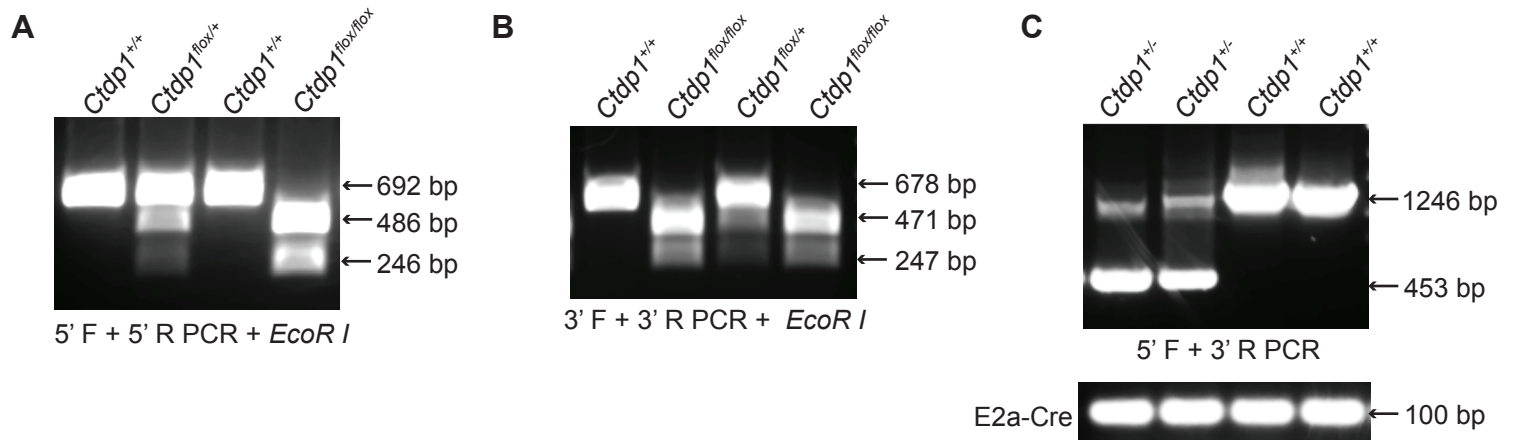


**Table S1. List of antibodies used in this study.**

| Name                    | Vendor                    | Cat#        |
|-------------------------|---------------------------|-------------|
| CTDP1                   | Bethyl Laboratories, Inc  | A301-172A   |
| HSC70                   | Santa Cruz Biotechnology  | sc-7298     |
| p27                     | Santa Cruz Biotechnology  | Sc-1641     |
| Cyclin E                | Santa Cruz Biotechnology  | Sc-247      |
| Cyclin B                | Santa Cruz Biotechnology  | Sc-166210   |
| Histone H3              | Cell Signaling Technology | 9715        |
| pHistone H3 S10         | Cell Signaling Technology | 9701        |
| $\beta$ -actin          | Santa Cruz Biotechnology  | sc-47778    |
| H2AX                    | Bethyl Laboratories, Inc  | A300-082A   |
| $\gamma$ H2AX (pSer139) | Novus Biologicals         | NB100-78356 |
| ATR                     | Cell Signaling Technology | 13934       |
| pATR S428               | Cell Signaling Technology | 2853        |
| ATM                     | Cell Signaling Technology | 2873S       |
| pATM                    | R&D System                | Af1655      |
| Chk1                    | Cell Signaling Technology | 2360        |
| pChk1 S317              | Cell Signaling Technology | 12302       |
| Chk2                    | Cell Signaling Technology | 2662        |
| pChk2 T68               | Cell Signaling Technology | 2661        |
| p53                     | Santa Cruz Biotechnology  | Sc-126      |
| FANCD2                  | Abcam                     | Ab108928    |
| RB                      | Cell Signaling Technology | 9309        |
| pRB S795                | Cell Signaling Technology | 9301        |
| pRB S780                | Cell Signaling Technology | 8180        |
| pRB S870/811            | Cell Signaling Technology | 8516        |
| Vimentin                | Cell Signaling Technology | 5741        |

**Figure S1.**

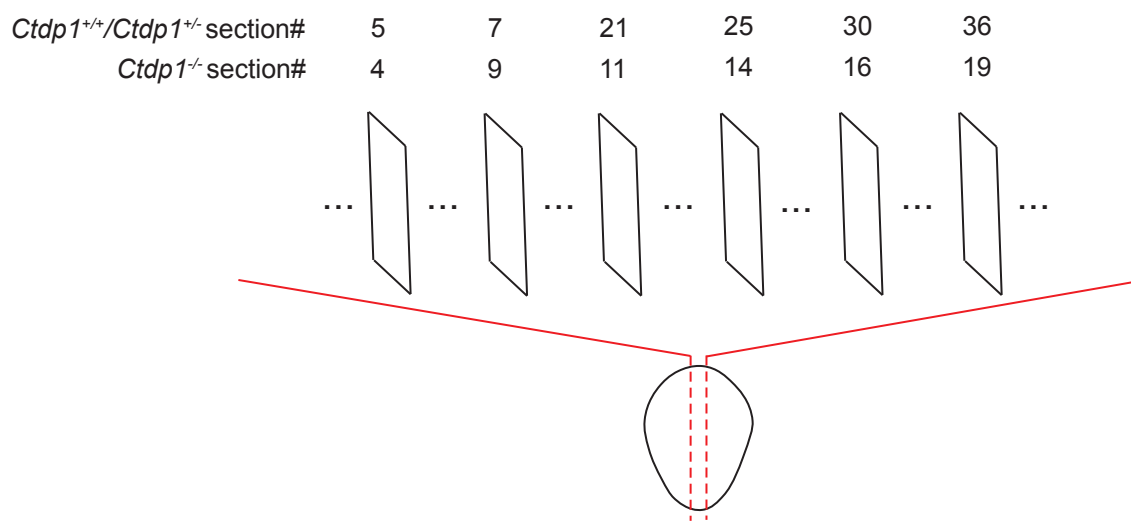


**Figure S1. Genotyping PCR reactions**

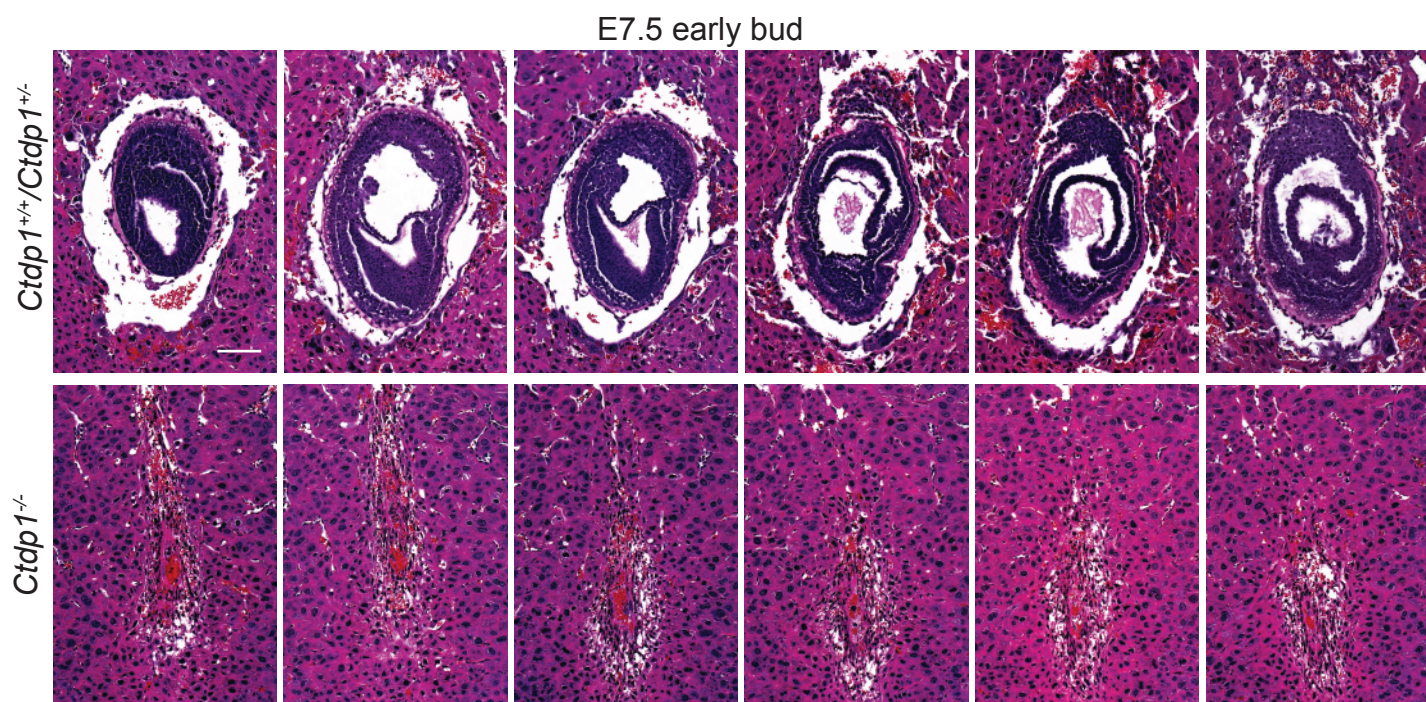
**A-B.** The representative genotyping results of the *Ctdp1<sup>flox/+</sup>* heterozygous intercross using 5'F + 5'R primers (**A**) and 3'F + 3'R primers (**B**). The expected sizes of PCR products after *EcoR I* digestion are indicated. *EcoR I* was used here to further distinguish the floxed allele and wild type allele since the size of their PCR products are similar. **C.** The representative genotyping results of the *Ctdp1<sup>flox/+</sup>;E2a-Cre* heterozygous intercross using full length 5'F + 3'R primers and E2a-Cre primers, respectively. The expected sizes of PCR products are indicated. The *Ctdp1<sup>-/-</sup>* genotype is not shown because there are no viable *Ctdp1<sup>-/-</sup>* pups.

**Figure S2.**

**A**



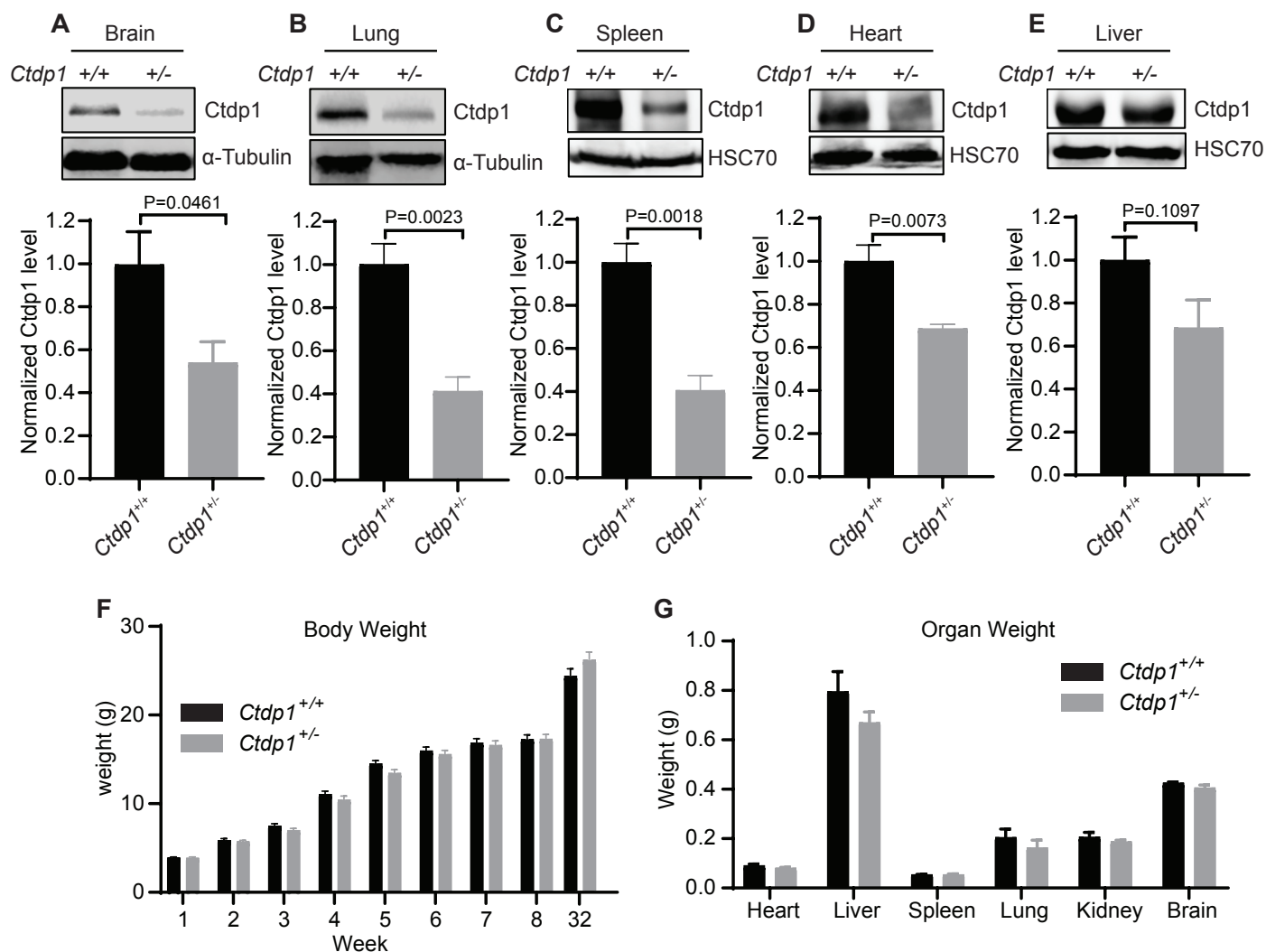
**B**



**Figure S2. H&E stained serial sagittal sections of representative mouse embryos at E7.5.**

**A.** Schematic showing the serial sections that were evaluated and their relative location within the maternal decidua corresponding to the H&E sections shown in Figure S1B. **B.** Selected representative serial sections of *Ctdp1*<sup>+/+</sup>/*Ctdp1*<sup>+/-</sup> and *Ctdp1*<sup>-/-</sup> embryos within the maternal decidua.

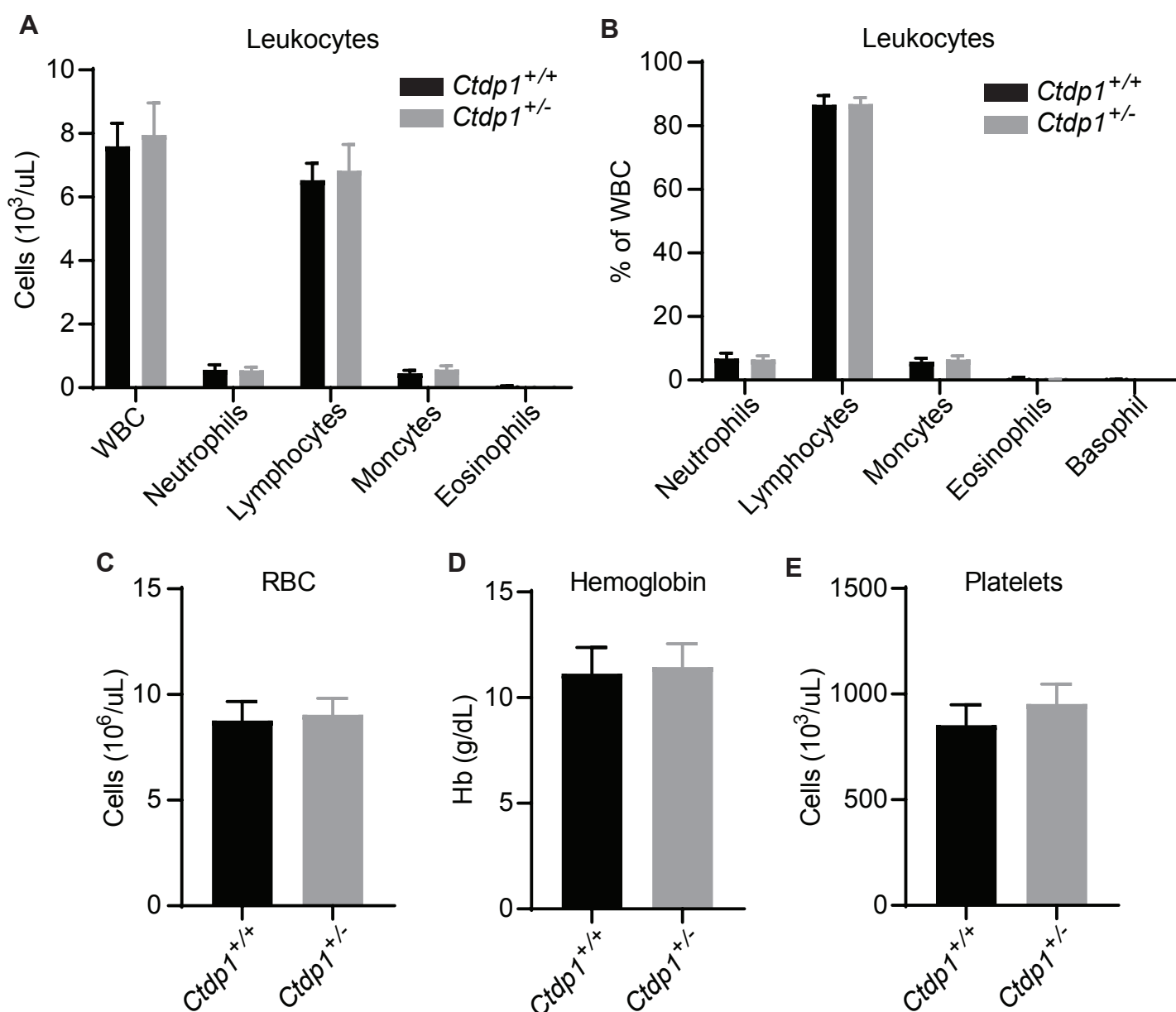
Figure S3.



**Figure S3. The Ctdp1 expression, body weight and organ weights of  $Ctdp1^{+/+}$  and  $Ctdp1^{+/-}$  mice.**

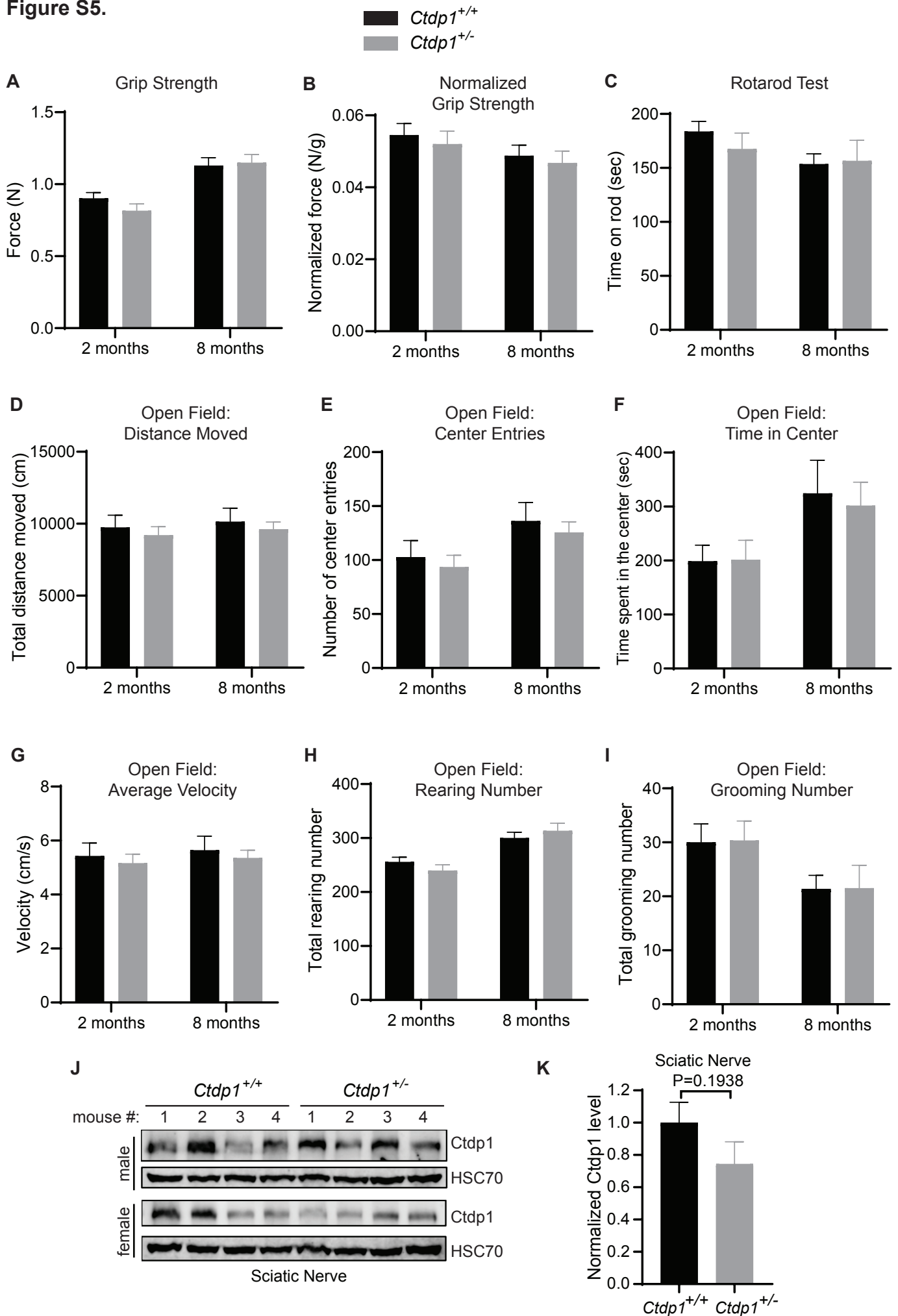
**A-E.** Western blot analysis of Ctdp1 expression of  $Ctdp1^{+/+}$  and  $Ctdp1^{+/-}$  mice at 5 weeks in the brain (**A**), lung (**B**), spleen (**C**), heart (**D**), and liver (**E**). Immunoblotting of  $\alpha$ -Tubulin or HSC70 was used as a loading control. Normalized Ctdp1 expression was quantified in 4 mice per group depicted in the bar graphs below the protein blots. Values represent the mean  $\pm$  SEM. Statistical significance was determined using Student's t-test and the P-values of the comparisons are displayed above the bar graphs. **F.** Body weight of  $Ctdp1^{+/+}$  and  $Ctdp1^{+/-}$  mice from 1-32 weeks. n = 20 per group for weeks 1-8. n = 4 per group at 32 weeks. **G.** Organ weights of  $Ctdp1^{+/+}$  and  $Ctdp1^{+/-}$  mice at 8 weeks. n = 6 per group.

Figure S4.

Figure S4. Complete blood evaluation of *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>+/-</sup> mice.

**A-B.** The numbers (**A**) and percentages (**B**) of different leukocyte groups in the blood of *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>+/-</sup> mice at 8 weeks. **C-E.** The number of red blood cells (RBC) (**C**), value of hemoglobin (**D**), and number of platelets (**E**) in the blood of *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>+/-</sup> mice at 8 weeks. For each of the measurements in panels A-E, n = 6 per group. Data are shown as mean  $\pm$  SEM.

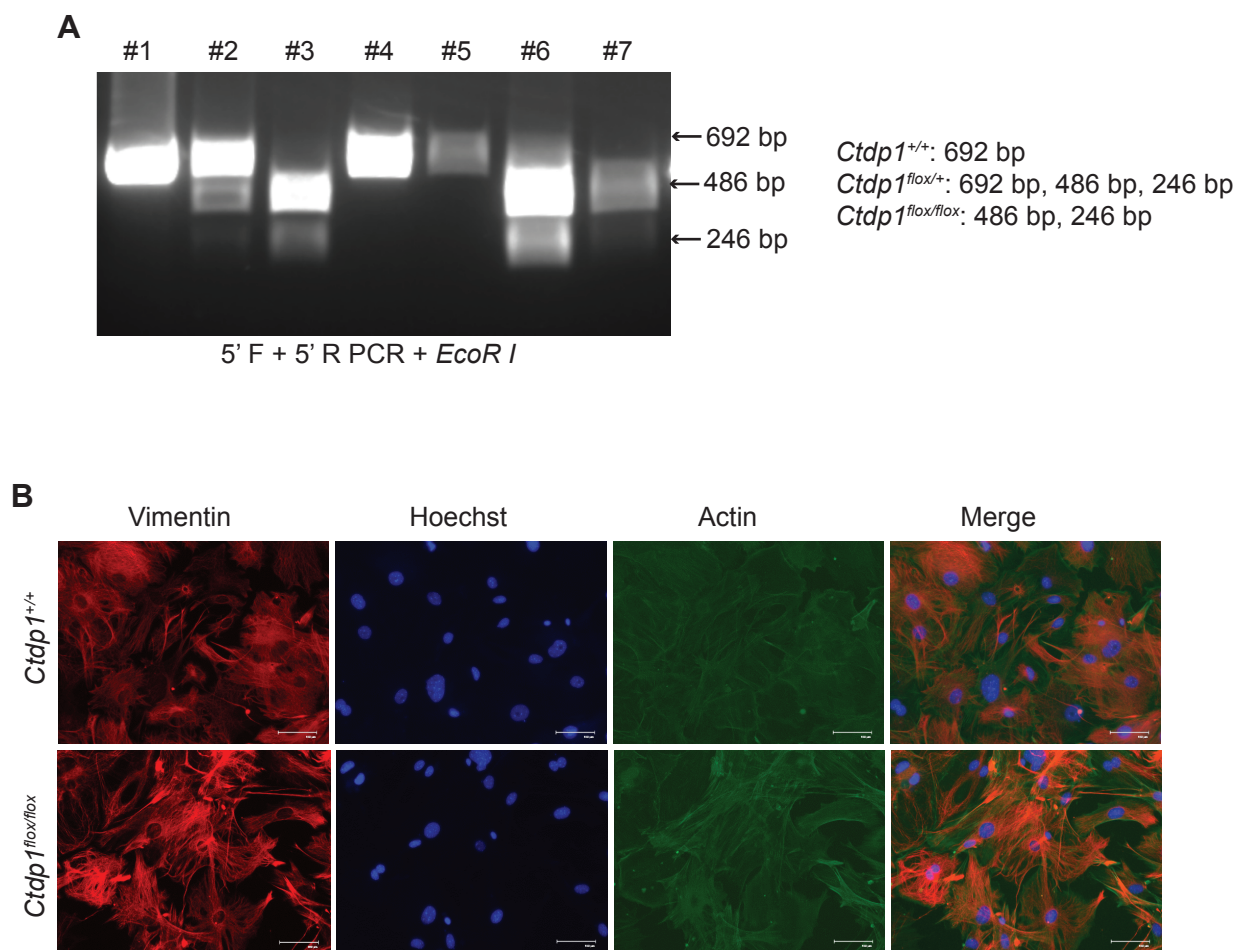
**Figure S5.**



**Figure S5. Locomotive and behavioral tests in *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice.**

**A.** Measurement of forepaw grip strength in *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice at 2 and 8 months. **B.** Normalized grip strength value of *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice at 2 and 8 months. **C.** Measurement of motor function and co-ordination using the rotarod test for *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice at 2 and 8 months. **D-I.** An open field test was performed at 2 and 8 months to evaluate mouse locomotor activity, including the following parameters: total distance moved (**D**), total number of entries in the center area (**E**), time spent in the center area (**F**), average velocity (**G**), total rearing number (**H**), and total grooming number (**I**). For mice at 2 months, n = 6 per group. For mice at 8 months, n = 8 per group. Data are shown as mean  $\pm$  SEM. **J.** Western blot analysis of the Ctdp1 protein level in the sciatic nerve of *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice at 8 months. **K.** Quantitation of the Ctdp1 protein level in the sciatic nerve of the *Ctdp1<sup>+/-</sup>* and *Ctdp1<sup>-/-</sup>* mice at 8 months. HSC70 was used as a loading control. n = 8 per group. The P-values are displayed above the bar graphs. Data are shown as mean  $\pm$  SEM.

**Figure S6.**



**Figure S6. The *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>flox/flox</sup> MEFs were successfully isolated.**

**A.** Genotyping of the seven embryos derived from a *Ctdp1*<sup>flox/+</sup> male and a *Ctdp1*<sup>flox/+</sup> female breeding. #1 and #3 were selected to establish *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>flox/flox</sup> MEFs, respectively.

**B.** Immunofluorescence staining of vimentin (fibroblast marker), actin (cytoskeletal marker), and Hoechst (nucleus marker) in *Ctdp1*<sup>+/+</sup> and *Ctdp1*<sup>flox/flox</sup> MEFs. Scale bar = 100  $\mu$ m.



Figure S7.

**REPAIR TEMPLATE with Genomic Sequence**

LoxP

EcoRI

Target Exons

5' LoxP forward Primer

5' LoxP reverse Primer

3' LoxP forward Primer

3' LoxP reverse Primer

TGCTGGCTTTGCCTTGGCAGCACCTTGAACAGTTTCCCCAGGAAAGAATCCTTTTTGTTTTCCAGCTGTC  
 TTTCCATGACCCTAGATATGTTGAGTATTCTTCTTCTCCAGTATTTCTGGAGGACATAATGCTTTTTGT  
 CTTCACTGTAAGACAGCAGATCACC<sup>EcoRI</sup>GCAGTGTGACAGTTGCCTGCTTTTCTTATGCTCTATGTAGAT  
 GACCAGTATTCTTAAATGATCTCTATTTCATTCTGCAATGTAGGTGGTGGGTGGCTGTTGCTATTTTTG  
 TTTGTTTCCATGTAAC<sup>Target Exon 3</sup>TGCAGTTGGTTTACTGGGAGAATGGACTCTTGTGCTGACTAGTACTGCCGAT  
 CTGACATAACTTCGTATAGCATA<sup>Target Exon 4</sup>CATTATACGAAGTTATGAATTC<sup>EcoRI</sup>TGCAGGTATGACCTAGAGCCCAGTT  
 TCTCATGTTTTCTTTTTTAAAAGAAAGACAGCATTACGTAGCTGTCTGTACAGGAGAGTTGTGTGCTA  
 GGATAGTAGTGTGGTAACCACTTGTGAAATCATAACCACCATTCACAGTTATGACAGATGTGCCTTT  
 CCACACAATGTTAACCAACCCTTCCACTCTTACAGGCTGCAGAGTAAAAATGGAAGGCAGCAGGTTCC  
 CCTTCCACAGCGACGGTTTCCATGGTGCACAGTGTGCCGGAGTTGATGGTGAGCTCTGAGGTGAGCAGA  
 GGACTCTGGAGCGTGGATTGATAGGCAGCCCCATCTGAATACTGACTGCTTCC<sup>5' LoxP forward Primer</sup>TAAGATGTAGCTCCGCT  
 GGCTGCCCGTTTTCTTTTTTCCGTTTCCATAAACAAC<sup>5' LoxP reverse Primer</sup>GTCTCTCCATGGATGCTTGGAAAGCCCCACAGCTC  
 TTAGTTTTGTA<sup>3' LoxP forward Primer</sup>GATTAGTCACCTTCTTGGTACTGC<sup>3' LoxP reverse Primer</sup>TGACACAGCAGCAGGGGTGGCTGCATTCCCCTTG  
 AGCCAGACTTTCTTAGAAATGCTGTGACAGGCTCCTAACAGGAAGCAGTGCTATGGCTAGGAACCTGTT  
 TGTGCTCTTTTCTTAATAAAATGAATTACGTTTTGAATCCAAATATATATACTTTGTCAATTTTTCTCAT  
 TTA<sup>Target Exon 3</sup>CTTTTGTAGCAAGCTGAGAAACTAGGAAGAGAGGATCAGCAGCGACTACATCGAAACAGAAA  
 ACTGTTTCTCATGGTTGACTTGGACCAGACCCTGATTCATACGACTGAGCAGCACTGTCCCAGATGTCC  
 AACAAA<sup>Target Exon 4</sup>GTGAGTGACTCCAGCTTTTCCCTTGGGAATTCATAACTTCGTATAGCATA<sup>Target Exon 3</sup>CATTATACGAAGTT  
 ATGGCTCTCACAAGAGTGTCCATTCCAAGTACACTCTCTTGTGTTAAGTGAGTTCC<sup>Target Exon 4</sup>TGGGAACCCTAT  
 ATGTGGGAGGCAGGTCAGTCAGCTGCTGTGGGCAGACTTCACATAGCTGTGTCTGGGCTGGGCCAGGTGG  
 CACGGGAAGTGCTCTCTCTCTTCCGTGGCATTAGCTTCTGTGT<sup>Target Exon 4</sup>CAGGTTGGCTCACACTTACTAGGGC  
 CCTTCAAGATAGAAGAGTTCAGAAACAGTCGCTGTGGAAACGGGGACCTGCTGCCTTCCATTTTTACTCT  
 GCAGCCTATAAGAGTGGAAAGGGTTTGGTTAACACTGCTGGGGGCATGCTCTTGGGAAGAGGTGTGTGTA  
 GAGTGCCTTAGAGTTAGATGTCTAGAACAAGAGGATATCTGAGGCCATGTT

**Primers**

5' LoxP forward Primer: 5'-GTGACATTTCTGTCGTCTAGTGGA-3'

5' LoxP reverse Primer: 5'-CTAATCAGTGGAAGAACCATGACG-3'

3' LoxP forward Primer: 5'-CAGCCAGCGGAGCTACATCTTAGG-3'

3' LoxP reverse Primer: 5'-CCCTAGTAAGTGTGAGCCAACCTG-3'

**Figure S7. Depiction of the *Easi*-CRISPR repair template used to generate the floxed *Ctdp1* allele.** The location of the *loxP* sites, targeted exons 3 and 4, *EcoRI* restriction site, and primer sites for PCR genotyping are highlighted.