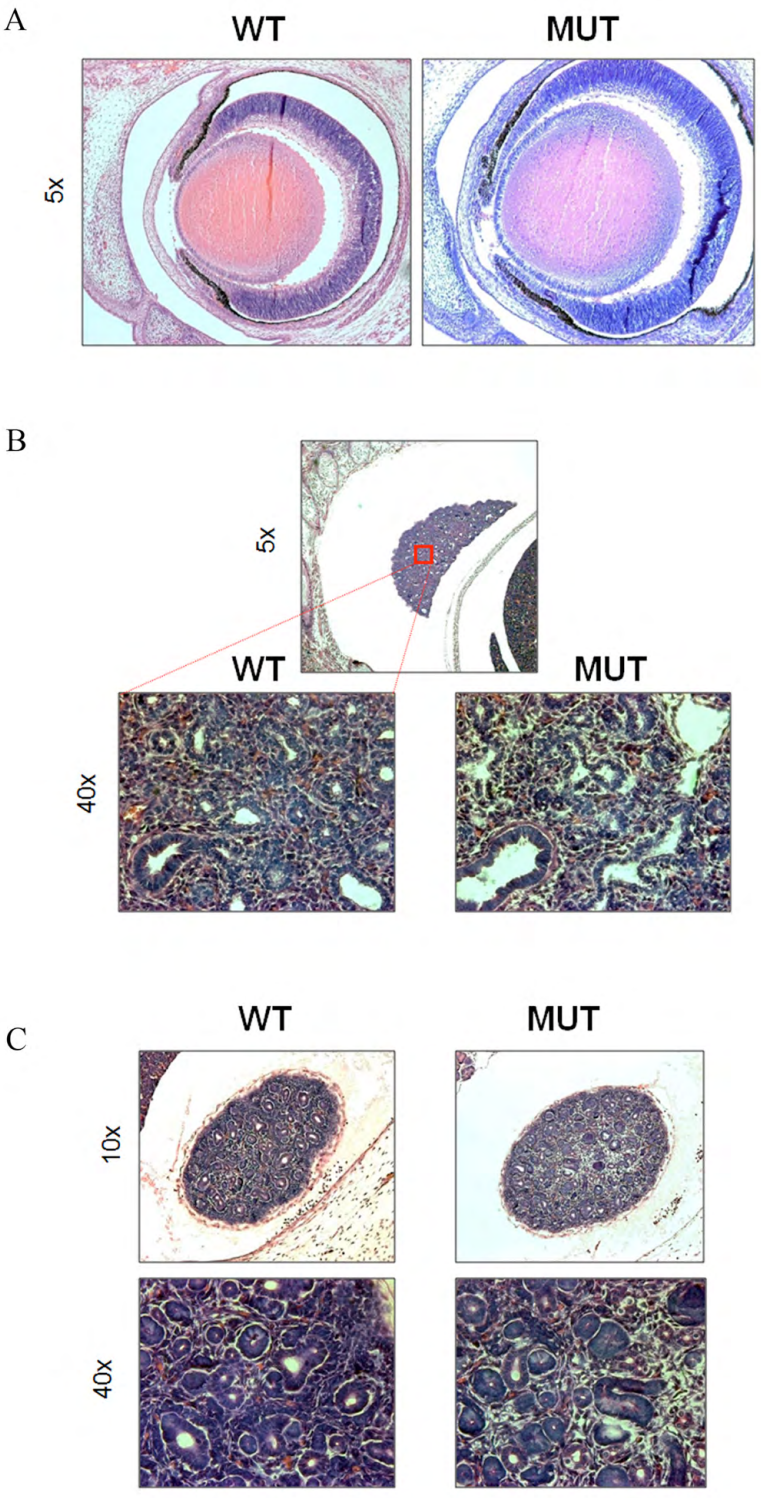

Fig. S1. The Pygo2-A342E mutation does not cause any obvious defect in mouse developing organs. Paraffin-embedded sections of the eye (**A**), lungs (**B**) and kidneys (**C**) from 15.5 days post-coitum embryos, were stained with Hematoxylin and Eosin. The magnification level is indicated on the left of the panels. WT, wild type.

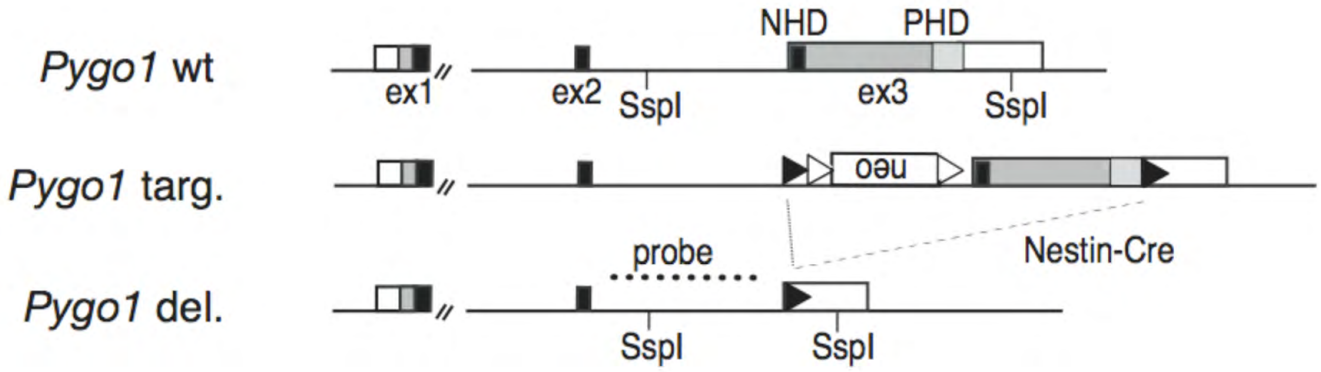

Fig. S2. Generation of the *Pygo1* knockout allele. The endogenous *Pygo1* gene has been replaced by a *LoxP*-containing *Pygo1* variant cloned in the targeting vector. *LoxP* sites are located on the opposite ends of the PHD finger coding sequence. After crossing with a CMV-Cre mouse line, the recombination leads to the production of a PHD-deleted protein. The recombination was confirmed with PCR using specific primers (not shown). wt, wild type.

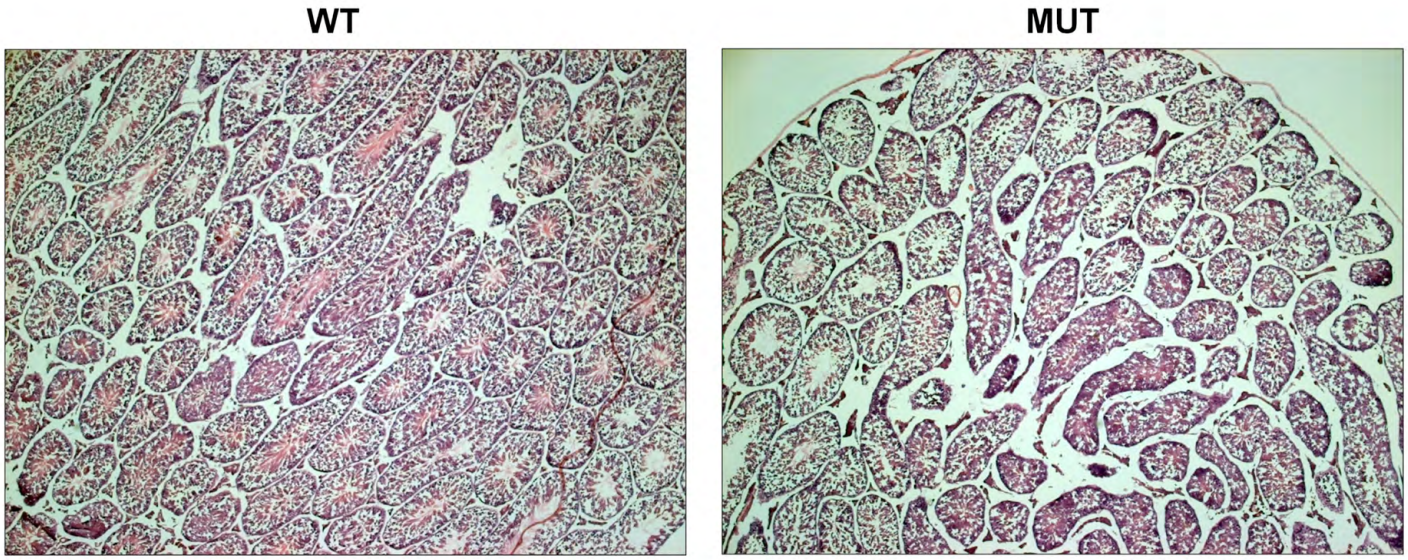

Fig. S3. Strong decrease of terminally differentiated sperm cells in the seminiferous tubules of MUT mice testes. Most of the seminiferous tubules in the MUT testis display a severe loss of terminally differentiated sperm cells normally present within the lumen (wild type on the left), as visualized by Hematoxylin and Eosin staining on 10 μm testis sections. WT, wild type.

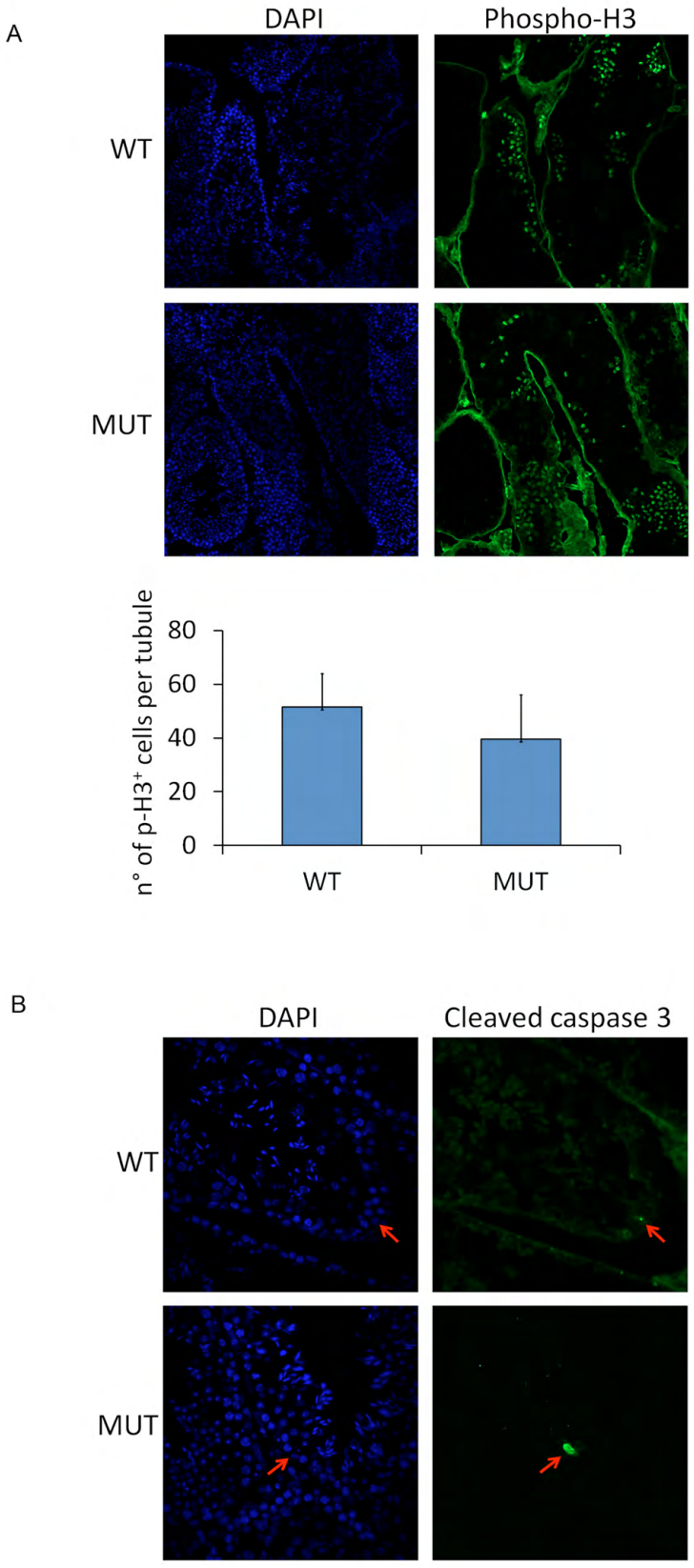

Fig. S4. Proliferation and apoptosis are not affected in the MUT testicles. (**A**) No quantitative difference in the proliferation of spermatocytes in the MUT testis, when compared to a control situation, was detected: the number of cells positive for phosphohistone H3, which marks mitotic cells, displays no statistically significant difference. (**B**) Very weak and rare signals positive for cleaved caspase 3, a marker for apoptosis, are detected, in our hands, in wild-type seminiferous tubules. No measurable increase is present in the MUT testis. DAPI counterstains cell nuclei (blue signal, A,B). WT, wild type.

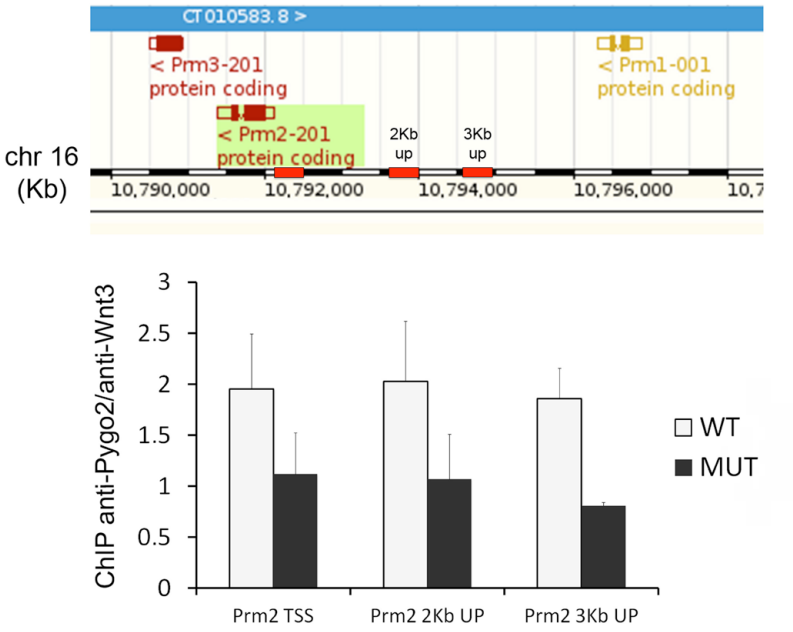

Fig. S5. Pygo2 binding to chromatin is detected within the intergenic region between *Prm1* and *Prm2* genes. (Top) Schematic representation of the locus from Ensembl genome browser (http://www.ensembl.org/Mus_musculus/Info/Index). The position of the amplified regions is indicated with red boxes. Note that the transcription of the *Prm2* gene proceeds from the right to the left. (Bottom) ChIP followed by quantitative PCR. Data are represented as the fold enrichment (compared to the input samples) obtained using the anti-Pygo2, over the enrichment measured when using the anti-Wnt3 antibody.