

**Figure S1. Schematic representation of mating schemes and CTNNB1 protein pools in oocytes and progeny blastocysts used in this work.**

CTNNB1 protein is depicted as rectangle with an N- (green) and C-terminal (yellow) portion. Paternally encoded protein is boxed blue, maternally encoded protein is boxed in red. The  $\beta\text{CatC}$  allele deletion results in complete removal of the CTNNB1 protein (illustrated as semi-transparent squares), while  $\beta\text{CatN}$  allele deletion results in a C-terminal CTNNB1 fragment (C-terminal (yellow) square). Zp3cre recombinates

floxed alleles in the maternal germline. The content of rounded rectangles beneath the mothers in each cross depict the maternal protein contribution to the embryo through the oocyte. The content of the rounded rectangles beneath the F1 generation depict the CTNNB1 protein pool at the 3.5 dpc blastocyst stage. For simplicity sake display of ZP3cre inheritance is omitted as irrelevant to the resultant embryos. Progeny labeled with (\*) received only half of the wild type maternal protein contribution at fertilization.

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WT  MATQADLMELDMAMEPDRKAAVSHWQQSYLDSGIHSGATTTAPSLSGKGNPEEEDVDTSQVLYEWE
Kem  -----
Bir  -----
Bir2 -----

WT  QGFSQSFTQEQVADIDGQYAMTRAQRVRAAMPETLDEGMQIPSTQFDDAAHPTNVQRLAEPQMLKH
Kem  -----
Bir  -----
Bir2 -----

WT  AVVNLINIQDDAELATRAIPELTKLLNDEDQVVVNKAAMVHQLSKKEASRHAIMRSPQMVSIAIVRT
Kem  -----
Bir  -----
Bir2 -----

WT  MQNTNDVETARCTAGTLLHNLSSHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLHLHQEG
Kem  -----
Bir  -----
Bir2 -----

WT  AKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNMIRTYTYEK
Kem  -----MRTYTYEK
Bir  -----MRTYTYEK
Bir2 -----

WT  LLWTTSRVLKVLVSVCSNKPATIVEAGGMQALGLHLTDPQSRLVQNCLWTLRNLSDAATKQEGMEGLL
Kem  LLWTTSRVLKVLVSVCSNKPATIVEAGGMQALGLHLTDPQSRLVQNCLWTLRNLSDAATKQEGMEGLL
Bir  LLWTTSRVLKVLVSVCSNKPATIVEAGGMQALGLHLTDPQSRLVQNCLWTLRNLSDAATKQEGMEGLL
Bir2 -----MATQGGMQALGLHLTDPQSRLVQNCLWTLRNLSDAATKQEGMEGLL

WT  GTLVQLLGSDDINVVTC AAGILSNLTCN NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALR
Kem  GTLVQLLGSDDINVVTC AAGILSNLTCN NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALR
Bir  GTLVQLLGSDDINVVTC AAGILSNLTCN NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALR
Bir2 GTLVQLLGSDDINVVTC AAGILSNLTCN NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALR

WT  HLTSRHQEAEMAQNAVRLHYGLP VVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRL
Kem  HLTSRHQEAEMAQNAVRLHYGLP VVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRL
Bir  HLTSRHQEAEMAQNAVRLHYGLP VVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRL
Bir2 HLTSRHQEAEMAQNAVRLHYGLP VVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRL

WT  VQLLVR AHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRI VIRGLNTIPLFVQLL
Kem  VQLLVR AHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRI VIRGLNTIPLFVQLL
Bir  VQLLVR AHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRI VIRGLNTIPLFVQLL
Bir2 VQLLVR AHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRI VIRGLNTIPLFVQLL

WT  YSPIENIQRVAAGVLC ELAQDKEAAEAIEAEGATAPL TELLSRNEGVATYAAA VLFMRSEDKPQDY
Kem  YSPIENIQRVAAGVLC ELAQDKEAAEAIEAEGATAPL TELLSRNEGVATYAAA VLFMRSEDKPQDY
Bir  YSPIENIQRVAAGVLC ELAQDKEAAEAIEAEGATAPL TELLSRNEGVATYAAA VLFMRSEDKPQDY
Bir2 YSPIENIQRVAAGVLC ELAQDKEAAEAIEAEGATAPL TELLSRNEGVATYAAA VLFMRSEDKPQDY

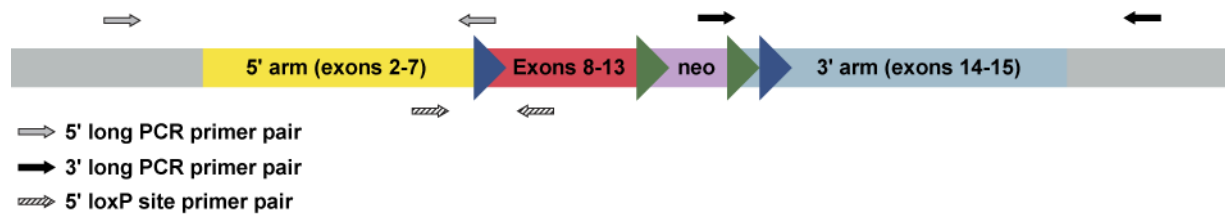
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Kem  KKRLSVELTSSLFRTEPMAWNETADLGLDIGAQGEALGYRQDDPSYRSFHSGGYGQDALGMDPMMEH
Bir  KKRLSVELTSSLFRTEPMAWNETADLGLDIGAQGEALGYRQDDPSYRSFHSGGYGQDALGMDPMMEH
Bir2 KKRLSVELTSSLFRTEPMAWNETADLGLDIGAQGEALGYRQDDPSYRSFHSGGYGQDALGMDPMMEH

WT  EMGGHHPGADYPVDGLPDLGHAQDLMDGLPPGDSNQLAWFD TDL
Kem  EMGGHHPGADYPVDGLPDLGHAQDLMDGLPPGDSNQLAWFD TDL
Bir  EMGGHHPGADYPVDGLPDLGHAQDLMDGLPPGDSNQLAWFD TDL
Bir2 EMGGHHPGADYPVDGLPDLGHAQDLMDGLPPGDSNQLAWFD TDL

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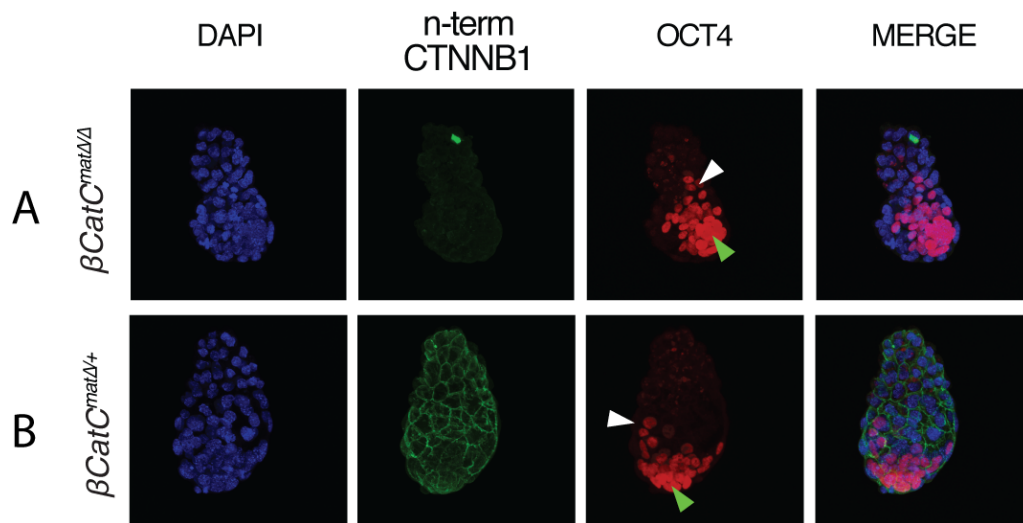
**Figure S2. Comparison of the wild type and truncated protein products produced by the *Ctnnb1* (wt), *Ctnnb1*<sup>tm2Kem</sup> (Kem) and *Ctnnb1*<sup>tm4Wbm</sup> (Bir and Bir2) alleles.**

Analysis of the sequences of the different alleles revealed that the *Ctnnb1*<sup>tm2Kem</sup> allele has one possible fragmented product produced from an alternative translation start site, whereas the *Ctnnb1*<sup>tm4Wbm</sup> allele has two possible products. Western blot analysis (Fig 1 C) shows that the fragment, a splice product of exons 1 to exon 8, Bir2, gives rise to the truncated CTNNB1<sup>tm4Wbm</sup>.



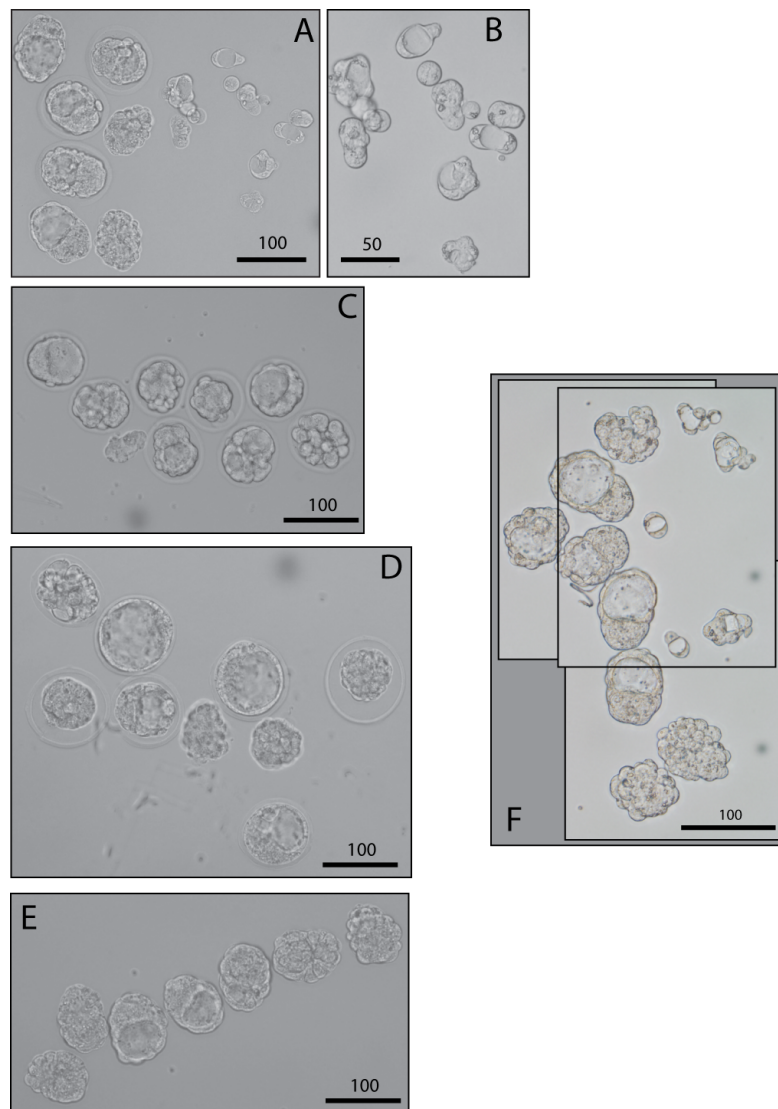
**Figure S3. Schematic representation of the  $\beta$ -catenin floxed allele designed to remove the C-terminal portion of the protein ( $\beta$ CatC).**

Floxed sites are indicated by blue arrowheads and frt sites by green arrowheads. Grey arrows indicate the position of the primer pairs used to determine correct recombination of the 5' arm of the construct. Black arrows indicate the position of the primer pairs used to determine correct recombination of the 3' arm of the construct. Patterned arrows indicate the primer pair used to determine whether or not the 5' loxP site was intact.



**Figure S4. 4.5 dpc blastocysts derived from maternal-zygotic  $\beta$ -catenin null females.**

CTNNB1 and OCT4 expression analysis in  $\beta\text{Cat}^{\text{mat}\Delta/\Delta}$  (A) and  $\beta\text{Cat}^{\text{mat}\Delta/+}$  (B) implanting embryos. At 4.5 dpc mutant ICMs remain OCT4 positive (green arrowhead). PE cells are also OCT4 positive and well visible in mutant and control (white arrowhead).



**Figure S5. Representative images of litters isolated from maternal-zygotic  $\beta$ -catenin null females at 3.5 dpc** (A, C-E) Representative 3.5 dpc litters of  $\beta$ CatC<sup>fl</sup>:Zp3-cre female mated with a  $\beta$ CatC<sup>mat $\Delta$ /+</sup>  male. (A) Litter containing presumably normal blastocysts, uncompact morulae without a zona pellucida, and numerous trophoblastic vesicles. (B) Higher magnification of trophoblastic vesicles of litter shown in (A) (C-E) Litters containing normal blastocysts, compacted and uncompact morulae with and without zona pellucidae. (F) Representative litter at 3.5 dpc of a  $\beta$ CatN<sup>f</sup>/ $\beta$ CatC<sup>f</sup>:Zp3-cre female mated with a  $\beta$ CatC<sup>mat $\Delta$ /+</sup>  male. Litter contains normal and abnormal blastocysts, uncompact morulae without zonae and several trophoblastic vesicles.