

Table S1. Antibodies and dilutions used in this study.

Antibody	Source	Catalog #	Lot #	Dilution
Primary Antibodies				
pan-ERM (IgM)	Gift from F. Solomon (MIT)	Hybridoma supernatant (13H9)		1:200
GFP	Molecular Probes	A11122	1828014	1:1000
ACTR-II (H-65)	Santa Cruz Biotechnology	sc-25451	B2009	1:2000
GAPDH	Abcam	ab9485	808033	1:1000
Phospho-Smad1/5/9	Cell Signaling Technology	13820	3	1:4000
Smad1	Cell Signaling Technology	6944	5	1:4000
Phospho-Akt	Cell Signaling Technology	4060	23	1:8000
Akt (pan)	Cell Signaling Technology	4691	20	1:50,000
Secondary Antibodies				
HRP-conjugated mouse anti-rabbit IgG	Santa Cruz Biotechnology	sc-2357	I2215	1:10,000
Cy2-conjugated goat anti-mouse IgG	Jackson Immunoresearch Labs	115-225-146	133889	1:200
Cy3-conjugated goat anti-rabbit IgG	Jackson Immunoresearch Labs	111-165-144	134845	1:500
Cy3-conjugated goat anti-mouse IgM	Jackson Immunoresearch Labs	115-165-075	115625	1:500

Figure S1. GFP expression is detected in transfected DSC neurons. Western blots of untransfected, whole cell DSC lysates and dsRed^ΔDSC lysates were probed with anti-ActRIIA and anti-GFP antibodies demonstrating expression of GFP in transfected neurons only. Detection of GAPDH provided a loading control.

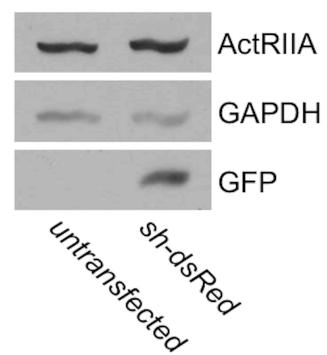


Figure S2. Knockdown of ActRIIA does not effect the expression of the remaining type II BMP receptors, ActRIIB and BMPR2. Western blots of dsRed^ΔDSC and AIIA^ΔDSC whole cell lysates were probed with anti-ActRIIA, anti-ActRIIB and anti-BMPR2 antibodies demonstrating selective loss of ActRIIA expression in the presence of *sh-AIIA*. Detection of GAPDH provided a loading control. This analysis also confirms that all three type II BMP receptors are expressed in DSC neurons.

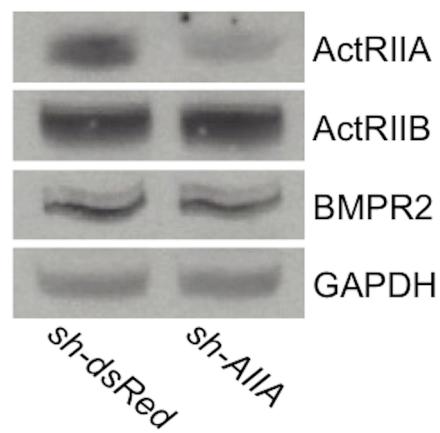


Figure S3. Amino acid sequence alignment of mouse ActRIIA and mouse ActRIIB.

The amino acid sequences for mouse ActRIIA (NCBI accession # NP_031422.3) and mouse ActRIIB (NCBI accession # NP_031423.1) were aligned using the NCBI BLAST Multiple Alignment tool. The *Lys* and *Glu* mutated in ActRIIA and ActRIIB, respectively, are highlighted in yellow and the *Val* residues mutated in ActRIIA V3 are highlighted in green. Note that the numbering for the full-length amino acid sequences shown here differs from numbering used throughout the paper, which is derived from the model of BMP7 bound to the ECD of ActRIIA (PDB ID: 1LX5; Greenwald et al., 2003).

ActRIIA 1	MGAAAKLAFA VFLISCSSGA ILGRSETQEC LFFNANWERD RTNQTGVEPC	50
ActRIIB 1	M-TAPWAALA LLWGSCLAGS GRGEAETREC IYYNANWELE RTNQSGLERC	49
ActRIIA 51	YGDKDKRRC FATWKNISGS IEIVKQGCWL DDINCYDRTD CIEKKDSPEV	100
ActRIIB 50	EGEQDKRLHC YASWRNSSGT IELVKKGCWL DDFNCYDRQE CVATEENPQV	99
ActRIIA 101	YFCCCEGNMC NEKFSYFPEM EVTQPTSNPV TPKPPYYNIL LYSLVPLMLI	150
ActRIIB 100	YFCCCEGNFC NERFTHLPEP GGPEVTYEPPTATPLLLTVL AYSLLPIGGL	149
ActRIIA 151	AGIVICAFWV YRHHKMAYPP VLV----- -----PTQD	177
ActRIIB 150	SLIVLLAFWM YRHRKPPYGH VDIHEVRQCQ RWAGRRDGCA DSFKPLPFQD	199
ActRIIA 178	PGPPPPSPPLL GLKPLQLLEV KARGRFGCVW KAQLLNEYVA VKIFPIQDK	227
ActRIIB 200	PGPPPPSPLV GLKPLQLLEI KARGRFGCVW KAQLMNDFVA VKIFPLQDKQ	249
ActRIIA 228	SWQNEYEVYS LPGMKHENIL QFIGAEKRGT SVDVDLWLIT AFHEKGSSLSD	277
ActRIIB 250	SWQSEREIFS TPGMKHENLL QFIAAEKRGS NLEVELWLIT AFHDKGSLTD	299
ActRIIA 278	FLKANVVSWN ELCHIAETMA RGLAYLHEDI PGLK-DGHKP AISHRDIKSK	326
ActRIIB 300	YLKGNIITWN ELCHVAETMS RGLSYLHEDV PWCRGEGHKP SIAHRDFKSK	349
ActRIIA 327	NVLLKNNLTA CIADFLALK FEAGKSAGDT HGQVGTRRYM APEVLEGAIN	376
ActRIIB 350	NVLLKSDLTA VLADFLGLAVR FEPGKPPGDT HGQVGTRRYM APEVLEGAIN	399
ActRIIA 377	FQRDAFLRID MYAMGLVLWE LASRCTAADG PVDEYMLPFE EEIGQHPSLE	426
ActRIIB 400	FQRDAFLRID MYAMGLVLWE LVSRCKAADG PVDEYMLPFE EEIGQHPSLE	449
ActRIIA 427	DMQE[VV]HKK KRPVLRDYWQ KHAGMAMLCE TIEECWDHDA EARLSAGCVG	476
ActRIIB 450	ELQEVVVHKK MRPTIKDHWL KHPGLAQLCV TIEECWDHDA EARLSAGCVE	499
ActRIIA 477	ERITQMQLT NIITTEDIVT VVTMVTNVDF PPKESSL	513
ActRIIB 500	ERVSLIRRSP NGTTSDCLVS LVTSVTNVDL LPKESSI	536

Figure S4. Mutation of ActRIIB *Glu*⁷⁵ does not rescue BMP7-evoked chemotaxis.

Chemotaxis in response to 50 ng/mL BMP7 (mean \pm s.e.m.). Chemotaxis indices for dsRed^ΔWEHI cells co-expressing ActRIIB (*lane 1*, CI = 41.7 ± 3.9) and ActRIIB E75K (*lane 3*, CI = 19.8 ± 2.2). Chemotaxis indices for AIIA^ΔWEHI cells co-expressing ActRIIB (*lane 2*, CI = 8.7 ± 11) and ActRIIB E75K (*lane 4*, CI = -16 ± 1.0). In dsRed^ΔWEHI cells co-expressing ActRIIB, BMP7-evoked chemotaxis differs significantly from chemotaxis in dsRed^ΔWEHI cells co-expressing ActRIIB E75K (* $P < 0.05$, n = 2) and from chemotaxis in AIIA^ΔWEHI cells co-expressing ActRIIB E75K (** $P < 0.005$, n = 2) (Student's two tailed *t*-test).

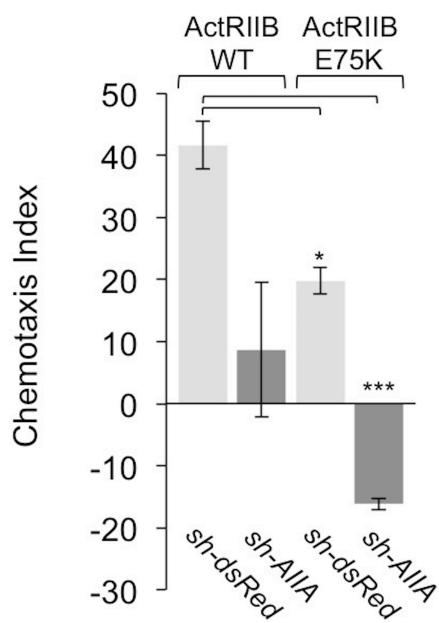
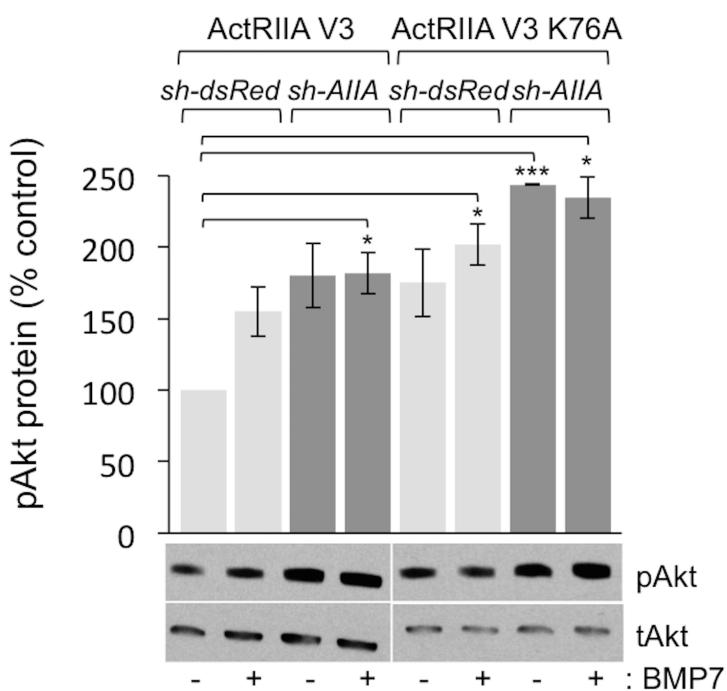


Figure S5. Loss of ActRIIA and expression of ActRIIA K76A results in unregulated increases in pAkt levels. All samples are shown with respect to pAkt levels in unstimulated, dsRed^ΔWEHI lysates expressing ActRIIA V3 (*lane 1*). Significant differences were observed in pAkt levels between unstimulated, dsRed^ΔWEHI lysates co-expressing ActRIIA V3 and WEHI cells stimulated with BMP7 including AIIA^ΔWEHI lysates co-expressing ActRIIA V3 (*lanes 1 and 4*, 82% over control), dsRed^ΔWEHI lysates co-expressing ActRIIA V3 K76A (*lanes 1 and 6*, 87% over control) and AIIA^ΔWEHI lysates co-expressing ActRIIA V3 K76A (*lanes 1 and 8*, 135% over control) (* $P < 0.05$, Student's two tailed *t*-test). The difference in pAkt levels between dsRed^ΔWEHI lysates co-expressing ActRIIA V3 (*lane 1*) and AIIA^ΔWEHI lysates co-expressing ActRIIA V3 K76A (*lane 7*, 144% over control) in the absence of BMP7 is highly significant (** $P < 0.0001$, Student's two tailed *t*-test). Increases in pAkt levels in the absence of BMP7 stimulation including AIIA^ΔWEHI lysates co-expressing ActRIIA V3 (*lane 3*, 80% over control) and dsRed^ΔWEHI lysates co-expressing ActRIIA V3 K76A (*lane 5*, 75% over control) were also observed.



List of Symbols and Abbreviations

ActRIIA	Activin A receptor type IIA
ActRIIB	Activin A receptor type IIB
ALK	Activin receptor-like kinase
BISC	BMP-induced signaling complex
BMP	Bone morphogenetic protein
BMPR2	BMP receptor type 2
CI	Chemotaxis index
DSC	Dorsal spinal cord
ECD	Extracellular domain
EGFP	Enhanced Green Fluorescent Protein
FACS	Fluorescence-activated cell sorting
GCAD	Growth cone area decrease
LIMK1	Lim domain kinase 1
PDB	Protein Data Bank
PI3K	Phosphoinositide 3-kinase
PFC	Preformed complex
RNAi	RNA interference
shRNA	short hairpin RNA
TBS	Tris-buffered saline
TGF β	Transforming growth factor beta