: control/UAS::GFP, n=8; *Cdon*^{ATG} MO/UAS::GFP, n=9; control/UAS::Cdon, n=12; *Cdon*^{ATG} MO/UAS::Cdon, n=20; control/UAS::CdonΔFnIII(2), n=13; *Cdon*^{ATG} MO/UAS::CdonΔFnIII(2), n=17; control/UAS::CdonΔFnIII(3), n=10; *Cdon*^{ATG} MO/UAS::CdonΔFnIII(3), n=17. Error bars represent s.e.m. Note that the expansion of the *pax2.1*-positive optic stalk domain generated by *cdon*^{ATG} MO injection was less evident than that reported in Fig. 4l, likely owing to MO injection at two-four cells' stage (see Methods). Scale bar: 100 μ m.



Supplementary Figure 11. *cCd^{ATG}* MO efficiently interfere with *Cdon* expression. **a, b)** Carboxyfluorescein conjugated chick *Cdon* MO (*cCd^{ATG}*) and control MO were targeted by electroporation in the optic region of HH8 chick embryos and analyzed at HH14 when *Cdon* is abundantly expressed in the eye (compare MO distribution in **a** with *in situ* signal in **b**). Targeted eyes were dissected and processed for WB analysis with antibodies against mouse *Cdon* normalized to α -tubulin levels **(c)**. **c, d)** *cCd^{ATG}* MO interferes with *Cdon* levels in the targeted eyes (n=8 electroporated eyes for each condition) (N.D.V, normalized density values). oc, optic cup. Scale bars: 200 μ m.



Supplementary Figure 12. Cdon overexpression modifies Shh protein distribution in the optic stalk neuroepithelium. **a-l**) Confocal analysis of coronal sections at the level of the optic vesicle of HH14 chick embryos electroporated at HH8 with a construct carrying mCherry (**a-c**), Cdon (**d-f**), or its deleted derivatives Cdon Δ FnIII(1-2) (**g-i**) and Cdon Δ FnIII(3) (**j-l**). Sections were immunostained with antibodies against mCherry (**a**), Cdon (**d, g, j**) and Shh (**b, e, h, k**). Shh protein localizes to Cdon expressing cells (**d-f**) in which it accumulates at the basal region of the neuroepithelium (**e, f** white arrow). A similar accumulation is observed in the presence of the Cdon Δ FnIII(1-2) construct (**g-i** white arrow) but was hardly detectable in mCherry or Cdon Δ FnIII(3) expressing cells (**b, c** and **j-l**). **m**) Coronal section of HH14 chicken embryo stained with Hoechst at the level of the optic vesicles to illustrate the areas selected to quantify Shh immunostaining in Cdon overexpressing cells. **n**) The graph represents the quantification of Shh accumulation in electroporated cells. *p<0.05, **p<0.01, ***p<0.001; Student's *t*-test. Note that there is no statistical difference in Shh levels of Cdon and Cdon Δ FnIII(1-2) overexpressing cells (proximal, *p*=0.074; distal, *p*=0.7). The number of quantified sections (1 section per embryo) is indicated in the graph labels. The number of analysed embryos is the following: Cherry, *n*=7; Cdon, *n*=11; Cdon Δ FnIII(1-2), *n*=14 and Cdon Δ FnIII(3), *n*=9. Error bars represent s.e.m. Scale bar: 50 μ m.



Supplementary Figure 13. Cdon promotes morphological changes of the basolateral end-foot of neuroepithelial cells. Confocal analysis of coronal sections at the level of HH14 chicken optic stalk electroporated at HH8 with a construct carrying mCherry (**a-c**) Cdon (**d-f**), or its deleted derivatives CdonΔFnIII(1-2) (**g-i**) and CdonΔFnIII(3) (**j-l**). Sections in (**a-l**) were immunostained with antibodies against Cherry (**a**) Cdon (**d, g, j**) and Shh (**b, e, h, k**). Note how cells electroporated with Cdon (**d**) or CdonΔFnIII(1-2) (**g**) present an enlarged basal end-foot when compared to mCherry or CdonΔFnIII(3) neuroepithelial cells (**a, j** arrows). This enlarged end-foot is a preferential site of Shh accumulation (**e, h**). Note the filopodial-like structures in the basal end-foot of Cdon expressing cell (**d**, asterisks). Scale bar: 10 μ m.

Supplementary Table 1. List of the morpholinos used in this study

Name	Sequence (5'-3')	Modification	Specificity	Working concentration
<i>MO</i> ^{ct}	CCTCTTACCTCAGTTACAATTATA	3'- Lissamine	-	160uM-200uM
<i>cdon</i> ^{ATG}	ATAATCTCAGGCCACCGTCCTCCAT	3'- Lissamine	<i>Danio Rerio</i>	160uM
<i>cdon</i> ^{spl8}	ACTGTATGAACCTTCTCACCTGC	-	<i>Danio Rerio</i>	200uM
<i>cdon</i> ^{spl11a}	AGGAACTAGAGAATGAATCCAACCA	-	<i>Danio Rerio</i>	200uM
<i>cdon</i> ^{spl11d}	GCAGTAACCTCACCTGGCTCAAGGT	-	<i>Danio Rerio</i>	200uM
<i>cdon</i> ^{spl14}	GACGGTACTTCAGACTCTCACCTT	-	<i>Danio Rerio</i>	400uM
<i>cMO</i> ^{ct}	CCTCTTACCTCAGTTACAATTATA	3'-Carboxyfluorescein	-	2mM
<i>cCdron</i> ^{ATG}	CCGACTGCATAGCGCCGGACAGCA	3'-Carboxyfluorescein	<i>Gallus gallus</i>	2mM

Note: **a** and **d** in *cdon*^{spl11a} and *cdon*^{spl11d} MO denote splice “acceptor” and “donor”, respectively.

Supplementary References

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