Supplementary figure 1: Full genomic deletion strain of *ogr-2* by CRISPR/Cas9

(A) Illustration of *ogr-2*. The transcript's chromosomal region is denoted. Blue: Exons. Green: UTRs. Pink and purple: protein segments corresponding to the four exons. The SPK domain locus is denoted. (B) Illustration of the strategy used to generate a complete gene deletion mutant using the CRISPR/Cas9 system. The entire ORF of the *ogr-2* gene was removed by two simultaneous cuts: the first before the start codon and the second after the stop codon, followed by NHEJ repair. (C) Agarose gel electrophoresis images of PCR products spanning the *ogr-2* locus. A deletion of 1736 bp in a heterozygous population is presented in the product on the right. (D) Sequence of the *ogr-2* locus. The locations of genotyping primers and sgRNAs binding sites are indicated. The extent of each deletion is denoted in red.

Supplementary figure 2: Both *ogr-2Δ(huj1)* and *ogr-2Δ(huj18)* alleles result in lower progeny and changes in meiotic progression

(A) The relative number of nuclei in the mitotic and LZ stages in wild type, *ogr-2Δ(huj1),* and *ogr-2Δ(huj18)*. (B) Brood size and embryonic lethality (Emb) in wild-type, *ogr-2Δ(huj1)* and *ogr-2Δ(huj18)*. *p* values calculated by the two-tailed Mann-Whitney test are indicated.

Supplementary figure 3: Deletion of o*gr-2* does not lead to a significant increase in the number of pH3-positive nuclei.

(A) The proliferative zone of wild type and *ogr-2Δ* gonads stained with DAPI (blue) and Histone H3 pS10 (red). Bar = 25 µM. (B) The mean number of pH3 nuclei per gonad.

Supplementary figure 4: Deletion of o*gr-2* does not lead to a change in X chromosome pairing levels. (A) LZ and mid-pachytene stages of wild type and *ogr-2Δ* stained with DAPI (blue) and HIM-8 (red). Bar = 5 µM. (B) The mean level of HIM-8 pairing; n indicates the number of gonads scored.

Supplementary figure 5: Control staining of FLAG antibodies

Gonad of N2 stained with DAPI and FLAG antibody. Bar = 40 µM