#### **Supplemental Information**

Table S1. qRT-PCR primers and shRNA sequences.

## Figure S1. The expanded lipidomic composition of sea urchin and mammalian LLC-PK1 cilia.

HPLC-MS/MS quantification and chromatograms of diverse sterols from ciliated sea urchin embryos (**A**, **B**) and LLC-PK1 cells (**C**, **D**).

(\*) =  $P \le 0.05$ , Student's t test.

See also Figure 1 and Figure 4.

# Figure S2. Cilia-associated oxysterols cause SMO to accumulate in cilia and activate the HH pathway through the CBP.

(A) Ciliary (ARL13B, red) and nuclear (DAPI, blue) immunofluorescence of NIH/3T3 cells stably expressing mouse SMO-EGFP or SMO<sup>Y134F</sup>-EGFP treated with vehicle (ethanol) or 30  $\mu$ M 7 $\beta$ ,27-OHC or 24(*S*),25-EC 30  $\mu$ M. Cilia-associated oxysterols cause SMO to accumulate in cilia. Y134F substitution in the CRD blocks the effect of 7 $\beta$ ,27-OHC but not 24(*S*),25-EC on ciliary accumulation. Scale bars: main, 10 $\mu$ m; insert, 1 $\mu$ m.

(**B**) Cilia-associated oxysterol probe synthesis. Copper(II) sulfate pentahydrate, CuSO4 5H2O; dichloromethane, DCM; 4-dimethylaminopyridine, DMAP; N,N'-dimethylformamide, DMF; ethynylmagnesium bromide, HCCMgBr; lithium aluminum hydride, LAH; manganese dioxide, MnO<sub>2</sub>; pyridinium chlorochromate, PCC; tert-butyldimethylsilyl chloride, TBS-Cl; tetrahydropyran, THF; and tetra-n-butylammonium, TBAF.

(C) Ciliary (ARL13B, red) and nuclear (DAPI, blue) immunofluorescence of NIH/3T3 cells stably expressing mouse SMO-, SMO<sup>D259R</sup>-, SMO<sup>N450D</sup> -, or SMO<sup>Y134F, D259R</sup>-EGFP. Substitutions of the CBP, and combined substitution in the CRD and CBP, block SMO accumulation in cilia. Scale bars: main, 10µm; insert, 1µm.

(**D**) Luciferase activity of ciliated  $Smo^{-/-}$  MEFs co-transfected with *Gli*-luciferase reporter and SMO SMOM2 with the indicated substitutions and treated with vehicle (DMSO), 1µg/ml SHH, or 100nM SAG. Data are normalized to luciferase activity of SMO-expressing cells treated with vehicle. Substitution of the CRD and/or CBP attenuates the activity of SHH and SAG.

(E) Ciliary (ARL13B, red) and nuclear (DAPI, blue) immunofluorescence of NIH/3T3 cells stably expressing mouse SMOM2-EGFP or SMO<sup>Y134F, D259R</sup>-EGFP. Combined substitutions of the CRD and CBP block SMOM2 accumulation in cilia. Scale bars: main, 10 $\mu$ m; insert, 1 $\mu$ m. (\*) = P  $\leq$  0.05, Student's t test.

See also Figure 1 and Figure 2.

Figure S3. Sterol and oxysterol synthases are expressed in HH-pathway associated medulloblastoma, and pharmacologic inhibition of HSD11β2 blocks accumulation of SMO in cilia and HH pathway activation.

(A) RNA sequencing of medulloblastomas from P35 *Math1-Cre*  $SmoM2^{c/wt}$  mice compared to control cerebella of P35  $SmoM2^{c/wt}$  littermates shows diverse changes in sterol and oxysterol synthase gene expression in HH-pathway associated medulloblastoma.

(**B**) qRT-PCR assessment of  $Hsd11\beta2$  expression in P35 control  $SmoM2^{c/wt}$  cerebella and Math1-*Cre SmoM2*<sup>c/wt</sup> medulloblastomas. Data are normalized to expression in control cerebella.  $Hsd11\beta2$  expression is 585±45-fold higher in HH-pathway associated medulloblastoma.</sup>

(C) Immunoblot of equal quantities of protein lysate from human HH (n=2), Group 3 (n=3) and Group 4 (n=3) medulloblastomas shows that HSD11 $\beta$ 2 expression is specific to HH-pathway associated medulloblastoma.

(**D**) Re-analysis of human transcriptome data SPR008292 indicates sterol and oxysterol synthases are expressed in all molecular subgroups of human medulloblastoma. Data are shown in arbitrary units.

(E) Immunoblot of lysates from  $Ptch1^{-/-}$  MEFs transduced with scrambled or anti-*Hsd11β2* shRNAs demonstrate of HSD11β2 without altering β-actin expression.

(F) Immunofluorescence of endogenous SMO (red) localization to cilia (ARL13B, green) in NIH/3T3 cells treated with vehicle (water),  $1\mu$ g/ml SHH or 100nM SAG, with or without 400nM CNX. Pharmacologic inhibition of HSD11 $\beta$ 2 blocks accumulation of SMO in cilia by SHH or SAG. Scale bar,  $1\mu$ m.

(**G**, **H**) Fluorescence of 5nM BODIPY-CYA 5nM (green) and nuclei (Hoechst, blue) in HEK293T cells transfected with SMO and treated with vehicle (DMSA), 50nM CYA or 400nM CNX. Data are normalized to vehicle-treated cells. In contrast to CYA, CNX does not compete with CYA-BODIPY to bind SMO. Scale bar, 10µm.

(I) Luciferase activity of ciliated NIH/3T3 cells co-transfected with *Gli*-luciferase reporter and empty vector or HSD11 $\beta$ 2 and treated with vehicle (DMSO) or 100nM SAG. Data are normalized to luciferase activity of vehicle-treated cells treated with empty vector. HSD11 $\beta$ 2 expression is not sufficient to activate the HH pathway.

(J) Luciferase activity of ciliated NIH/3T3 cells co-transfected with *Gli*-luciferase reporter and empty vector or HSD11 $\beta$ 2 and treated with 1 $\mu$ g/ml SHH and vehicle (water) or CNX. Data are normalized to maximal activity. HSD11 $\beta$ 2 expression increases the IC50 of CNX.

(**K**) qRT-PCR assessment of *Hsd11\beta2* and *Cyp27a1* expression in ciliated NIH/3T3 and LLC-PK1 cells. Data are shown in arbitrary units. NIH/3T3 cells express *Hsd11\beta2* and *Cyp27a1*, but LLC-PK1 cells, which do not transduce HH signals, do not express *Cyp27a1*.

(L) qRT-PCR assessment of  $Hsd11\beta2$  expression in ciliated  $Ptch1^{-/-}$  MEFs transduced with scrambled control or  $Hsd11\beta2$  shRNAs and treated with 1mM M $\beta$ CD vehicle or 30 $\mu$ M of the indicated oxysterols. Data are normalized to expression in cells transduced with scrambled shRNA and treated with vehicle.  $Hsd11\beta2$  knockdown (KD) suppresses  $Hsd11\beta2$ .

(M) qRT-PCR assessment of *Cyp27a1* expression in ciliated *Ptch1*<sup>-/-</sup> MEFs transduced with scrambled control or *Cyp27a1* shRNAs and treated with 1mM M $\beta$ CD vehicle or 30 $\mu$ M of the indicated oxysterols. Data are normalized to expression in cells transduced with scrambled shRNA and treated with vehicle. *Cyp27a1* KD suppresses *Cyp27a1*.

(\*) =  $P \le 0.05$ , Student's t test.

See also Figures 3 and 4.

#### Figure S4. The expanded lipidomic composition of medulloblastoma.

(A) Sterol mass spectrometry from  $SmoM2^c$  cerebella normalized to sample weight during development (white), adulthood (black) and tumorigenesis (grey and blue).

(**B**) Sterol mass spectrometry normalized to sample weight from P35  $Ptch1^{c/c}$  control (black) and *Math1-Cre Ptch1<sup>c/c</sup>* tumor mice (grey) shows that 7k-C and desmosterol are enriched and 24k-C and 24,25-EC are suppressed in HH-pathway associated medulloblastoma.

(C) Cholesterol mass spectrometry normalized to sample weight during development (white), adulthood (black) and in two different genetic models of HH-pathway associated medulloblastoma (grey and blue). In contrast to sterols, cholesterol is suppressed during cerebellar development and tumorigenesis.

(**D**) Oxysterol chromatogram from *Math1-Cre Ptch1<sup>c/c</sup>* tumor mice. (\*) =  $P \le 0.05$ , Student's t test. See also Figure 5.

### Figure S5. Pharmacologic inhibition of HSD11β2 blocks oncogenic HH pathway activation.

(**A**, **B**) qRT-PCR assessment of *Mt2* and *Nr3c1 Gli1* expression in P7 and P35 control *Hsd11\beta2<sup>c/c</sup>* cerebella, P7 *Math1-Cre SmoM2<sup>c/wt</sup> Hsd11\beta2<sup>c/c</sup>* and P35 *Math1-Cre SmoM2<sup>c/wt</sup> Hsd11\beta2<sup>c/c</sup>* medulloblastomas. Data are normalized to expression in control cerebella. Homozygous deletion of *Hsd11\beta2* does not alter expression of glucocorticoid target genes during cerebellar development or oncogenesis.

(**C**, **D**) Immunofluorescence for apoptotic cells (TUNEL, red) and nuclei (DAPI, blue) from P35 *Math1-Cre Ptch1<sup>c/c</sup>* medulloblastoma following 14 consecutive days of vehicle (water) or  $100\mu g/g$  CNX intraperitoneal injection. Pharmacologic inhibition of HSD11β2 does not increase tumor apoptosis, in contrast to glucocorticoid administration (Heine et al., 2011; Heine and Rowitch, 2009). Scale bar,  $100\mu m$ .

(E) qRT-PCR assessment of *Gli1* expression by ciliated ASZ *Ptch1<sup>ko/ko</sup> p53*-mutant mouse basal cell carcinoma cells treated with vehicle (water) or  $10\mu$ M CNX. Data are normalized to expression in vehicle-treated cells. Pharmacologic inhibition of HSD11β2 blocks oncogenic HH pathway activation in basal cell cancer.

(**F**) qRT-PCR assessment of *Gli1* expression by ciliated Med1 *Ptch1<sup>ko/wt</sup>* mouse medulloblastoma cells treated with vehicle (water) or 400nM CNX. Data are normalized to expression in vehicle-treated cells. Pharmacologic inhibition of HSD11 $\beta$ 2 blocks oncogenic HH pathway activation in medulloblastoma.

(G) HPLC-MS/MS measurement of CNX in control P35 *Math1-Cre Ptch1<sup>c/c</sup>* medulloblastomas 2 hours after intraperitoneal injection of vehicle (water) or  $100\mu$ g/g CNX. CNX crosses the blood brain barrier.

(H) Gross images of P21 control  $Ptch1^{c/c}$  and  $Math1-Cre\ Ptch1^{c/c}$  brains following 14 consecutive days of vehicle (water) or 100µg/g CNX intraperitoneal injection. Pharmacologic inhibition of HSD11β2 attenuates the growth of HH-pathway associated medulloblastoma caused by inactivation of PTCH1. Scale bar, 5mm.

(I) Sagittal H&E-stained sections of P21 control  $Ptch1^{c/c}$  cerebella and  $Math1-Cre Ptch1^{c/c}$  medulloblastomas following 14 consecutive days of vehicle (water) or 100µg/g CNX intraperitoneal injection. Pharmacologic inhibition of HSD11β2 reduces the number of small round blue tumor cells in HH-pathway associated medulloblastoma. Scale bar, 1mm.

(\*) =  $P \le 0.05$ , Student's t test.

See also Figure 5.





Α



SMO + 7β,27-DHC





SMO<sup>Y134F</sup>+ 24(S),25-EC

SMO + 24(S),25-EC



SMO-EGFP ARL13B DAPI NIH/3T3

Raleigh et al. Fig. S2





D

Smo<sup>2-</sup> MEF HH reporter activity



NIH/3T3



Ε SMOM2 SMOM2<sup>Y134F-D259R</sup> 1

Compound 2

NIH/3T3



CNX

0.0 Vehicle CYA



NIH/3T3

Κ

CNX (µM)



Raleigh et al. Fig. S3

BODIPY-CYA Hoechst

SNX



Raleigh et al. Fig. S4



#### Raleigh et al. Fig. S5