SUPPLEMENTAL MATERIAL

Kuchmiy et al., https://doi.org/jem.10.1084/20160900

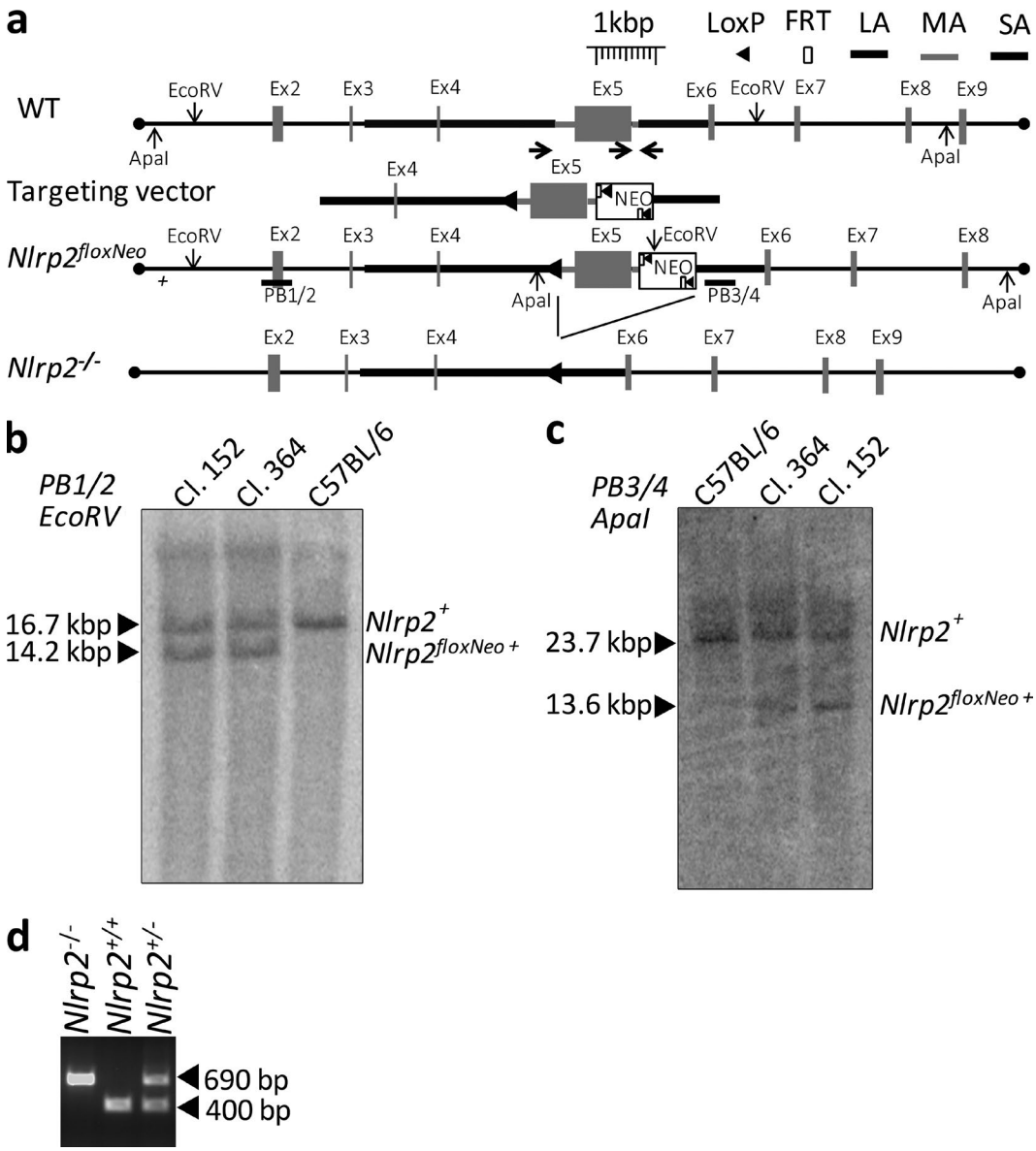

Figure S1. **Description and genotyping of *Nlrp2*$^{-/-}$ mice.** (a) *Nlrp2*$^{-/-}$ mice were generated by flanking exon 5, which encodes most of the central NACHT ATPase domain, with LoxP sites using homologous recombination in C57BL/6 ES cells. The FRT-flanked neomycin-resistance cassette was removed by breeding chimera mice to FLP recombinase-expressing mice, and Nlrp2 knockout mice were obtained after breeding mice to appropriate Cre recombinase–expressing animals. The hybridization regions of genotyping primers are indicated by horizontal arrows. Restriction enzymes EcoRV and ApaI used for Southern blotting are indicated, as are probes PB1/2 and PB3/4 for Southern blotting. (b and c) Southern blotting confirmation of homologous recombination in selected ES clones for the 5′ (b) and 3′ (c) flanking regions. (d) PCR genotyping of WT, *Nlrp2* heterozygous, and knockout mice. kbp, kilo base pairs; LA, long arm of homology; MA, middle fragment; SA, short arm of homology; LoxP, site for Cre recombinase recognition; FRT, site for FLP recombinase recognition; Ex, exon; NEO, neomycin resistance gene.

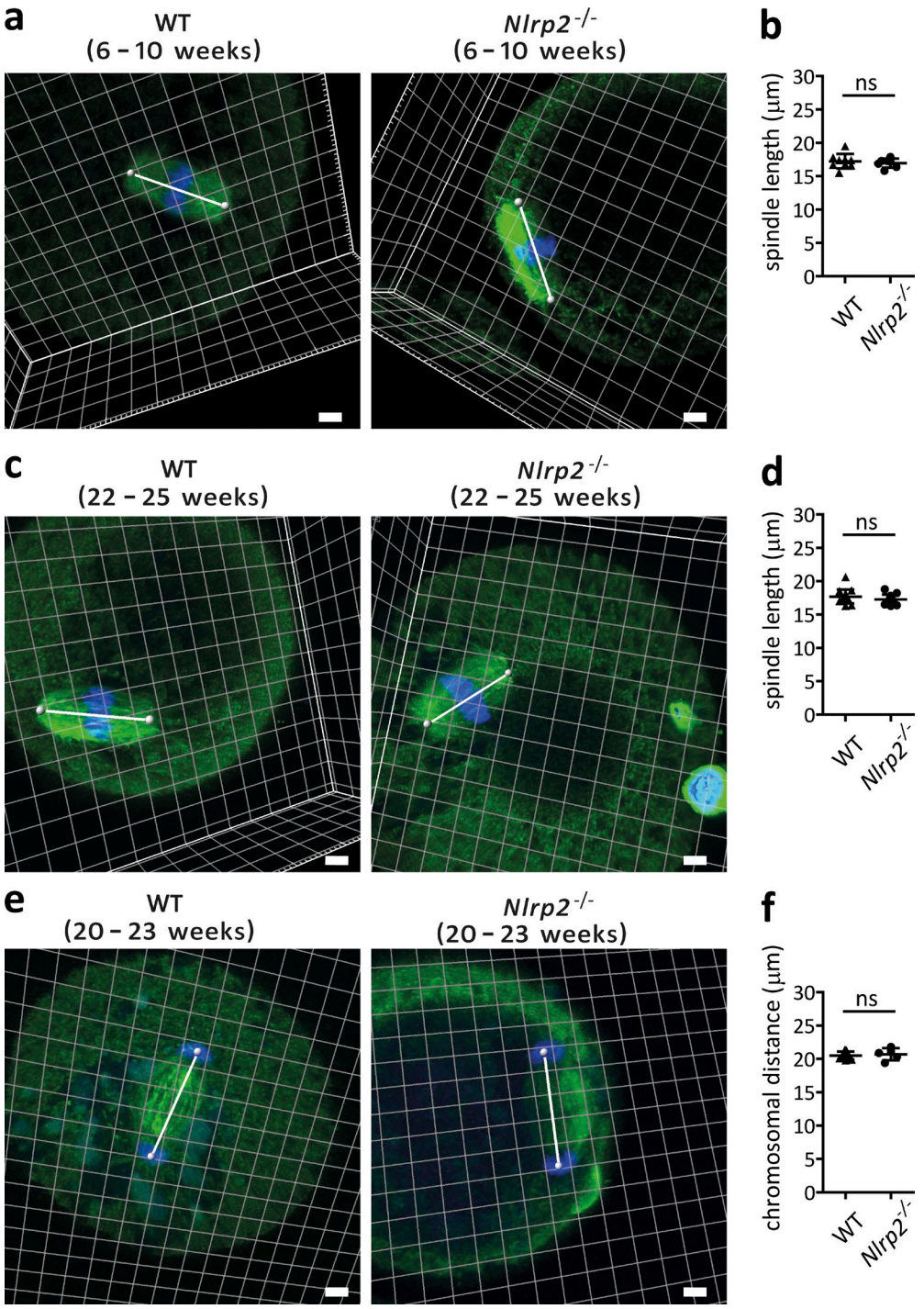

Figure S2. **Defective parthenogenetic activation is not associated with aberrant spindle morphology in MII oocytes of mature adult *Nlrp2*$^{-/-}$ mice.** (a–d) Metaphase II (MII) oocytes of WT and *Nlrp2*$^{-/-}$ mice of the indicated ages were stained for α-tubulin (green) and DAPI (blue) to visualize spindle morphology (a and c), and to quantify spindle length (b and d) in Imaris software. (e and f) Defective parthenogenetic activation is not associated with aberrant chromosome segregation in MII oocytes of mature adult Nlrp2$^{-/-}$ mice. Metaphase II (MII) oocytes of WT and *Nlrp2*$^{-/-}$ mice of the indicated ages were triggered to undergo parthenogenetic activation for 1 h before cells were stained for α-tubulin (green) and DAPI (blue; e), and the distance between chromosome sets was determined in Imaris software (f). Data represents at least three biological repeats. Statistical significance was determined by Student's *t* test; $P < 0.05$ was considered statistically significant. On fluorescent micrographs grid/scale bars are equal to 5 µm.

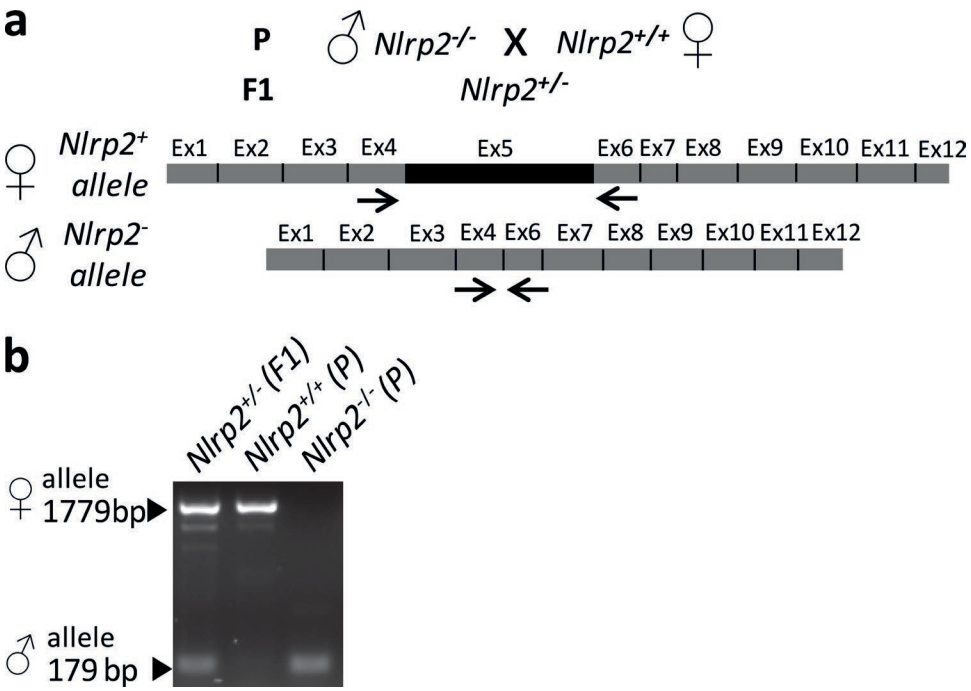

Figure S3. ***Nlrp2* is not imprinted.** (a) Schematic representation of the breeding strategy used to investigate *Nlrp2* imprinting in oocytes. (b) Oocytes of female pups from the breeding couples depicted in a were collected, and cDNA was prepared to analyze the parental *Nlrp2* alleles that were actively transcribed.

Table S1. ***Nlrp2*$^{-/-}$ mice are born with expected Mendelian ratios from heterozygous parents**

Genotype of pups	Pups born	Empirical genotype ratio	Expected genotype ratio	Statistical significance
	n	%	%	
Nlrp2$^{+/+}$	24	26.7	25.0	n.s.
Nlrp2$^{+/-}$	44	48.9	50.0	n.s.
Nlrp2$^{-/-}$	22	24.4	25.0	n.s.