

## Supplementary Materials for

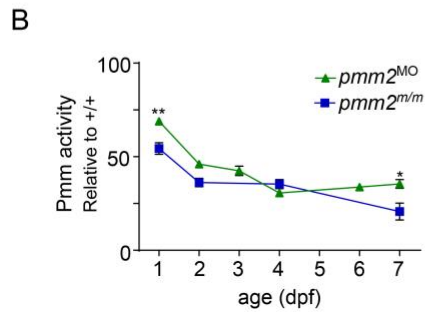
### **Protease-dependent defects in N-cadherin processing drive PMM2-CDG pathogenesis**

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**A**

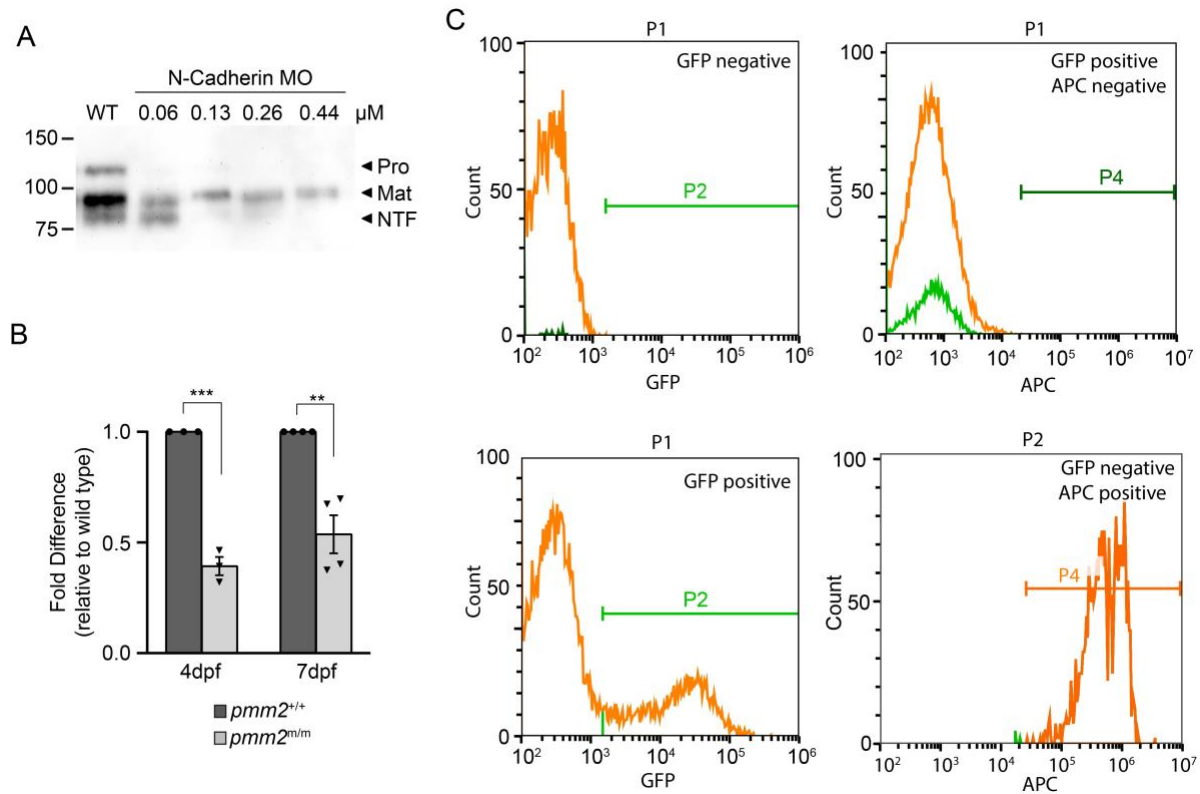
Human <i>PMM2</i>	---MAAPGPALCLF <b><u>DVD</u></b> GTLTAP <b><u>R</u></b> QKITKEMDDFLQKLRQKIKIGVVGGSDFEKVQEQLG
	LCLFDVDGTLTA RQK T +M +FL KL+Q++K+GVVGGSD +K++EQLG
Zebrafish <i>pmm2</i>	<b><u>MSGSTVDSTTLCLFDVDGTLTAARQ</u></b> KATADMHEFLSKLKGRVKVGVVGGSDLDKIKEQLG
	e1 le2
Human <i>PMM2</i>	NDVVEKYDYVFPENGLVAYKDGKLLCRQNIQSHLGEALIQDLINCLSYIAKIKLPKKRG
	+DV+++ DYVF ENGLVAY+ GKL QNIQ++LGE ++Q+ IN+CL+Y++KIKLPKKRG
Zebrafish <i>pmm2</i>	<b><u>DDVVD</u></b> RVDYV <b><u>FA</u></b> ENGLVAY <b><u>RFGKLH</u></b> SVQNIQAYLGEDILQEFINFLNLSKIKLPKKRG
	le3 e4 le5
Human <i>PMM2</i>	TFIEF <b><u>R</u></b> NGMLNVSPIG <b><u>R</u></b> SCSQEE <b><u>R</u></b> IEFYELDKKENIRQKFVADLRKEFAGKGLTFSIGGQ
	TFIEFRNGMLNVSPIGRSCSQ+ERIEF+ELDKKE IR+ FV+ L++EFAGKGL FSIGGQ
Zebrafish <i>pmm2</i>	<b><u>TFIEFR</u></b> NGMLNVSPIG <b><u>RSCSQ</u></b> GERIE <b><u>FFELDK</u></b> KEKIRETFVSVLKEEFAGKGLAFS <b><u>IGGQ</u></b>
	le6 le7
Human <i>PMM2</i>	I <b><u>S</u></b> <b><u>F</u></b> DVFPDGWDKRYCLRHVENDGYKTIYFFGDKTMPGGNDHEIFTDPRTMGYSVTAPEDT
	ISFDVFP+GWDKRYCL VE D Y+ I+FFGDKTMPGGND+EIF DPRT+G+ V +PEDT
Zebrafish <i>pmm2</i>	<b><u>ISFDV</u></b> <b><u>F</u></b> PEGWDKRYCL <b><u>GIVEKDSYGH</u></b> I <b><u>HFFGDK</u></b> TM <b><u>PG</u></b> NDYEIFVDPRTIGHEVKSPEdT
	le8
Human <i>PMM2</i>	RRIC-ELLFS
	+RIC EL FS
Zebrafish <i>pmm2</i>	GRICRELFFS



**Fig. S1.**

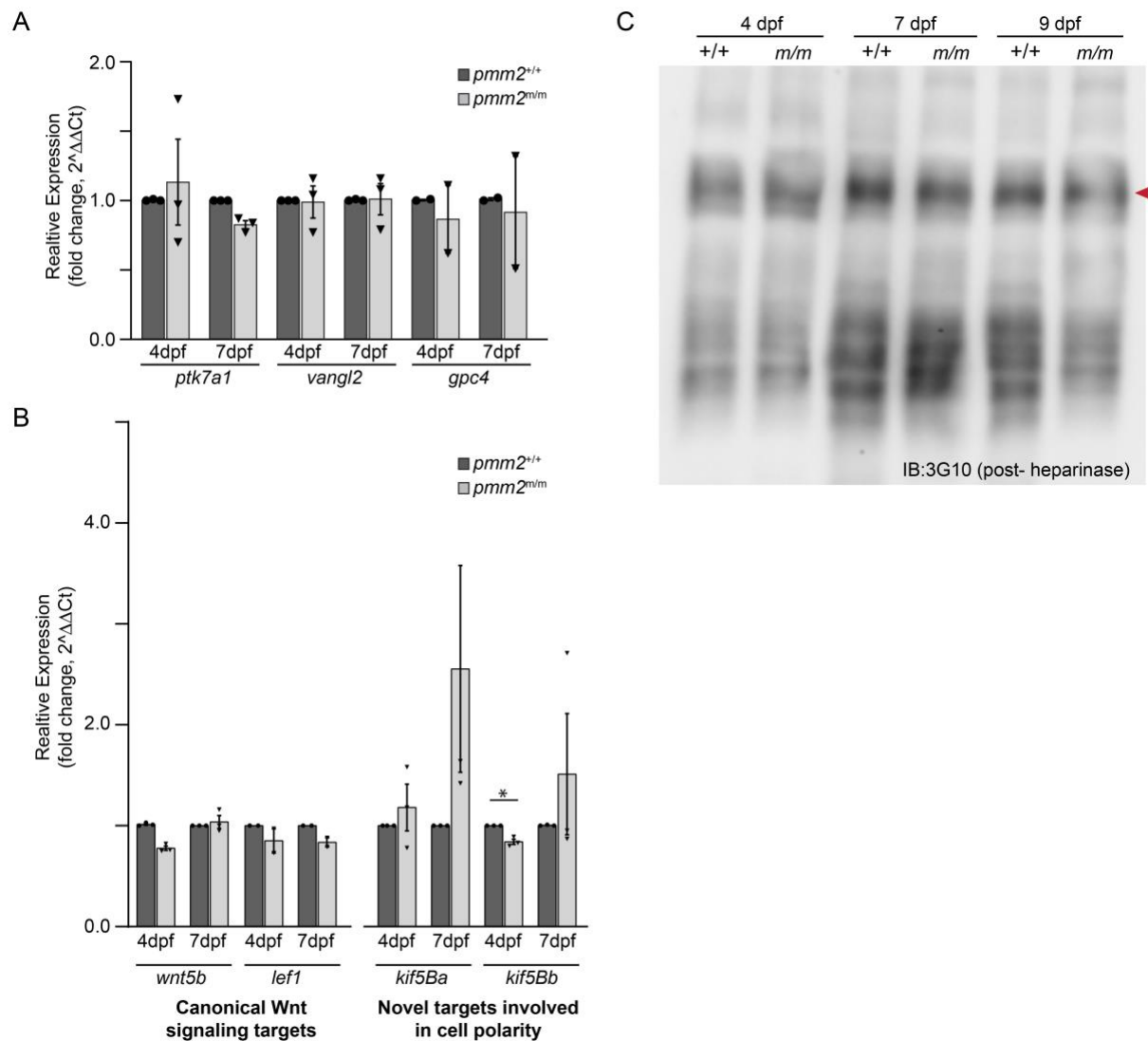
**A** Alignment between zebrafish and human *pmm2* enzymes. Bolded underlined residues comprise the substrate binding site, two of which are lost in the one functional *pmm2* transcript made in mutants. Bolded red residue indicates site of the zebrafish mutation

**B .** Graph compares Pmm2 enzyme activity in morphant and mutant embryos 1-7dpf



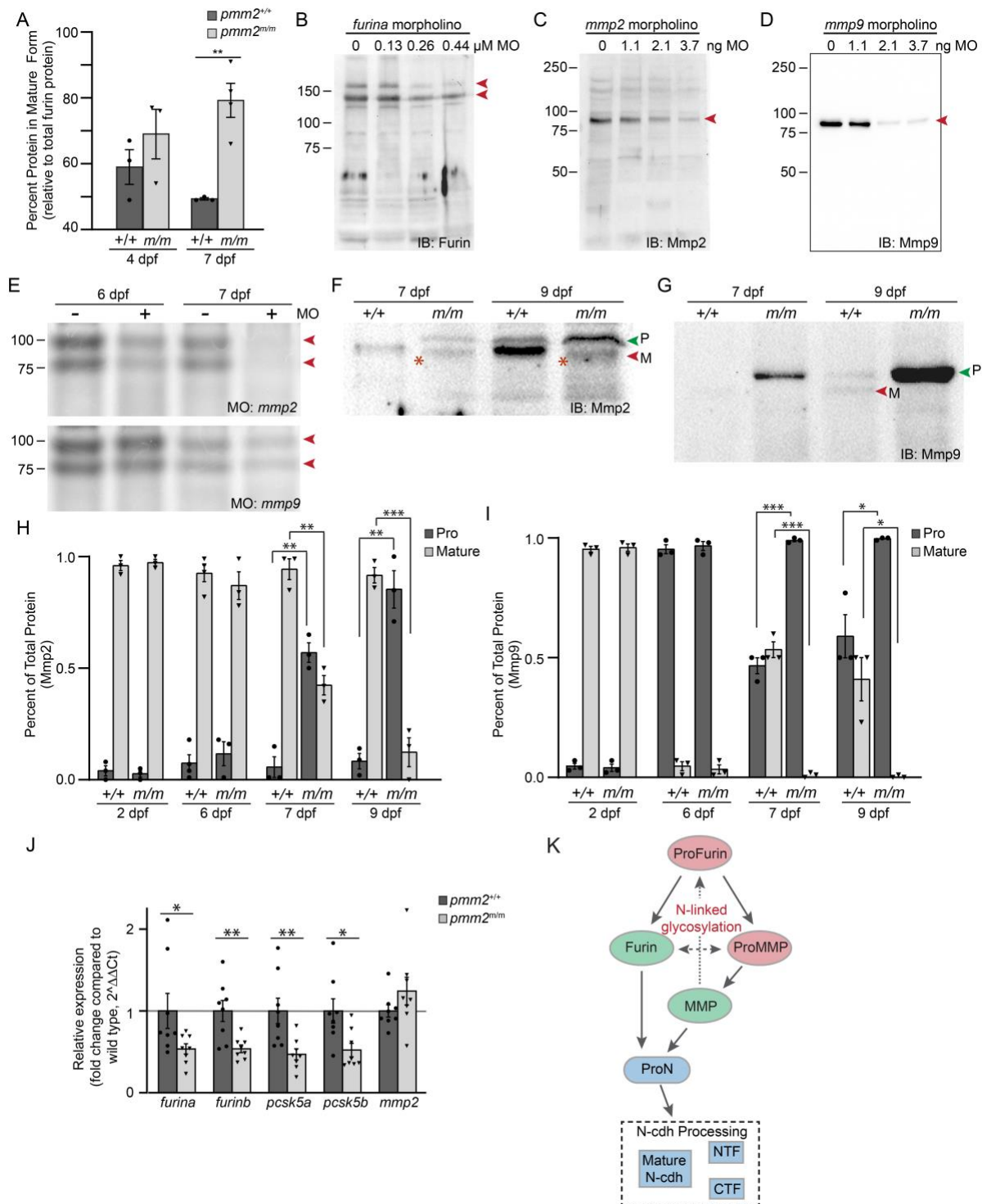
**Fig. S2.**

- A** Representative western blot of N-cadherin knockdown in 4dpf embryo lysates show antibody specifically recognizes the pro, mature (Mat), and N-terminal fragments.
- B** Quantitative RT-PCR of N-cadherin transcript abundance show steady state levels are reduced in *pmm2*<sup>m/m</sup> embryos compared to *pmm2*<sup>+/+</sup>.
- C** Representative plots from Flow Cytometry analyses of cell surface N-cadherin show controls for gate selection of GFP<sup>+</sup> and N-cadherin<sup>+</sup> cell populations.



**Fig. S3**

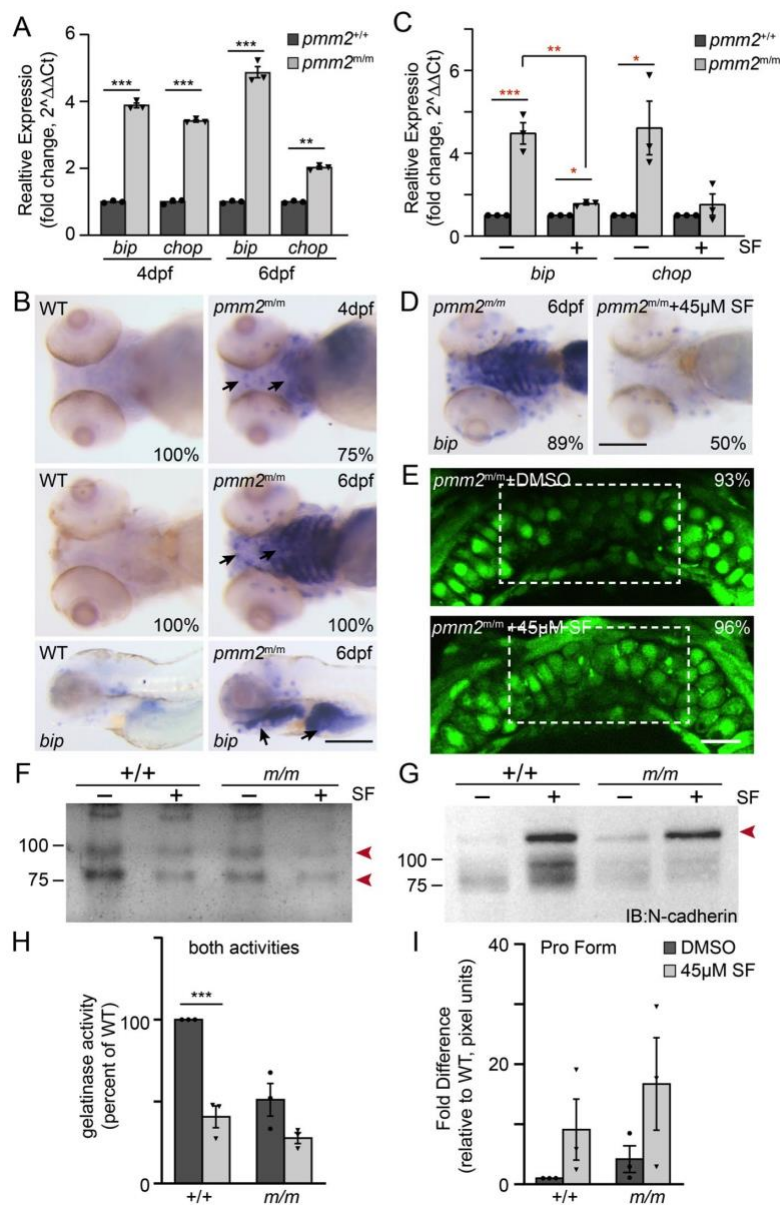
- A,B** Quantitative RT-PCR of transcript abundance of several targets of (A) non-canonical or (B) canonical Wnt show steady state levels are not statistically altered by *pmm2* deficiency. The one exception is two novel genes involved non-Wnt mediated cell polarity, *kif5Ba* and *kif5Bb*, which are highly variable in *pmm2*<sup>m/m</sup> embryos.
- C** Representative western blot of global glypican analyses in embryos 4,7,9dpf show very little difference in global abundance between *pmm2*<sup>+/+</sup> and *pmm2*<sup>m/m</sup> embryos.



**Fig. S4.**

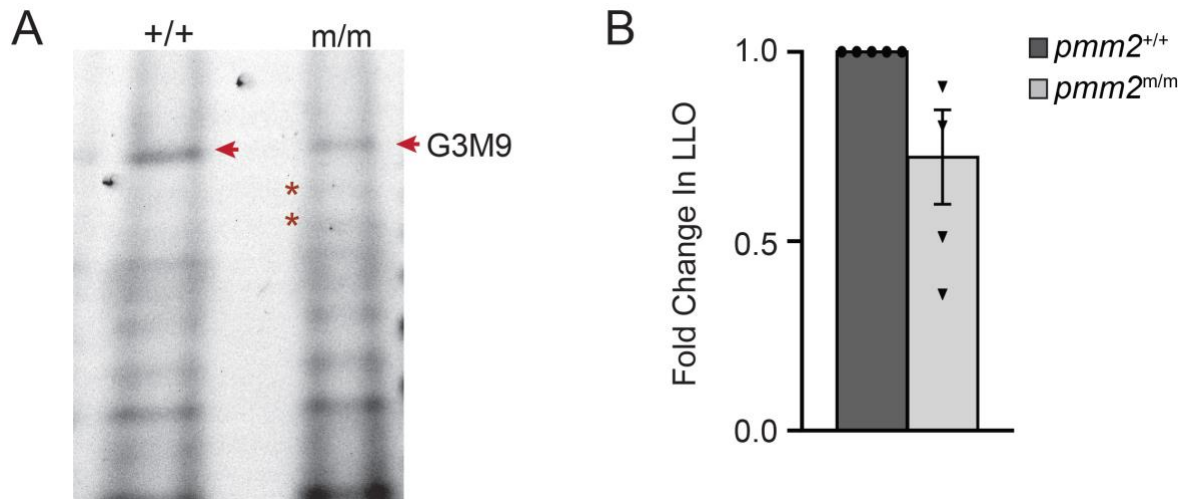
**A** Graph quantitating the percent of total furin protein present in the mature form on western blots from embryonic lysates shows increased abundance of mature furin relative

- to total protein at 4 and 7dpf in *pmm2* mutants. n=3 experiments of 15 embryos per sample per experiment. Error=SEM, Student's t-test, \*\*p<0.01
- B Representative western blot of *furina* morpholino-mediated knockdown in 4dpf embryo lysates show antibody specifically recognizes protein bands consistent with pro and mature forms.
- C Representative western blot of *mmp2* morpholino-mediated knockdown in 4dpf embryo lysates show antibody specifically recognizes protein bands consistent with pro and mature forms.
- D Representative western blot of *mmp9* morpholino-mediated knockdown in 4dpf embryo lysates show antibody specifically recognizes protein bands consistent with mature form.
- E Gelatin zymography of 6 and 7dpf embryo lysates in which either *mmp2* or *mmp9* expression was morpholino inhibited show Mmp2 contributes the majority of gelatinase activity at these stages. Red arrows highlight key activities.
- F,G Enlarged images of western blots shown in Fig 4. Pro (P) and mature (M) forms of either Mmp2 or Mmp9 are indicated with arrows. The shift in size of mature Mmp2 (noted at both 7 and 9dpf) is indicated with red stars
- H,I Graph quantitating the percent of total protein present in the Pro (dark box) or Mature (light box) form of either Mmp2 or Mmp9 on western blots of *pmm2*<sup>+/+</sup> and *pmm2*<sup>m/m</sup> embryonic lysates 2-9dpf. n=3 experiments of 15 embryos per sample per experiment. Error=SEM, Student's t-test, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001
- J Quantitative RT-PCR of transcript abundance of multiple protein proconvertases and *mmp2* show steady state levels of several enzymes is reduced in *pmm2*<sup>m/m</sup> embryos compared to *pmm2*<sup>+/+</sup>. n=5-6 experiments of 10-15 embryos per sample per experiment. Error=SEM, Student's t test, \*p<0.05, \*\*p<0.01.
- K Schematic summarizes model of interactions between PCs (like furin), Mmps, and N-cadherin indicating that N-glycosylation impacts this relationship and N-cadherin processing.



**Fig. S5. Sulphoraphane treatment does not improve cartilage phenotypes.** A) qPCR analyses of *bip* and *chop* transcript abundance at 4 and 6 dpf. n=3 experiments with 15 embryos per sample. Error=SEM, Student's t-test, \*\*p<0.01, \*\*\*p<0.001. B) In situ hybridization for *bip* 4 and 6 dpf. Black arrows highlight increased staining in *pmm2*<sup>m/m</sup> embryos. Percent values indicate the number of scored embryos exhibiting pictured phenotype. n=15-20 embryos over 4

experiments. Scale bars= 100µm. C) qPCR analyses of *bip* and *chop* transcript abundance at 6 dpf show SF treatment reduces their abundance. n=3 experiments with 15 embryos per sample. Error=SEM, Dunnett's test, \*p<0.05, \*\*\*p<0.001. D) In situ hybridization for *bip* 6dpf show SF locally decreases transcript abundance. Percent values indicate the number of scored embryos exhibiting pictured phenotype. n=15-20embryos over 3 experiments. Scale bars = 100µm. E) Confocal analyses of *flil1a*:EGFP positive cartilages show no improvement following SF treatment. Percent values indicate the number of scored embryos exhibiting pictured phenotype. n=16 embryos over 3 experiments. Scale bars = 10µm. F) In gel zymography shows SF treatment further reduces gelatinase (Mmp activity in both *pmm2*<sup>+/+</sup> and *pmm2*<sup>m/m</sup> embryos. Red arrows denote key activities mediated by Mmp2. n=3 experiments with 15 embryos per sample per experiment. G) Graphic quantitation of zymography analyses of SF treatment. n=3 experiments with 15 embryos per sample per experiment. Error=SEM, Student's t-test, \*\*\*p<0.001. H) Representative western blot of N-cadherin processing shows SF treatment increases abundance of Pro N-cadherin in both *pmm2*<sup>+/+</sup> and *pmm2*<sup>m/m</sup> embryos. n=3 experiments. I) Graphic quantitation of western blot analyses of Pro N-cadherin in SF treated embryos. . n=3 experiments with 15 embryos per sample per experiment. Error=SEM, Student's t-test, \*\*\*p<0.001



**Fig. S6. LLO levels trend down in *pmm2* mutants but the reduction is not statistically significant.**

- A Representative gel of LLO analyses by FACE. Red asterisks highlight increased abundance of two species, likely assembly intermediates, in *pmm2*<sup>m/m</sup> embryos
- B Quantitation of LLO abundance in *pmm2*<sup>+/+</sup> and *pmm2*<sup>m/m</sup> embryos 6dpf.

qPCR	<i>mmp2</i> for	GGCGAGTTCTGTAAGTTTCCA
	<i>mmp2</i> rev	TCATCTCGACCCTGAGAGGT
	<i>mmp9</i> for	ATCTGTGTTTCGTGACGTTTCC
	<i>mmp9</i> rev	CATCCGCTAGCTGTGTGTTG
	<i>mmp13</i> for	TCCAGCGATGTGAGTCTGAG
	<i>mmp13</i> rev	TCCAGCTTTCCAGACACCT
	<i>mmp2</i> for	CATGGATGGAGAAGCCGACA
	<i>mmp2</i> rev	AGCAGACCATCCTTGCCATC
	<i>furina</i> for	CACCGATCCCAAGTTTGCAC
	<i>furina</i> rev	GACACGACGACTCCTTGTCC
	<i>furinb</i> for	ATGGTTTCGTGAGTCACGGG
	<i>furinb</i> rev	TGAACCCCTCTATGGCTGGA
	<i>furina</i> for	CGATGTTAACGATGGCGACC
	<i>furina</i> rev	CTATTGGTGTAGCCGTCGCA
	<i>pcsk5a</i> for	AACCGGTGGGCAGTCAAAAT
	<i>pcsk5a</i> rev	CACTAGCCCACCTATCTGGC
	<i>pcsk5a</i> set 2 for	AGCCGTGTCCTTCATACTGC
	<i>pcsk5a</i> set 2 rev	TGGGTCTTCCACCTCTCCTT
	<i>pcsk5b</i> for	TCACTGTTTCATGCGACGGTT
	<i>pcsk5b</i> rev	TCAAGATACCAGGGCTTGCG
	<i>mmp2</i> for	GGCGAGTTCTGTAAGTTTCCA
	<i>mmp2</i> rev	TCATCTCGACCCTGAGAGGT
	<i>mmp9</i> for	ATCTGTGTTTCGTGACGTTTCC
in situ		
	<i>bip</i> for	GTGTAAAACGACGGCCAGTAG
	<i>bip</i> rev	TTCACTTACCTACTGGGCCC
	<i>chop</i> for	GTGTAAAACGACGGCCAGTAG
	<i>chop</i> rev	TTCACTTACCTACTGGGCCC

**Supplemental Table I. Sequences of primers used in this study.**

