

Fig. S1. Phylogenetic analysis of classical cadherins. Extended version of the tree in Fig.1. Dachsous cadherin proteins were used as an outgroup. The phylogenetic tree was constructed with the maximum likelihood method in IQ-tree. The number at the nodes indicates the bootstrap support from the maximum likelihood method.

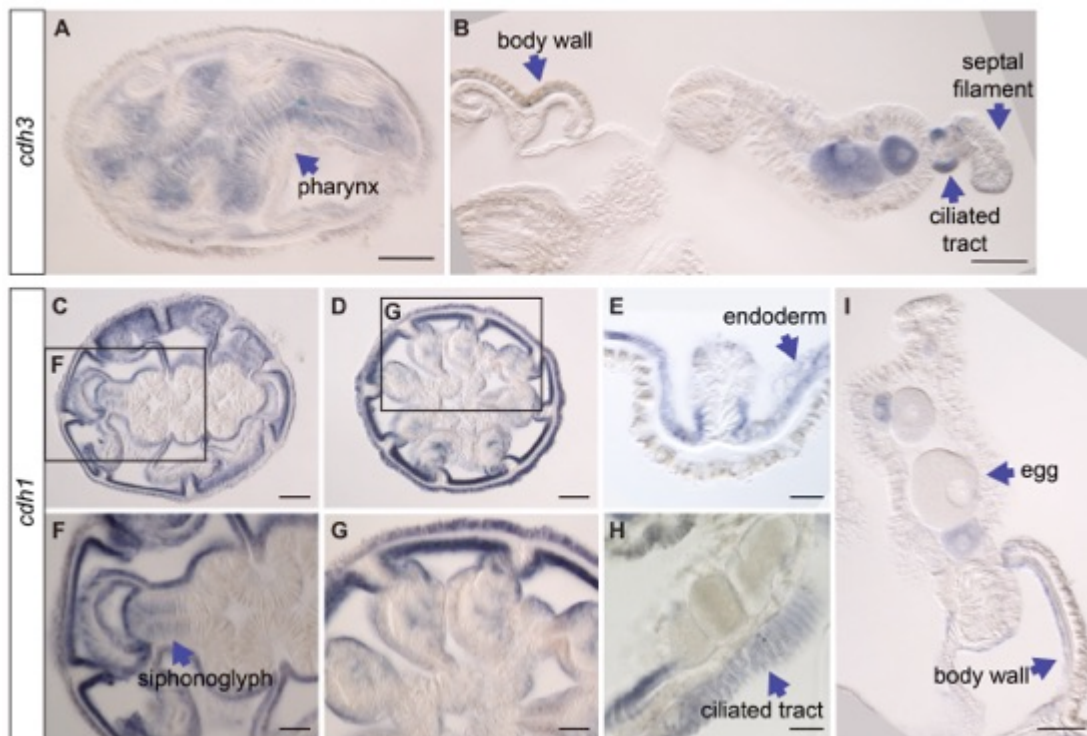


Fig. S2. *cdh1* and *cdh3* expression in adults and juveniles. (A-B) *cdh3* is expressed in the ectoderm of the pharynx, septal filaments and ciliated tract and in the oocytes. (C-I) *cdh1* is expressed in the endoderm, ciliated tract, ciliated lobe of the pharynx – siphonoglyph and small oocytes. Scale bar A-D, I: 100 μ m. Scale bar E-H: 50 μ m.

Cdh1	MSAGRLAAVLTTPLLFLLSLLKTFQLAKAQDTLIEVNFDEGRPARSSVYLFDS-SGDVFS	59
Cdh3	--MGLDGSASLGFVLVFTLLSLLTITGHAQTIESASVPENEPEGFRVFSFPSPSNEIYS	58
	* . . . * : : : : * . . . : : * : * . . . * . . * * : * * * * : : * *	
Cdh1	LYQA---DPTVPLLFQISEVGHVTSTQEIYEIIGKTNKYDLTVLQRPGETLGGIAITL	115
Cdh3	FFRALDTASQSALRLFDISEDGVVTKNPLVYTDGEENLYVLTVLRQRGMTEGGIAWTL	118
	: : : * . . . * : : *	
Cdh1	RITILDVNNFHPVFQSQGEHYEGFVKEGTAENTIVEGLEQCHATDRDTSGIRGYSIISG	175
Cdh3	RITVTDTNFQPTFGA--DLYLGYIAEAAQGTTVGGLEKCHAEDKDRSGIDRYEIVSG	175
	* * * : * . * * * : * * * : * * * : * * * * * * * * * * * * * * * *	
Cdh1	NEKGYFKVETVQIGSGVTSRKFLVLKTTGKPIVRDDNNPYIMLTVQVTDGGNPSHSGTAN	235
Cdh3	NERGYFVAETKTVG---AQKFLVLKATNTRIVRDPARPSITLTVRANDGGGL--HGTR	229
	* * : * * * * . * * * : * : *	
Cdh1	IRVNVEDANDQTPVFESSQYRETAENTPIQTSVLRVRATDKDDGTNGGIYYMKNPVNS	295
Cdh3	IQIDIQDTNPPVFQSEYTVTVGEDTPVMTSILRVRARDADIGRNGGIYYLRNTQ--	287
	* : : : : * : : : * * * * . * * * * : * : * * * * * * * * * * * * * * * *	
Cdh1	YFTIDAITGVIRVAKTLDYNARDKHTLYISARDRGDPPTSAAEATVEISLRENIQGWPLP	355
Cdh3	DFTIDAITGVIRPRLMLDFQSQQRTLEVLTARDRGSSPKAA-NVNVQVTRSDISGYPPV	346
	* *	
	Cdh3 antibody 1	
Cdh1	DS--ADPKENTKPYFP-QSRYTFSIREDFPPKALLVMRAADNDPIGPNKRLRYSLSGNG	412
Cdh3	VVPSSSDRNRPPVFEKSSFTLSIREDFPVNGAIQVVKANDPDAGSTNGQLRYSLSGN-	405
	: . . . *	
Cdh1	VSKFAIDPESGVVTLTDSVDYENTPNNHVDLTVTATDQ--GPGSLSATTQLLIEIQDVD	470
Cdh3	--NNFAIDSTSGVVTLQTQLEYKGNPAQDVIDLVVATDRNGQSGALSASVNLKIEVLDVD	464
	. : *	
Cdh1	ENKNSPRFDPQQAILEISENLKQNSLVTTVSATSDSDSVGNPSSPDGKVVYSIVGGTGLGV	530
Cdh3	DNNAPVFNPPQLELTVSEDSAVGRTIRRVSATDSD----DGSDGQVVYSIIQSGGLGV	519
	: * : *	
Cdh1	FRVDSNTGEVKVAVPSLDREGTSQYTLVVKASDNATFPRSSRLFLMINLLDEDDNFPYFS	590
Cdh3	FQVQATTGDLIVAAP-LDREKMSFYDLVIKAEDKATFPKSSNLYVMVKIQDVEDHFPQFT	578
	* : * : : . * * * : * * . *	
Cdh1	QPIYIAQVPENQPSGTFVTVVVGRADEGFNPSYTVITPGVPYKIEPSTGVIRTSLDQ	650
Cdh3	QPMYYAKAPEKSPENTFVTVVVDHDLGESVSYSI-TGASSFKIVPTSGLILTTGPIDL	637
	* * : * * : * : * : * . *	
Cdh1	SEL-STRELQVIV-RVSTAGSKTADGQVNITVISKVNRPPVFKNTPYSVKVPEEMGPLPN	708
Cdh3	TTEPSTYELVVTATSTNYGTTKRATGQVNVEITSKTESPPVFKNTPYAVSVPENQGSIAN	697
	: * * * * * . . . : * * * * * : * * . : * * * * * * * * * * * * * *	
Cdh1	LFCIAAVDSLSPVQYTLAPGADGLFEVDKDSGRHLTKNSFNENVDRYNLRIEARTSSV	768
Cdh3	LVCVAAIDTKGQPVYIYSIESRG-EPFGIDSKSGRFSLSQSFYETADKYRIQISAQSGTA	756
	* . * : * * * : . * * * : . *	

Cdh3 antibody 2

Cdh1	QEVA--SASLTVEVTEEKDLPKFSSDSYQLTVDESAAAGTTLAPGLLIIDSDTSSDQFDC	826
Cdh3	PNIMTSSSDVAITIKDEKDPQFSQSEYKVSVPEDASVRSTLSRGIRFVDEDTLSTQLEC	816
	: : * : : : : : : : * * * * * : : * : : * : : : * * * * * : : :	
Cdh1	SMEAITSLHTLYNFEVTQQSGRCFLRVQAGGKLD AHLASKYTFNVRATDRNFRNMFATAQ	886
Cdh3	SMEEMTSRIPLDYL SVVQDGGECKFVIE--KTLDTFVASKFTFDMKVTDKNFPGMFATK	874
	** : * * * : : * . * . * . * . * : : : . * : : * * * * * : : * * * * * : :	
Cdh1	VEVNVIDVNDHKPEFLQESYWLSVPSSTPAGSSLVTVQAEDMDIGTNAQVRYELLRQEN-	945
Cdh3	VEVTVTDNTNTYTPVFSRTSFWASKPDTLPTDTSVMQLSII DKDMGSLGEVTYQLIDPTVS	934
	** . * * * : . * * * : * : * * * . : * : : * : : : . * * * : . * * * : :	
Cdh1	-----SERFILNDNNQLSTASTLTPNVRYQLLIRASDSATRNPSSAQVPVYVSVYSPSE	999
Cdh3	AGETSGYDRFRVDDSGMIESTNILTANTLYKLQAKAKDGGSPALEATVDVFISVYPSD	993
	: * * : * . . : : : . * * . * : * : * . * : * . * . : . * * * : * * * * * : :	
Cdh1	SPIVFDKSSYNQNL PEDSSANTLVFTAKATRSGSSSGITYELVGGYKQIGEAMFSIKPDT	1059
Cdh3	TPVRF SQNPYSASIAENSPLNTEVFRATATKSGSSSGIAYSLVGGQIENGNTMFSIDS-S	1052
	: * : * . : . * . : : * * * * * * . * * * : * * * * * : : * * * * * : :	
Cdh1	GQVYL IKKLD FETKSYFPIAVRAKYSGGAI ELASEVVAKVTV DVNDNGPRFAFHESKST	1119
Cdh3	GRVLLLRLQDRERTKSYKLYVRGTYTGGSLTLATDVECLVTVTDVNDNTPLFTFDRV NKQ	1112
	* : * * : * * * * * . . : : * . * . * : * * * * * : * * * * * * * * . * * . . * *	
Cdh1	VVIDSFSAKDTQLVQARALDADSGSLGEVTYGIDGGRSTSNLFPNINVKTGMIFATREIL	1179
Cdh3	FVVDNYAPANTI IATLRAVDSDEGANAQVTMSIQGT-VPSNAPFTIDTPSNVLKTTTKLS	1171
	. * * : : : : * : . * * * * * . * : : * * * . * * * * * . : : : : * : : :	
Cdh1	YTQGS SYIIIVVATD GATDGSQKIQKFTVNVQVLDTPRPPSFPQKTY SAPVTETAGVGD T	1239
Cdh3	--TVIDYQITVRATDKG--SPPQYSETTVIVKVLNIQTTPVFGQAKYTVDVQENTKVGQQ	1227
	. * * * * * . . : : * * * : * * * * * * * * * . * * . * * : * * : * * :	
Cdh1	VTTVRAVYKPN AFLKYTFVSGNEDNTFCVNGFGIISVAKSLDREKVAGYTLGMRVTLGQ	1299
Cdh3	VISVKATYGD SNGLLQYSFVSGNLGDAFCIDSSGQITVAQPLDREVLPSYTLRVRVALGN	1287
	* : * * * . . * . * : * * * * * * * : * * * : * * * * * * : . * * * : * * * * * :	
Cdh1	HVDDTTVYVNLTDINDDAPHFTSAIYRRS I KEGLAEDTEILPPVIAVDHDFG SNGKILYS	1359
Cdh3	NEDFTEV FVSLTDINDDSPTFTKSVYEFFANEDISSGTS-IGKVAATDRDSGSHGQISYR	1346
	: * * * : * . * * * * * * * * * : * * : : * . : * * . * : * * * * * * * *	
Cdh1	ILSGVHPDWDK YFNIDSATGKIT--TKMTLDYETHKSHTL FIRAEDNGSPKRLSGIAQVD	1417
Cdh3	FLYASDIQSMDFDL DQTTGIIISLASGSLDYEDISMHVLFVRAEDNGAN-KLSAIAEVR	1405
	: * . . : . * : * . * * * * : : : * * * . * . * * : * * * * * : : * * . * * * :	
Cdh1	IDVIDRNDNSPVFAAAFYRAKISLGAVKGT SVLQVHATDLDSGQNGQITYSIIQGN EEEA	1477
Cdh3	IYLRDINDNDPKFSAASYHAKLSLDAPVLEHVQVTATDLDTANNGRIRYSIVAGNQEGA	1465
	* : * * * . *	
Cdh1	FTI-NEQGVILVDKSLTTVAADKFS LKVEARDKNASPRSGSVTVEINVYLPDGP PMFVVS	1536
Cdh3	FQVLT DNGLIRVAKSLTTVAASSFLLTLEAADSGDPERKGSVNVQVNVFLPDGPPKFVLD	1525
	* : . : * : *	

Cdh1	PVTVYVKEGVPANHRVAGVKAATSEALTYTLLSGNEAGMFRINPSTGSLDATRELDYEER	1596
Cdh3	PVIVNATEGIAANQRVAVAKAATSEALKYEILSGNTNDMFAINPSSGVILTTRELDYEEA ** * ..** : ** : *** .***** . * : **** . ** ***** : * : *****	1585
Cdh1	RRYELKIEARDTRDRSAMVELIIIVVNINDNKPTFVDIVDGQIDRKAIGTCSPTDIAEGE	1656
Cdh3	TGYIMNIIARDTRDRSASVQVIINVVNINDNEPMFPGETNGQIDRKVAGPFAPGFI---- * : * ***** * : * * ***** : * * . . : ***** . * : * *	1641
Cdh1	VITRLGAFDRD-GDEITFIVPDDVKDLFKIDSRGVVTAKKPIEDLPKIYFPNVKALDNGE	1715
Cdh3	-ATRLTAVDKDIGDRVYKISIEAENYFTIDERGQLICKNDLKGIASPFRFTIEARDGGL *** * . * : * ** . : : : : . : : * . ** . ** : . * : : : . : * . : : * * . *	1700
Cdh1	PPQETDVKVRLVVFHYRPDQKHVRVNVREDTPTGSVIATVRRYFPNGIVSLLLPEKANFS	1775
Cdh3	PQKVHTANVLLVFKYRPKQPVRVTVPETTRAGTVITRVPRYFPPTGEFSIVYPENTNFT * : . : * ***** : *** . * * * : * : * : * * ***** . * . : : * : * : * :	1760
Cdh1	VRANGDVILLTPLDYESQQFHRMTVREEL--GNQTNVDVDEVVVLDVNDNRPIWMERERL	1833
Cdh3	IDNDGNVTLNRPLDYEEIAFTLITVREKQASGPLENYIDVEITVLDVNDNAPVFTMISTL : : * : * * ***** . * : ***** : * * * : ***** . ***** * : : . *	1820
Cdh1	ARVNTNSRAGAQVYQLEARDEDDGSSGLVGYQLKSPSNDAKRKRSPQHPFTINPKTRQ	1893
Cdh3	GRVNSNSRAGATAFQLQARDLDSGNSGLIGFQLENIP-----TLFMINPLTRQ .*** : ***** . : *** : *** * . ** . ** : * : * : . * * * * *	1868
Cdh1	MEVAG-SLKDQRYDLDFVAFDYGIPRLTSDTITLNVDSAGQQLPPRFKVSYHFMVSED	1952
Cdh3	IEVGQPRQLTSRYGLDIIIPFDYKPSVNGTKATVDIE--TVQSPPVFNESYTFTVSER : ** . * : . ** . ** : : ***** * : . . . * : : : : : * * * * . : * * * * *	1925
Cdh1	AKYLSLVGII LARSISGARLDYKIVSGNVGDKFIAMGDGRILLNSLLDFERDQTQYNLKV	2012
Cdh3	APTMTKIGDVTAVSVSGARLSYTIIEGNTGDKFLAKDNGDIVLNSLLDFERDQSVFNLKV * : : * : * * : ***** . * . : . ** . ***** : * . : * : ***** : : *****	1985
Cdh1	KATEQIPDGLDSTVDVKIDVINANDHFPYFDQQLYSVQIPESTAVGVLVQEVTAKDCDCL	2072
Cdh3	EAKEQIPKGLSSEVDVTITVINANDHFPYFDQQLYSVQIPESTAVGVLVQEVTAKDCDCL : * . ***** . ** . * * * . * ***** . ***** : * : : : ***** . ** : : ***** : *****	2045
Cdh1	SSCTCSPGFLTYISIEPSKEQGGKFYIDPATGKISVSVVALDYEDQRYHLLKVYATDKGKKS	2132
Cdh3	SDCTCQVGLKYSVEAG---TSFD-IDQTGAIVVARTLDYETSKVQLKVMASDQGEKV * . ***** . * * . ** : * . . * * * * : : ***** . : : ***** * : * : *	2100
Cdh1	FQGLCFVNVTLTNVNDNRPTFLKSAYEFRVAEGAATGESLAIVVAVDADGDAVT---YSK	2189
Cdh3	FTAVTFVVTLEDTNDNAPVFKRNDYLFRTADASTGSMIGAVIARDQDQDDIEKVRYSV * . : * * * * * : . ***** . * : . * * * : . * : * . . : * * * * * : * *	2160
Cdh1	AGGALQFSVDQSTGVITLNSALDP-NKNQYTLQVMAKDSGGLTSTVSVTFNVADANNVNP	2248
Cdh3	VS-GTEFNVNTEGTGLTVAKDLSTGAKSEYSMEIRATDSTK-SNDARVRVNVEYKNMYRP . . . : * . * : . ***** : . * . * . : : : : * . ** . . . * . * * * * *	2218
Cdh1	QFTNCGTVSIRENDPRDTKITQLTATDADRQNGQITYSIEDASSQTLFSIEPRTGVVRS	2308
Cdh3	EFTKCGKATIQENLLKGQLIATVTATDRDQGRNGEVEYKIVPVGQDFFFTINNKTGEVIT : * : * . . : * : * * . : * : * : ***** * : * : * : * : * : * * * * : * * * * *	2278

Cdh1	LTSLDRENKDSYNAI IKAEDGSSKQDESERLLWYCYLTINVEDVNDNRPYFLAAKYFGSV	2368
Cdh3	TSSLDRETKATYTVI IITAEDGGHGKDPARLMSYCFLEVEVQDVNDNYPFITRAYLGS I :*****.* :*..**.****. :* :***: **:* :*:***** * *:: *::**:	2338
Cdh1	FSSAPNGSNILTVQATDADSGSNAKIKYALLDSAGGLFRLDSSGILRTNTNPARLQLETG	2428
Cdh3	QNTKPIGTSVLTVSATDPDAGDNAKITAFKSPNDKFEIDSTSGDIRTKVALTGTK---D . : * * : : : **.**** * : * . **.****. : . . : . : ** : ** : . : : .	2395
Cdh1	KKLLLEVSAKDVESIAGTQPGKPKTYTTQIEILVSNEEPPKFSQQVYTASINENMETGST	2488
Cdh3	VNEKMTVVASNTEAIQGGDAN-NRDRETEVTIYITDLAPPVCDKNLFTARILESLSVNSD : : * * . : . * : * : . . * : : * : : * * . : : : * * * * *	2454
Cdh1	VTRITATSSTGAEISYENVDTNPRAKILFRVQPDGYIITGDRPDYERG---TTYNMQFA	2544
Cdh3	VLKVSAQAPGGKSIVYSPVKANADIDEKFSVETNGQIKTASQLDYEQLSPGDKTFKLQVR * : : * : * * . * . * . : * * . * * : * * * * . : * * * * . * : : * .	2514
Cdh1	AKDKKTLLYSTVKVVINIIDVNDVSPAFLLAINTRNARVLENKPAPTKVISMKAIDDDGS	2604
Cdh3	AQEENTNLYSTCSVAITLEDVNDKPTFDLG--NYDARVRENAPIGTTVITIKATDRDTG * : : : * * * * . * . : * * * * . * : * * . . : * * * * * * . * : : * * * * .	2572
Cdh1	EPHRRVTY--EMKDNPNFQIDASTGMITTKTTLTLDREVTPKYDVEVTAKDGVN-----KES	2657
Cdh3	DAG-VVTYFLKAGSDEHFAIDVNSGTLTTKKSFDREGQSLFSVIVVIARDKGNP GALSEE : * * * : . : : * * . : * : * * : : * * * * : . * * * * * * . *	2631
Cdh1	AILYITVVDQNDQPPVFAPKSYAISVPEDSPIGTSVLDIYATDADVGENAKITYFISKGD	2717
Cdh3	VAVKVLVVDENDSPQFDQAEFQTSVSESATIGTSILEVVATDQDIGDNAKLEYFISGGD . : : * * : * . * * * . : * * * . : * * : : * * * * : * * * * : * * * * * * *	2691
Cdh1	PEGKFSIVTS---PVKGLVNGKLDKFETKSSYTLVETATDGKFSDTAVVTVTIQDVND	2773
Cdh3	GRFWFAVQTISKGRTYGEVQVDARLDFETKSSYTDVTATDGRFSATTRVLITITDAND . * : : * . * * : * . : * * * * * * : * * * * * * * * * * * * * * *	2751
Cdh1	LPPVF-----SSPLYESRIQENTGPGAGVVMVTASDIDSPTISFSLDDRKDYFQIT	2825
Cdh3	IVPFMFTLTPTLLSPIYTGRVSEMTGSGVEVLKVYAVDTDSPNIQYTLGSS-SYFTI- : * : * * * * * . * : * * * * * . * : * * * * * * . : : : . . * * *	2809
Cdh1	PIRASGPGNVWVDIRTGSKQLDREESPVKVFVTVIANDGKHTAQAEIRVNLTDVNDNAPR	2885
Cdh3	--AARQEGGKFGVGIISTGSQPLDREATPIFSFNVLAKDGVHTGSAYIEINVTDINDNQPR * * . : * * * * * : * * * * : * . * : * * * * * . * . : * * * * * * * *	2867
Cdh1	FPASPYIGYVEENKPSGTSVMYIQAVDDDDPLAGGNAKLSYELTDSAGDKFSIDPLSGLI	2945
Cdh3	FPNSLYVGYVEENKAAGTSVMYVQAHHDDDDPYLGGNAEIRYTLTDNAGGKFKIDANTALV * * * * : * * * * * * : * * * * * * * * * * * * : * * * . * . * . * * * . : . * :	2927
Cdh1	KTKVTFDREQTPNKFKVRVKATDAGNPRLSASVDGIIHVSDANDHKPKFTEKFRGVSVAE	3005
Cdh3	TTEEILDRETSFNSFTITVLATDQGANKLSTTKVATIYVTDANDHAPVFTKRIFRGTVSE . * : : * * * : * . * . : * * * * * : * * : : . * : * * * * * * * * : : * * : * :	2987
Cdh1	NAPPGYSVLRVTATDEDVGPNAEFVVFVVQGNDPHAFYIDPFNGTVLVSGILDYEEKKEY	3065
Cdh3	DVRPGYVVTVSATDTDGPNAELEFVVTHGNEPAAFYVDPSKGTVHVSGILNYTLRKS Y : . * * * * * * : * * * * * . * * * * * : * * : * * * * * * * * * * * * * * * * * *	3047

Cdh1	TITLTVADRGMPLQGDDETAYVVEILDANDNAPEFIPKIYNASVLEDVGARQPVLTVTA	3125
Cdh3	NLTVTVSDRGMPLVSDNSPAYVLITITDANDNAPIFIPNQYNKTVAEEDLAVGSPVVVTA	3107
	.:*:**:*:** * .:.* **:* * ***** **: * * * * .:.* .:.* **:	
Cdh1	VKDSGPNGNFTFAIDPRSDPDDAFTIEPNPNNASIGIIRTRVPLDQEKTPSFHLKVTAT	3185
Cdh3	VDYDSGDNAKFVFDITG-GNPDDLFEVVPNPDPNSSLGIVRTRLPLDRETTPIHLEITAK	3166
	** ** * .:.* * * .:*** * : **:*:*:**:*:**:*:**:* * .:.* .:.* :	
Cdh1	DAGGLQGEGERINVIDVNDNGPWFVPPFFVQGQIKEGVSARQFVTKLKAYDPDAFVKDQV	3245
Cdh3	DTGGLTGKAHVWLTLLDVNDNGPWFQPPFFVQGIKENVNVKQFVTKVSANPDPTKNGAP	3226
	*:** * .:.* * .:.*:**:**:** * **:*:**:* * .:.*:**:.* ** * : :	
Cdh1	ITFSIYNGTVGENFKLDPVSVTNEVDLHSYGVFDREAAPVWKIGIEAVDNGPKPKQNF	3305
Cdh3	FTYAIYNGTVSGNFADFIATITNVTTDMSSSGTFDRETTTWTIGIAGTDS-GRPAKSNF	3285
	:*:**:**.* ** * * .:.* * .:.* * * **:* * .:.* ** .:.* * .:.* :	
	Cdh1 antibodies 1 and 2 (against extracellular domain)	
Cdh1	TYVYVDVLDVNDNAPKDGSLLIIVNAYDGNFTGGVIGKPYQDDDFDGDENTYELNSQSP	3365
Cdh3	TYVYVDVQDDNDNEPCDGRMTIIVNSYNGKFRGGPIAKTYIRDADYDGDVNTYTLQSQTG	3345
	***** * ** * * * : **:*:*:** * * .:.* **:* * ** * ** * * * * :	
Cdh1	GSYFRVNEGNGDITAAPMIPMGEYNLKIRVTEK-----DSPSTVTSSVRVLVRR	3415
Cdh3	GNFTVDTTTGEISAAKDI PVGEYSLVISVTEVNTGNPPRANEVNFPKVTISRATVIVRD	3405
	*:** * * : .:.*:** **:*:**.* * ** * : * .:.* ** .:.* :	
Cdh1	IDKEAVDNGVAVEFTDMRKVGYFVGDYKGFEDVLASTLGVPTGDIKIFSVQKAHDNGLA	3475
Cdh3	ITSKAVSNSVALQISDMRKVEYFVGDYHDVVVVELSRMFGVSSSGIEVFSVQPSPIKUMA	3465
	* .:.*.* .:.*:**:**:** **:*:**.* .:.* * : ** * .:.*:**:** * : : *	
Cdh1	VVVFFT-VAAKDSYMPHWDVSVKLVDAAKPLESLGLKVSRLGMDECSKGNVQSVGVAKN	3534
Cdh3	LDVQFAVKTGSDYEYTKPYDVIRVVTNDRERLTLNLGLKVTSTIGIDMCALER--ERVGKGIN	3523
	: * * : .:.*.* **:* :.* : * .:.*:**:** * * : .:.* * * .:.* *	
Cdh1	ILVRSSNFSVASGDYGVKVPAPASSLTIVSIDILPKCLYEAVFPPEKRCRPHNPCLHGGKC	3594
Cdh3	VVETSSAYKIASGDYGVKVPAPASSITLVSMDDVLRDKYVTIIEPGKNCNENPCLNGGTC	3583
	: : ** : .:.*:**:**:**:**:**: : * : : * * .:.* .:.*:**:** * :	
Cdh1	YETVPDCPGFVCKPTGYHGPLCEMTTRTFYGNYSIWLPKLMTYSLSDLEFEFMKTADG	3654
Cdh3	HDTVPAQ-WRVCQPRGYRGPHCEQTRTRFRGTSYIWLPKLTAYDIRELSFEFTTEFKDG	3642
	::** ** **:* **:* ** * ** * * .:.*:**:** * .:.* * * * : ** * :	
Cdh1	LLVYQGPREGANGLKDFIAVVLRRGGRVELFVSLGLDPVTVKMDKGPRLDDGEWHTVQV	3714
Cdh3	LMLYQGPLKPGDNNGAKDFLAVFLDEGLVVRVSLGYEPITINMTRRPNLNDKEWHTVQI	3702
	*:**:** : * ** **:*:**.* **:* : ** * : **:* : * .:.* ** **:* :	
Cdh1	LRNMKD---IEI IIDRCSTALLEHKPDGTVVENRKSCHVYGRMLGRSVFLDGFGLQIGG	3771
Cdh3	IRDVIDRKMIRVIIDRCQSAQIV-EENGRVFEKRDTCETGRVKGRSVYLNFGPLQIGG	3761
	:*:* * * .:.*:**:**.* : : * * .:.*:**:** : ** * **:*:**:**:** * :	
Cdh1	VSNPNMDFPDIPYTGFKGCVRNIKDNHNLVDLKNPLKVVNAPEGCQLASACPE-CKNDGY	3830
Cdh3	VET-DLTFIGITTTGFRGCIRNIIDTEKMYDLRNPVKVVNAPEGCTLAGTCPNNCNDKGY	3820
	* .:.* : * .:.* **:*:**:** * .:.*:**:**:**:** * .:.*:** * .:.* **:	

Cdh1	CEP-LMARDSICVCPNGYSKGKHCGRGKASYLLASSFTEYLVAARRRRREVVPPPTEIFN	3889
Cdh3	CEPSLMAGKSMCVCDLGYTGRACNDRSEANYYLENSFSQFLLTGIRARRELIQPPVPLMN	3880
	*** ** .*:***: **:*: *:.*:*.* ** .***:***: . * ***: ** . : **	
Cdh1	RFYTTLALQVKLDEDATNVVFLASNRMGTEFQRVDVKDSKIRYVLRGARMVLVSFPQL	3949
Cdh3	EYYTHINLQVKLDPGKDCVLFSSNSLGTEFNRLDVKDHMLRYIFRLGDRMKVLSIPQY	3940
	.:** : ***** .:.*: **:*:* ***:**:* ***:** * ***:**	
Cdh1	NVTDGVYHSVIVRRHGDYAIMQLDYSGYVIGSLHSQRTLLDMSGGEIFSGGLPNITIVRI	4009
Cdh3	NISDGKYHSVMVNRREGNYAEMQIDYRAKMAGTTGGVQKLLNMGGGSIFTGGLPNITEVRV	4000
	*:** ***:**.*.*:* **:* . : * : . : **:*.*.* ***:***** **:	
Cdh1	IEAIVENDGSAVISTNVRN---DG---DGYAAD-----	4036
Cdh3	VEAIVQSGGDVILRTEDGKVLTSGIGVGGGMSFGAGSSVTLITIGSGVLTQRNILDSQSL	4060
	:***:..*..:.*: : . * . * : .	
Cdh1	-----VGGVHVR-----N	4044
Cdh3	FVRGIYKNGTVLYGSSSSSTFGMNVDDQGIPFKSSDTSSNGNGGVQISQGNPMTYGAGIQ	4120
	***: : :	
Cdh1	LQLSGPLNLVSRKRRASGTVSVLGDFFGGCIAGTSVNGANMESDPSIKVHRQNVLDGCPCL	4104
Cdh3	WTLSNPGRTOVGAGNSGGAVEVIGDMEGCTATNRFQGVSLDSPDEVRRQNVKGCPCA	4180
	.* . .:*:* ** * . .:*..*.* ***:** * ***	
	transmembrane	
Cdh1	SNFCANGGTCVDAMPYICAPGWTGPLCTIVVTAPPVGER-GTPFMHPAVIAIILLVML	4163
Cdh3	EGFCENGGTCVDGTPPYCLCSPGWTGPTCVLIVTAPNPGQRPGRVVSFFVIACVAVLL	4240
	..** *****. ***:* ***:** *.* ** * : : * ** * : **:	
	region	
Cdh1	<u>AIFIIMGAVILKRRPEPVVYADSTDTGHVHDNVRLYHDDGGGEEDNLGYDITKLMKYTY</u>	4223
Cdh3	<u>AVMVMGAVLLKRTPPPVI-PVMVEDGHVHDNIRPYHDEGAGEEDNFGYDITQLMKYTY</u>	4299
	*:***:***:* ** * : . : ***:** * ***:***:***:***:***:	
Cdh1	<u>IETTIAPPSVAPSK-----ASEDKISTSSDQPLLO</u>	4253
Cdh3	<u>VEGGYGGGGGYGGGGGYGDCTGGAAFGSAYAADGGGKGLSGVVEEVMVAEEKPLLO</u>	4359
	:* . . : . : : : **:	
Cdh1	<u>GRPPDAV--FGLTGKEPGPKPKMEGDDVGDFITTRVKITDREVFVLADELHIYRYEGD</u>	4311
Cdh3	<u>GAMEGYQQHGIIT--ITRRMMNADSVVGNFINSRVGEADREYILSYDALHIYRYEGD</u>	4417
	* . .*: : : . ***:**:* ***:** * ***:** * ***:**	
Cdh1	<u>DTDVDLSEIEPDEE-DEEYEQEFDLQKQWGPKFKLAKLYEDVDE</u>	4356
Cdh3	<u>DSDIDDLSELGSDEGGDDAEQSFDFLQDWGRKFENLNKIYNLDD-</u>	4462
	*:***:***: ** * : : ***.***:*** ***:** * ***:** *	

Fig. S3. Protein alignment of the full-length sequences of the Cdh1 and Cdh3. Cdh1 and Cdh3 antibody epitopes and transmembrane protein regions are underlined and recognized with the colors. Transmembrane regions were identified with the SMART protein domain annotation resource. Alignment was performed with the Clustal Omega Multiple Sequence Alignment tool.

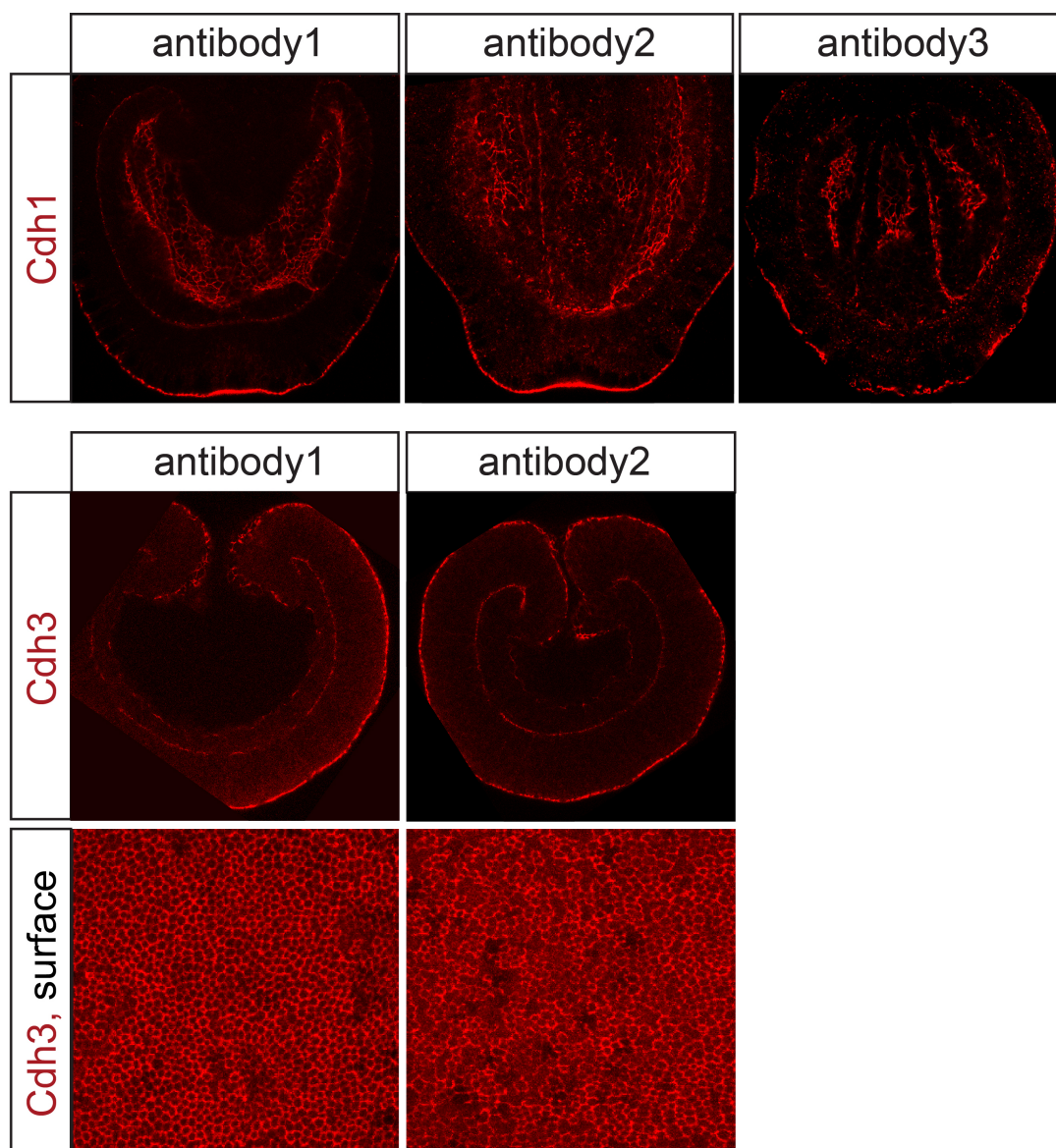


Fig. S4. Custom antibodies generated in different animals against different protein domains result in the same staining pattern. Cdh1 antibody1:domain1 (extracellular) and Cdh1 antibody2:domain1 were raised in rats; Cdh1 antibody3:domain3 (intracellular) was raised in a rabbit. All three custom Cdh1 antibodies show the same staining result. Monoclonal Cdh3 antibody1 and Cdh3 antibody2 were generated against different Cdh3 peptides and result in the same staining pattern.

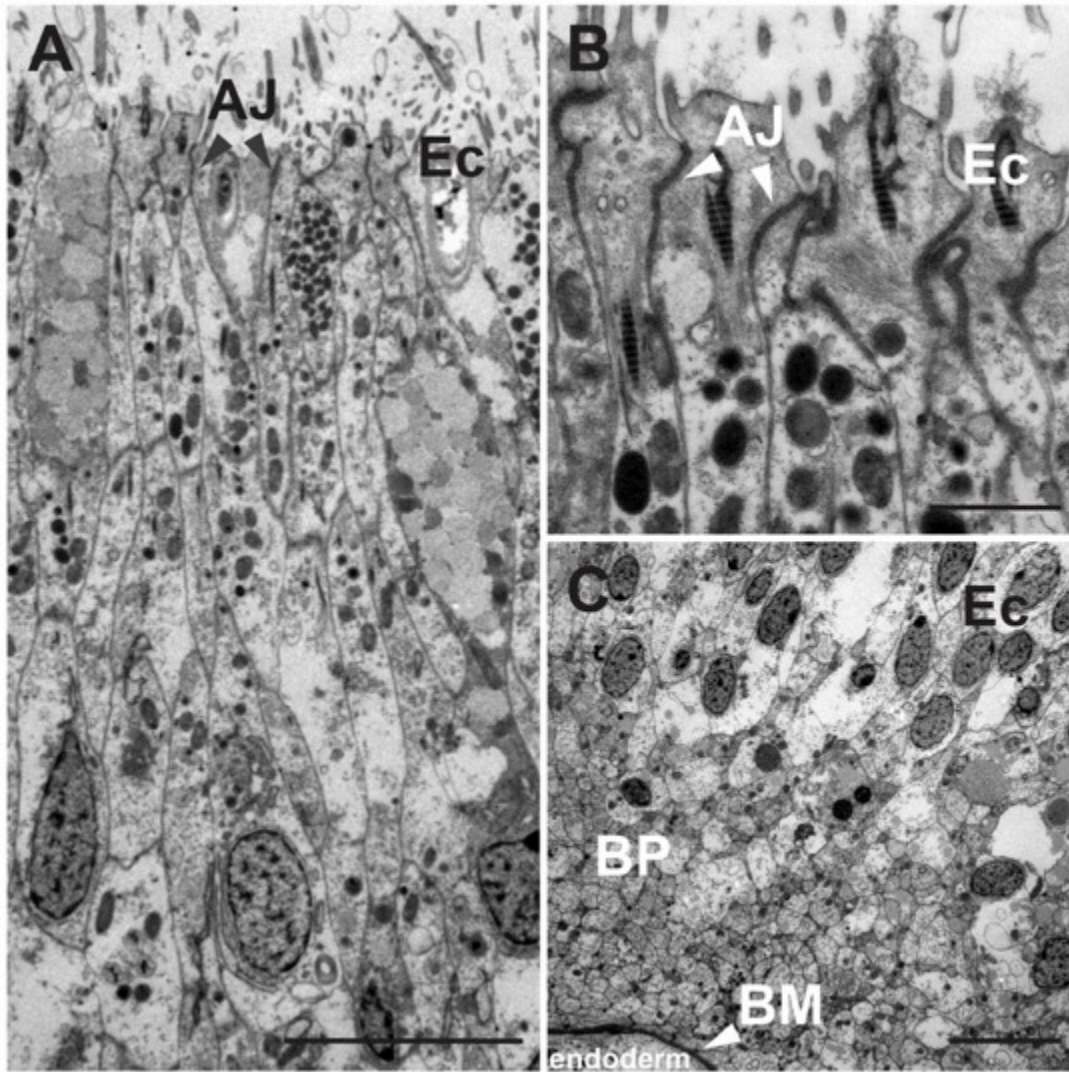


Fig. S5. TEM of the ectoderm of the apical organ. (A,B) Apical side of the ectodermal cells of the apical organ. (C) Basal side of the apical organ ectoderm. AJ apical junctions; Ec ectoderm; BP basal protrusions; BM basal membrane Scale bar A,C: 5 μ m. Scale bar B: 1 μ m.

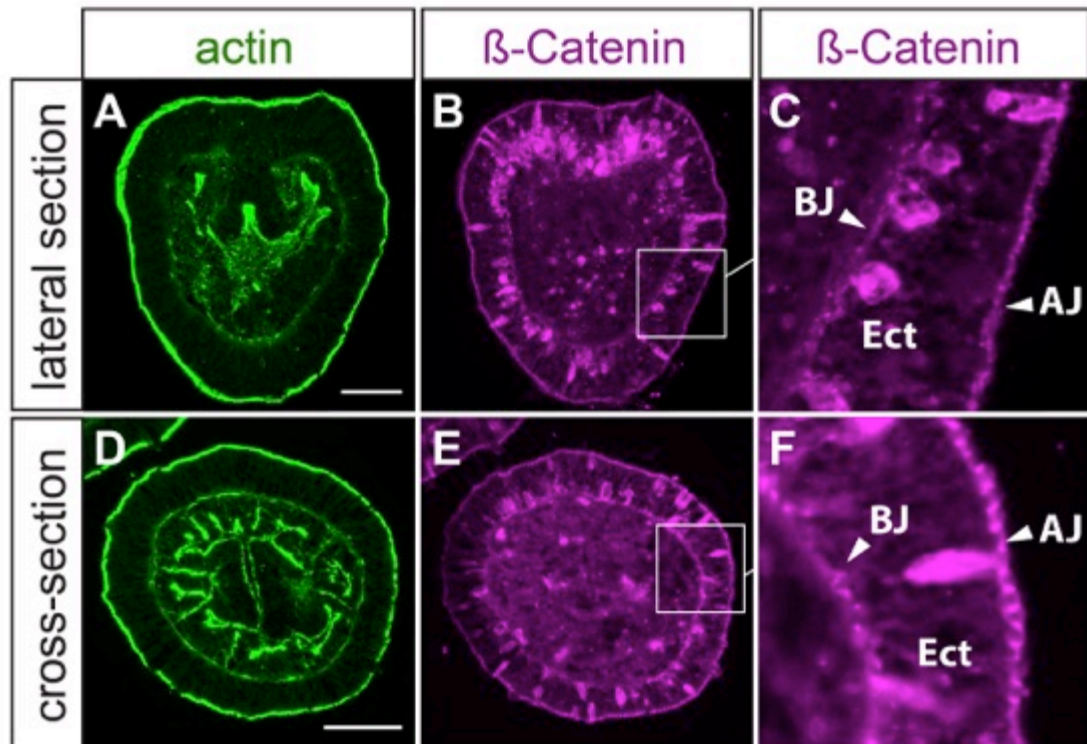


Fig. S6. β -Catenin is localized to the apical and basal adhesion junctions of the body wall ectoderm. β -Catenin antibody and phalloidin staining of vibratome sections of the 4 day old planula to exclude a possible penetration problem of the β -Catenin antibody. Please note that in vibratome sections, the β -Catenin antibody detects the basal junction in the ectoderm, but has a tendency to show unspecific staining in nematocytes and other subcellular structures. Scale bar 50 μ m.

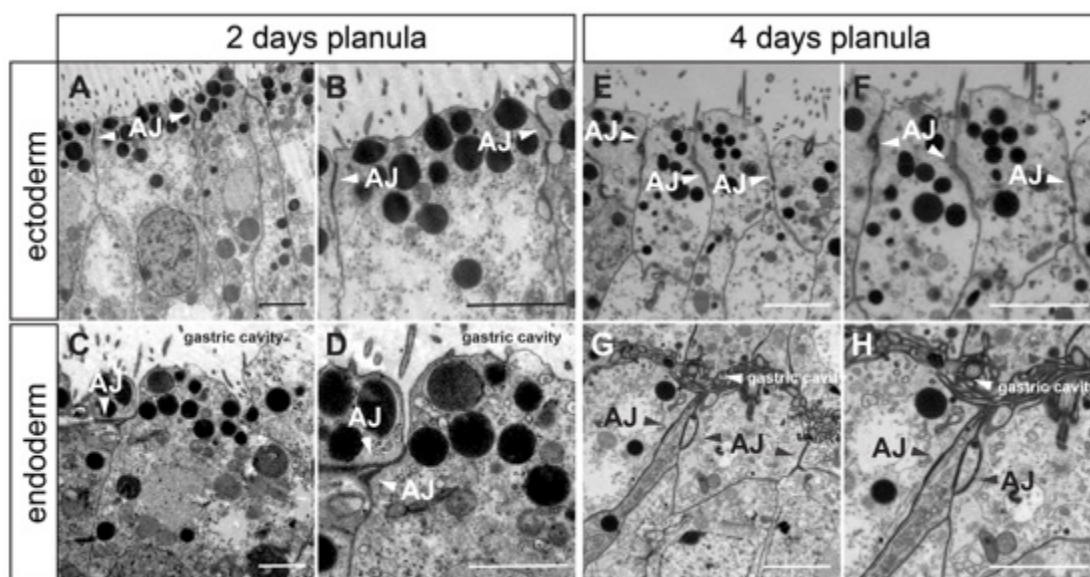


Fig. S7. TEM of the apical adherens junctions of the ectoderm and the endoderm. (A,B) ectoderm, 2 dpf planula; (C,D) endoderm, 2dpf planula; (E,F) ectoderm, 4 dpf planula; (G,H) endoderm, 4 dpf planula. Scale bar 2 μ m.

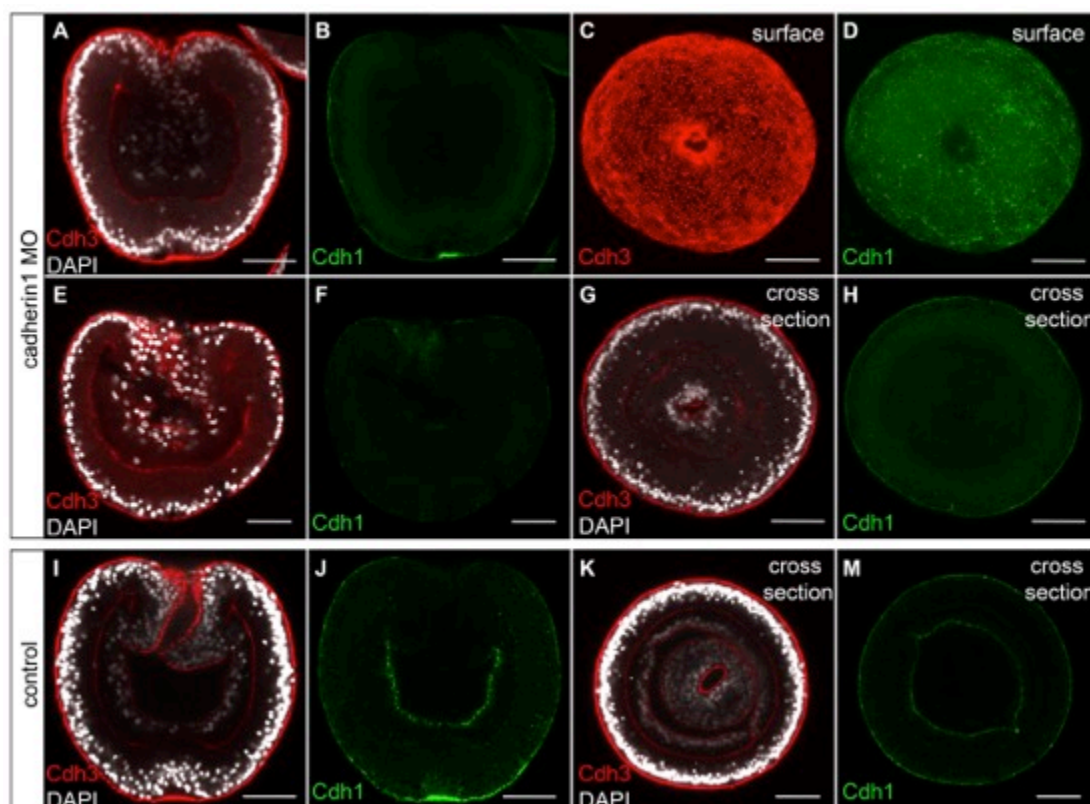
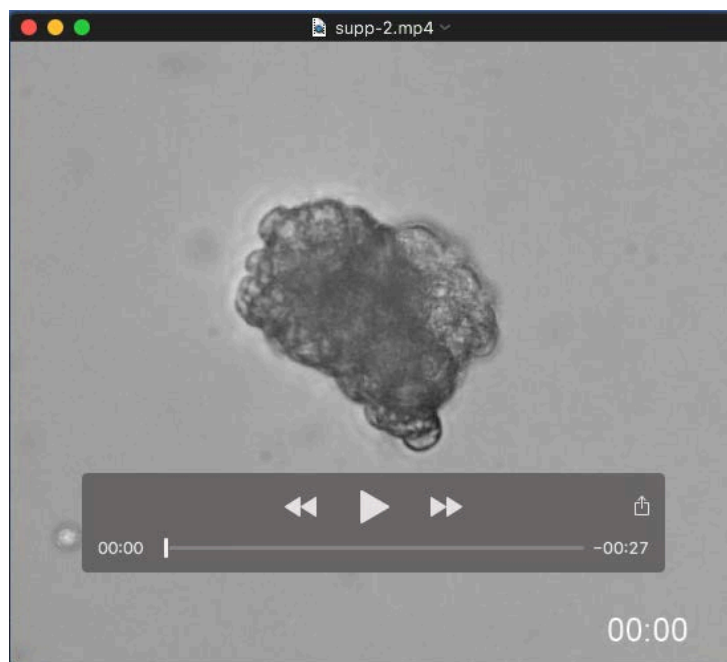
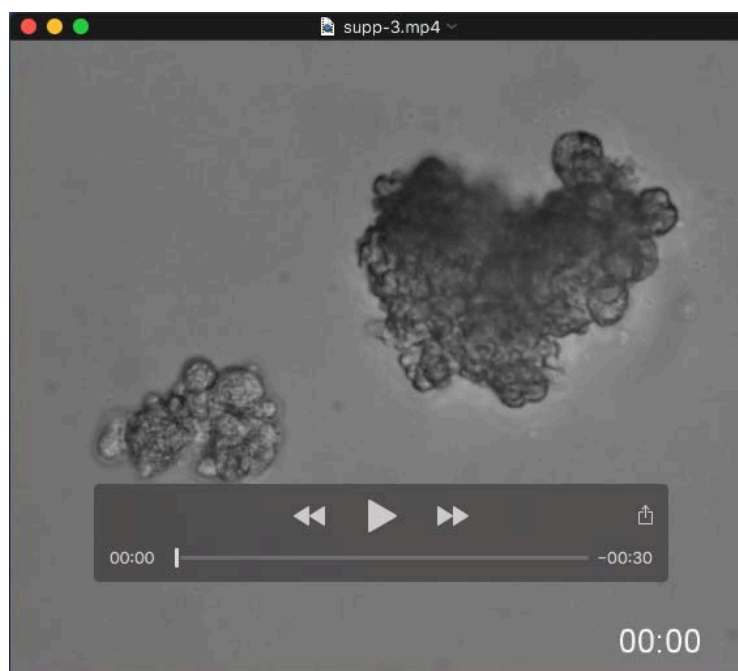


Fig. S8. Cdh1 and Cdh3 expression upon Cdh1 MO knockdown. (A-H) Cdh1 MO injected planula. (I-M) Uninjected control planula. Scale bar 50 μ m.



Movie 1 Std MO aggregate development. Time indicates hours and minutes.



Movie 2 Cdh3 MO aggregate development. Time indicates hours and minutes.