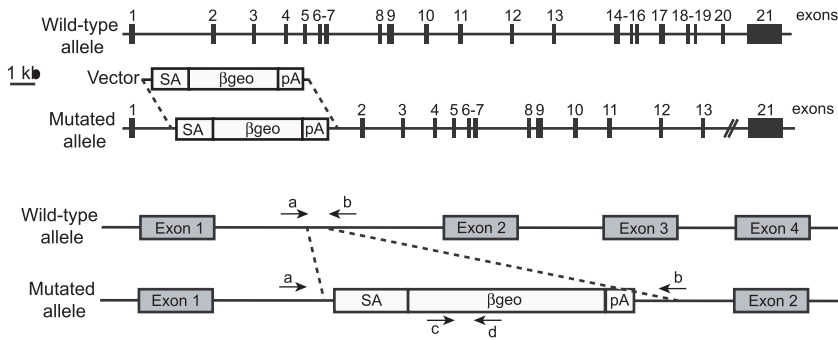


A



B

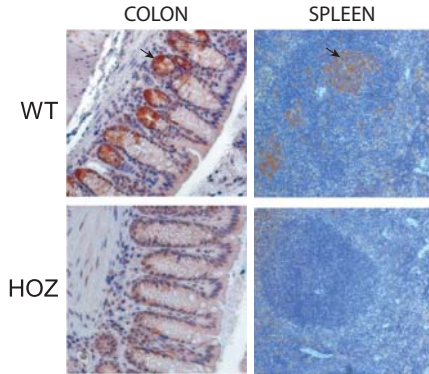
Genotype	WT	het	HOZ	number
Expected ratio	25%	50%	25%	
Observed mice	27%	52%	21%	149

$p=0,688$

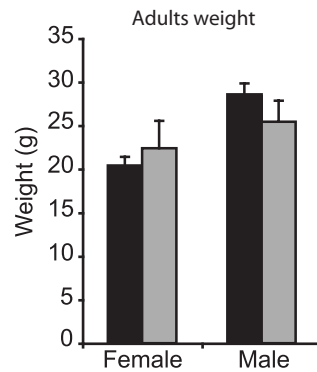
C



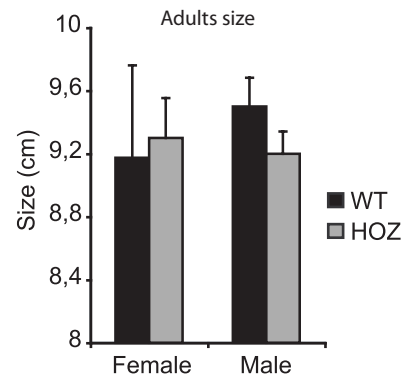
D



E



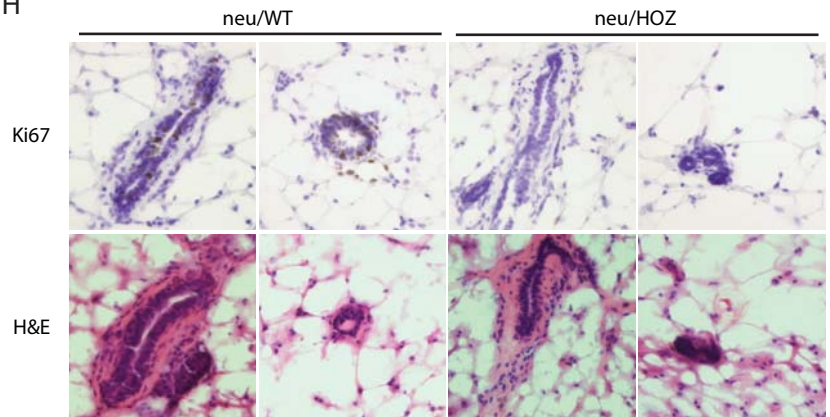
F



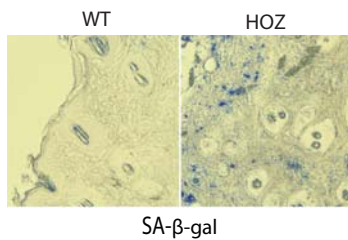
G

	WT	HOZ
Hemoglobin (g/L)	137,3	134,6
Hematocrit (%)	49,3	48,5
White blood count (*10 ⁹ cells/L)	2,2	2,0
Red blood count (*10 ¹² cells/L)	8,8	8,7
Platelet count (*10 ⁹ cells/L)	946,0	1064,6
Neutrophils (%)	11,5	14,9
Lymphocytes (%)	75,3	77,1
Monocytes (%)	0,9	1,0
Eosinophils (%)	7,0	6,2
Basophils (%)	0,1	0,1

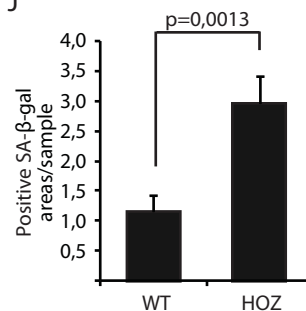
H



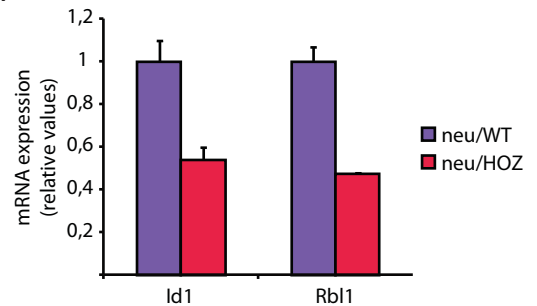
I



J



K



Supplemental figure 4.

Characterization of hypomorphic CIP2AHOZ mice. A) Gene-trap strategy for inhibition of CIP2A expression. Murine CIP2A wild-type allele and the corresponding CIP2A locus with gene-trap vector insertion are presented in the upper panel (exon structure is represented with filled boxes, the gene-trap vector by clear boxes). The pGTLxf gene-trap vector contains a splice acceptor site (SA), β -galactosidase reporter gene (β -geo) and a SV40 polyadenylation site (pA) inserted in CIP2A locus intron 1. The lower panel indicates the position of the genotyping primers, a-b for the wild-type allele, c-d for the mutated allele. B) Sex and genotype ratio in the litters. No significant difference was observed in genotype and sex ratio between WT and CIP2AHOZ mice. C) CIP2A protein expression in indicated WT and HOZ adult mouse organs. D) CIP2A immunoreactivity in WT and HOZ adult mouse organs was evaluated by immunohistochemistry. No CIP2A protein expression was detected in CIP2AHOZ tissues. Arrows indicate specific CIP2A staining in WT tissues. E, F) CIP2A depletion does not affect adult mouse weight. Average weights and sizes of adult males or females of each genotype are represented. G) CIP2A depletion does not affect hematopoietic stem cell function. No significant difference in blood characteristics between WT and CIP2AHOZ adult mice. H) Representative immunohistochemical stainings of Ki67 and hematoxylin and eosin (H&E) from neu/WT and neu/HOZ mouse mammary glands. 20x magnification. I) Representative SA- β -gal stained skin from DMBA-induced wild-type (WT) and CIP2AHOZ mouse skin. J) Number of positive SA- β -gal staining in DMBA-induced WT and CIP2AHOZ mouse skin (I). Shown is mean+ SEM from 5 WT and 9 CIP2AHOZ mice. P value by Student's t-test. K) RT-PCR analysis of E2F1 target genes from neu/WT and neu/HOZ mammary gland tumors. Shown is mean +SEM from 4 neu/WT and 8 neu/HOZ tumors.