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Enzyme rates of ACVR1<sup>WT</sup> and ACVR1<sup>R206H</sup> in response to different ligands.

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TGF- $\beta$  can trigger ACVR1<sup>R206H</sup> signaling by an alternative mechanism.

## Sequences of all knockout clones

In each case, the wild-type sequence is given on top and the mutant sequence for a particular allele is given underneath. Depending on the gene, we found between two and 4 alleles for each gene. Sequences in lower case represent mismatches to the reference sequence.

### Parental ACVR1 Knockout clone 1

#### Allele 1

```
608CAGTGGCTCGCCAGATTACACTGTTGGAGTGTG640  
CAGTGGCTCG-----TTGGAGTGTG
```

#### Allele 2

```
608CAGTGGCTCGCCAGATTACACTGTTGGAGTGTG640  
CAGTGGCTCGCCAGAT(309 nt deletion)
```

### Parental ACVR1 knockout clone 2

#### Allele 1

```
608CAGTGGCTCGCCAGATTACACTGTTGGAGTGTGT640  
(332 nt deletion)ACACTGTTGGAGTGTGT
```

#### Allele 2

```
608CAGTGGCTCGCCAGATTACACTGTTGGAGTGTGT640  
CAGTG-----TGTGT
```

### Parental ACVR2A knockout

#### Allele 1

```
682TCATGGCAAATGAATACGAAGTCTACAGTTTG714  
(396 nt deletion spanning Guide sequence)
```

#### Allele 2

```
682TCATGGCAAATGAATACGAAGTCTACAGTTTG714  
TCATGGCAAATGAATACGAA(243 nt deletion)
```

#### Allele 3

```
682TCATGGCAAATGAATACGAAGTCTACAGTTTG714  
TCATGGCAAATGAATACGAAGTCTA(18 nt deletion)
```

## Parental ACVR2B knockout

### Allele 1

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
(29 nt deletion) ACAGTTCATTGCTGCCGAGAAGCGA

### Allele 2

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
(195 nt deletion spanning Guide sequence)

## Parental ACVR2A/2B double knockout

### ACVR2A

#### Allele 1

<sup>682</sup>TCATGGCAAAATGAATACGAAGTCTACAGTTT<sup>714</sup>  
(225 nt deletion) TG

#### Allele 2

<sup>682</sup>TCATGGCAAAATGAATACGAAGTCTACAGTTT-G<sup>714</sup>  
TCATGGCAAAATGAATACGAAGTCTACAGTTT<sup>714</sup>

#### Allele 3

<sup>682</sup>TCATGGCAAAATGAATACGAAGTCTACAGTTT<sup>714</sup>  
TCATGGCAAAATGAATACGAAG(23 nt deletion)

### ACVR2B

#### Allele 1

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
AAGCACGAGAAC(189 nt deletion)

Allele 2 not detected

## HOM1 ACVR2A knockout

### Allele 1

<sup>682</sup>TCATGGCAAAATGAATACGAAGTCTACAGTTT<sup>714</sup>  
TCATGGCAAAATGAATACGAAGTCTACAGT(270 nt deletion)

### Allele 2

<sup>682</sup>TCATGGCAAATGAATACGAAGTCTACAGTTG<sup>714</sup>  
TCATGGCAAATGAA(29 nt deletion)

*Allele 3*

<sup>682</sup>TCATGGCAAATGAATACGAAGTCTACAGTTG<sup>714</sup>  
TCATGGCAAATGAATACGAA-----TG

**HOM1 ACVR2B knockout**

*Allele 1*

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
AAGCcaggtggatactg(202 nt deletion)

*Allele 2*

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
-----TTGCTGCCGAGAAGCGA

**HOM1 ACVR2A/2B double knockout**

**ACVR2A**

*Allele 1*

<sup>682</sup>TCATGGCAAATGAATACGAAGTCTACAGTTG<sup>714</sup>  
TCATGGCAAATGAATACGAAGT(49 nt insertion)

*Allele 2*

<sup>682</sup>TCATGGCAAATGAATACGAAGTCTACAGTTG<sup>714</sup>  
TCATGGCAAATGAATACGAAGTCTACAGTTT(39 nt insertion)

*Allele 3*

<sup>682</sup>TCATGGCAAATGAATACGAAGTCTACAGTTG<sup>714</sup>  
TCATGGCAAATGAATACGAAGTCTACAGTT-G

**ACVR2B**

*Allele 1*

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
AAGCACGAGAAC-----AGTTCATTGCTGCCGAGAAGCGA

*Allele 2*

<sup>718</sup>AAGCACGAGAACCTGCTACAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>

AAGCACGAG-----CTGCCGAGAAGCGA

*Allele 3*

<sup>718</sup>AAGCACGAGAACCTGCTA-CAGTTCATTGCTGCCGAGAAGCGA<sup>759</sup>  
AAGCACGAGAACCTGCTAACAGTTCATTGCTGCCGAGAAGCGA

**Parental ACVR1B/1C double knockout**

**ACVR1B**

*Allele 1*

<sup>337</sup>CTCAAGGAGCCTGAGCACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>  
CTCAAGG-----GGCCCGGTGGAGCTG

*Allele 2*

<sup>337</sup>CTCAAGGAGCCTGAGCACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>  
CTCAAGGAGCCTGAGCACCC-GTCCATGTGGGGCCCGGTGGAGCTG

**ACVR1C**

*Allele 1*

<sup>673</sup>TCCTCCAGAGATGAAAGATCTTGGTTTCGTGAGGCAGAAATTTAC<sup>717</sup>  
TCCTCCAGAGATGAAAGATCTTGGTTTC---ActttccaATTTAC

*Allele 2*

<sup>673</sup>TCCTCCAGAGATGAAAGATCTTGGTTTCGTGAGGCAGAAATTTAC<sup>717</sup>  
TCCTCCAGAGATGAAAGATC-----GTGAGGCAGAAATTTAC

*Allele 3*

<sup>673</sup>TCCTCCAGAGATGAAAGATCTTGGTTTCGTGAGGCAGAAATTTAC<sup>717</sup>  
TCCTCCAGAGATGAAAGATC(211 nt deletion)

**HOM1 ACVR1B/1C double knockout**

**ACVR1B**

*Allele 1*

<sup>337</sup>CTCAAGGAGCCTGAGCACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>  
CTCAAGGA-----TGTGGGGCCCGGTGGAGCTG

*Allele 2*

<sup>337</sup>CTCAAGGAGCCTGAGC-ACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>

CTCAAGGAGCCTGAGCCACCCGTCCATGTGGGGCCCGGTGGAGCTG

*Allele 3*

<sup>337</sup>CTCAAGGAGCCTGAGCACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>  
CTCAAGGA-----TGTGGGGCCCGGTGGAGCTG

*Allele 4*

<sup>337</sup>CTCAAGGAGCCTGAGCACCCGTCCATGTGGGGCCCGGTGGAGCTG<sup>381</sup>  
(38 nt deletion)TGGGGCCCGGTGGAGCTG

## **ACVR1C**

*Allele 1*

<sup>673</sup>TCCTCCAGAGATGAAAGATCTTGGTTTCGTGAGGCAGAAATTTAC<sup>717</sup>  
TCCTCCAGAGATGAAAGATCTTG-----TGAGGCAGAAATTTAC

*Allele 2* not detected

## **Parental SMAD6 knockout clone 1**

*Allele 1*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTAT-GCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCTATTGCGGTGTACGACC

*Allele 2*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACGACC<sup>1005</sup>  
GGG(227 nt insertion)

## **Parental SMAD6 knockout clone 2**

*Allele 1*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCTAT(136 nt deletion)

*Allele 2*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCT-TGCGGTGTACGACC

## **Parental SMAD7 knockout clone 1**

*Allele 1*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGCCTGG(>300 nt insertion)

*Allele 2*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGCCTGG(>300 nt deletion)

**Parental SMAD7 knockout clone 2**

*Allele 1*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGC(109 nt insertion)

*Allele 2* not detected.

**Parental SMAD6/SMAD7 double knockout clone 1**

**SMAD7**

*Allele 1*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGCC----GATCGGTCACACTGGTGCGTGGTGGCAT

*Allele 2*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGCCTGGG-----ACACTGGTGCGTGGTGGCAT

**SMAD6**

*Allele 1*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTAT-GCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCTATTGCGGTGTACGACC

*Allele 2*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTAT--GCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCTATTTGCGGTGTACGACC

**Parental SMAD6/SMAD7 double knockout clone 2**

**SMAD7**

*Allele 1*

<sup>887</sup>TTCTTCTGGAGCCTGGGGATCGGTCACACTGGTGCGTGGTGGCAT<sup>931</sup>  
TTCTTCTGGAGCCTGG--ATCGGTCACACTGGTGCGTGGTGGCAT

*Allele 2 not detected.*

**SMAD6**

*Allele 1*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACGACC<sup>1005</sup>  
G(>300 nt deletion)

*Allele 2*

<sup>961</sup>GGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACGACC<sup>1005</sup>  
GGGAGCACCGGACGCGCGTGGGCCGCCTCTA--CGGTGTACGACC

**Parental SMAD2/3 double knockout clone 1**

**SMAD2**

*Allele 1*

<sup>799</sup>ACTTACTCAGAACCTGCATTTT-GGTGTTTCGATAGCATATTATGAATTAAAT<sup>849</sup>  
ACTTACTCAGAACCTGCATTTTGGTGTTTCGATAGCATATTATGAATTAAAT

*Allele 2 not detected*

**SMAD3**

*Allele 1*

<sup>703</sup>ATTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATTCCTACTACGAGCT-----CGGGGAGACATTCCACGCCTCGC

*Allele 2*

<sup>703</sup>ATTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATTCCTACTACGAG-----ACATTCCACGCCTCGC

*Allele 3*

<sup>703</sup>ATTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATTCCTACTACGAGCTGAACCAGCG--TCGGGGAGACATTCCACGCCTCGC

**Parental SMAD2/3 double knockout clone 2**



## **SMAD2**

### *Allele 1*

<sup>799</sup>ACTTACTCAGAACCTGCATTTTGGTGTTCGATAGCATATTATGAATTAAAT<sup>849</sup>  
ACTTACTCAGAACCTGCATT--GGTGTTCGATAGCATATTATGAATTAAAT

### *Allele 2*

<sup>799</sup>ACTTACTCAGAACCTGCATTTT--GGTGTTCGATAGCATATTATGAATTAAAT<sup>849</sup>  
ACTTACTCAGAACCTGCATTTTGGTGTTCGATAGCATATTATGAATTAAAT

### *Allele 3*

<sup>799</sup>ACTTACTCAGAACCTGCATTTTGGTGTTCGATAGCATATTATGAATTAAAT<sup>849</sup>  
ACTTACTCAGAACCTG--TTTTGGTGTTCGATAGCATATTATGAATTAAAT

## **SMAD3**

### *Allele 1*

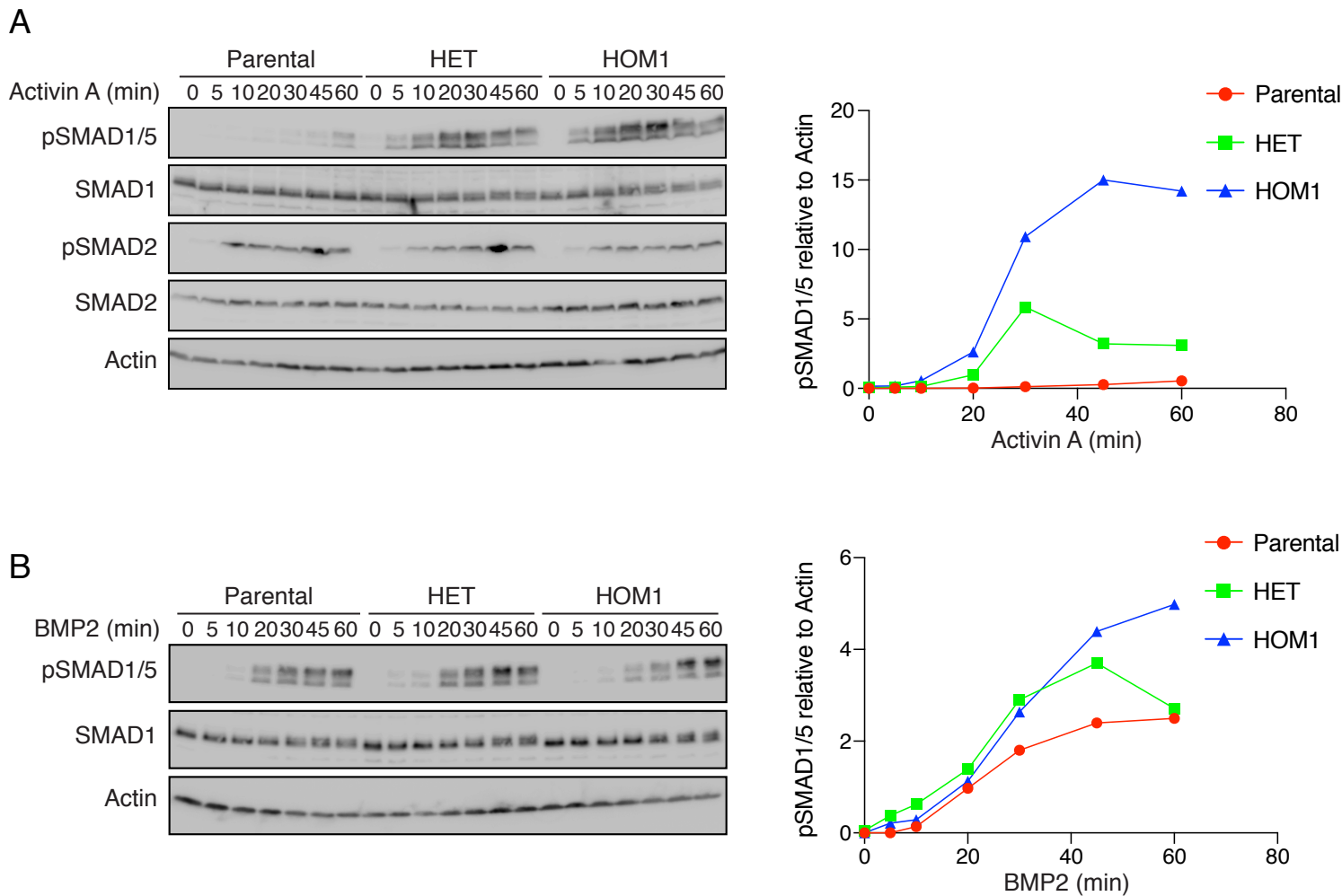
<sup>703</sup>ATCTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATCTCCTACTACGAGCTGAACCAGCG-----GGAGACATTCCACGCCTCGC

### *Allele 2*

<sup>703</sup>ATCTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATCTCCTACTACGAGCTGAACCAGCGC-----CACGCCTCGC

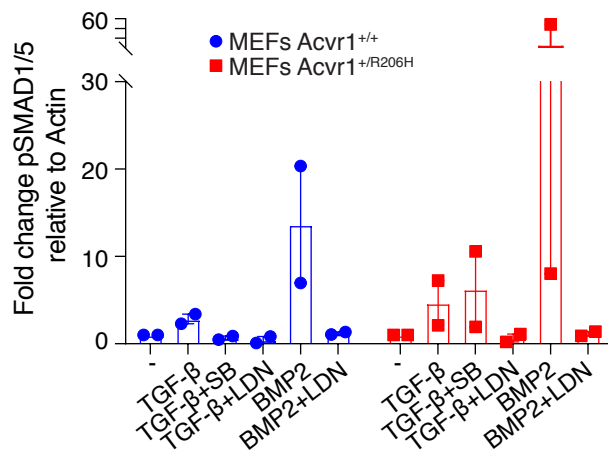
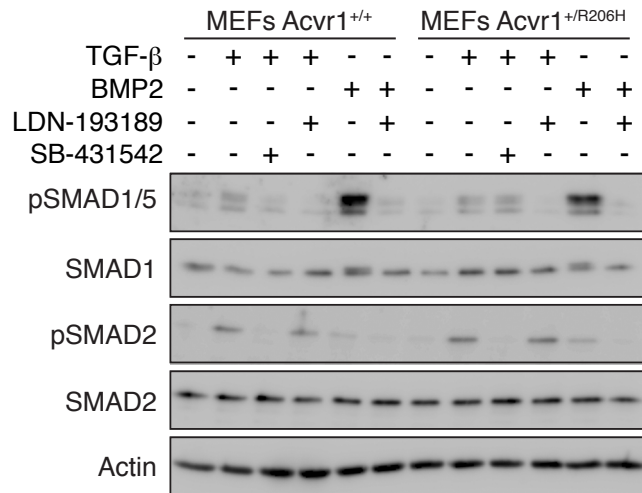
### *Allele 3*

<sup>703</sup>ATCTCCTACTACGAGCTGAACCAGCGCGTCGGGGAGACATTCCACGCCTCGC<sup>754</sup>  
ATCTCCTACTACGAGCTGAACCAGCG--TCGGGGAGACATTCCACGCCTCGC



**Appendix Figure S1. Enzyme rates of ACVR1<sup>WT</sup> and ACVR1<sup>R206H</sup> in response to different ligands.**

A, B. Parental HEK293T, HET and HOM1 cells were treated with Activin A (A) or BMP2 (B) for the times indicated. In all panels, Western blots of whole cell lysates were probed with the antibodies indicated. Quantifications are the levels of pSMAD1/5 normalized to Actin and are for one representative experiment. The relative initial phosphorylation rates after Activin A induction are:  $1.35 \times 10^{-5} \pm 2.13 \times 10^{-5}$ ,  $7.94 \times 10^{-4} \pm 2.37 \times 10^{-4}$ ,  $6.98 \times 10^{-3} \pm 2.01 \times 10^{-3} \text{ min}^{-1}$  for parental, HET and HOM1 respectively (A). The relative initial phosphorylation rates after BMP2 induction are:  $1.24 \times 10^{-3} \pm 1.09 \times 10^{-4}$ ,  $1.48 \times 10^{-3} \pm 1.49 \times 10^{-4}$ ,  $1.64 \times 10^{-3} \pm 2.98 \times 10^{-4} \text{ min}^{-1}$  for parental, HET, HOM1 respectively (B).



**Appendix Figure S2. TGF- $\beta$  can trigger ACVR1<sup>R206H</sup> signaling by an alternative mechanism.** MEFs from *Acvr1*<sup>+/+</sup> and *Acvr1*<sup>+R206H</sup> mice were treated with TGF- $\beta$  or BMP2 for 1 h, in the presence or absence of either 10  $\mu$ M SB-431542 or 1  $\mu$ M LDN-193189. In all panels, Western blots of whole cell lysates were probed with the antibodies indicated. Quantifications are the levels of pSMAD1/5 normalized to Actin, expressed as fold change relative to untreated of each cell line, and are the average  $\pm$  SEM of 2 independent experiments.