Expanded View Figures

Figure EV1. Generation of 11B mice and expression of *ARHGAP11A*/*Arhgap11a* and *ARHGAP11B* in foetal human neocortex and embryonic wild-type and 11B mouse neocortex.

A, B qPCR analysis of the expression of *ARHGAP11A* (A) and *ARHGAP11B* (B) in foetal human neocortex at the indicated developmental stages. The level of expression obtained at 12 wpc was set to 100, and the level of expression at the other stages is given relative to this. Data are the mean of 3 technical replicates from one foetus at each stage. Error bars indicate SD.

C, D FPKM values of *ARHGAP11A* (C) and *ARHGAP11B* (D) mRNAs in the indicated isolated cell populations of foetal (12–13 wpc) human neocortex; N, neuronal fraction, which includes bRG in G1. Data were taken from the previously reported transcriptome data set (Florio *et al*, 2015).

E Diagram showing the strategy of generating the *ARHGAP11B*-transgenic mouse line. Numbers in the ARHGAP11B protein indicate the amino acid residues in the truncated GAP domain (red) and the human-specific C-terminal sequence (green).

F, G qPCR analysis on *Arhgap11a* mRNA expression in wild-type (WT, solid line) and 11B (dashed line) mouse brain (F) and *mARHGAP11B* mRNA expression in the 11B mouse brain (G) at the indicated developmental and adult stages. The levels of expression obtained in 11B mouse embryos at E12.5 were set to 100, and the level of expression at the other stages is given relative to this. Data are the mean of 3 (WT) and 3 (11B) mice at each stage. Error bars indicate SD.

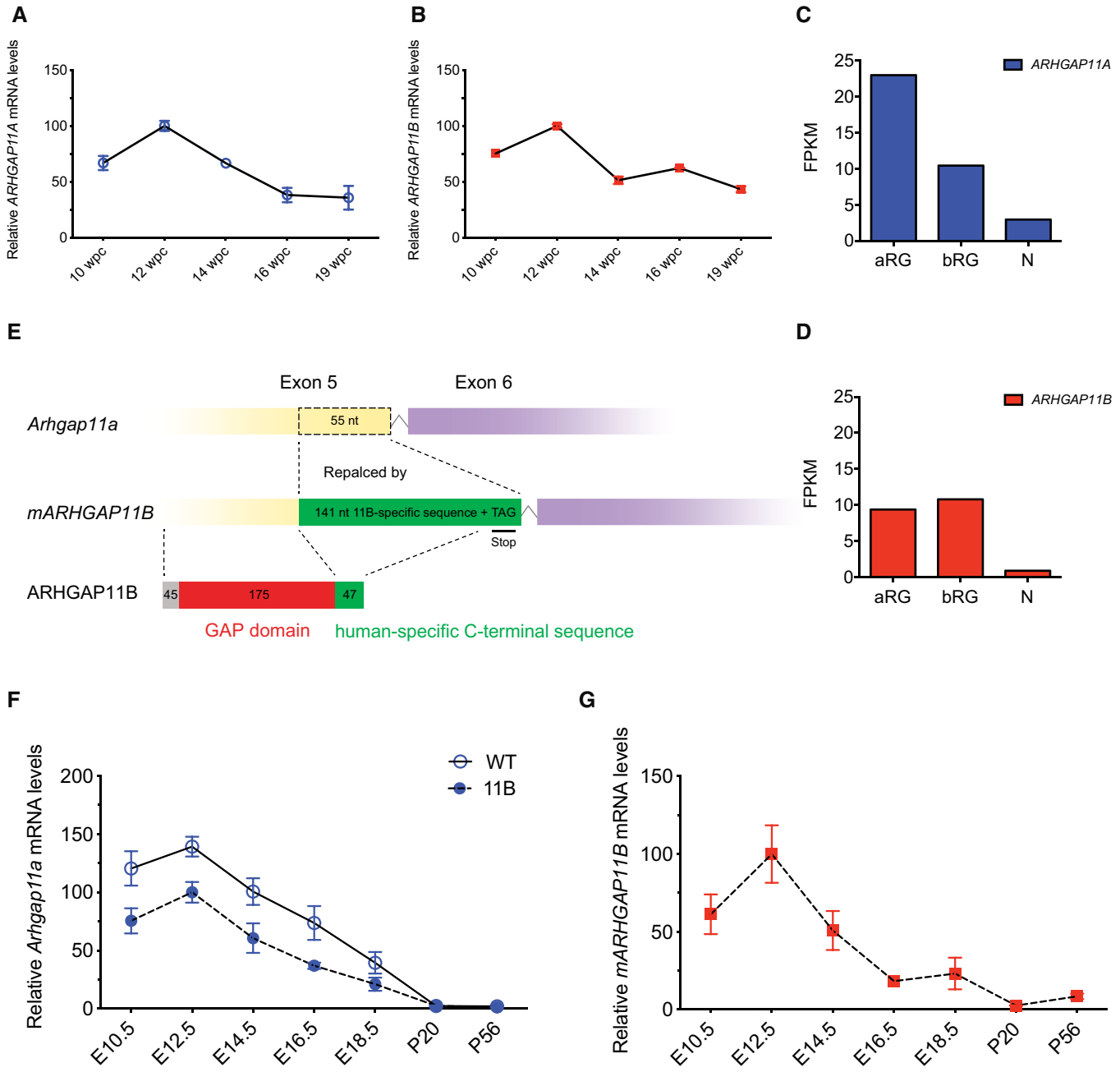

Figure EV1.

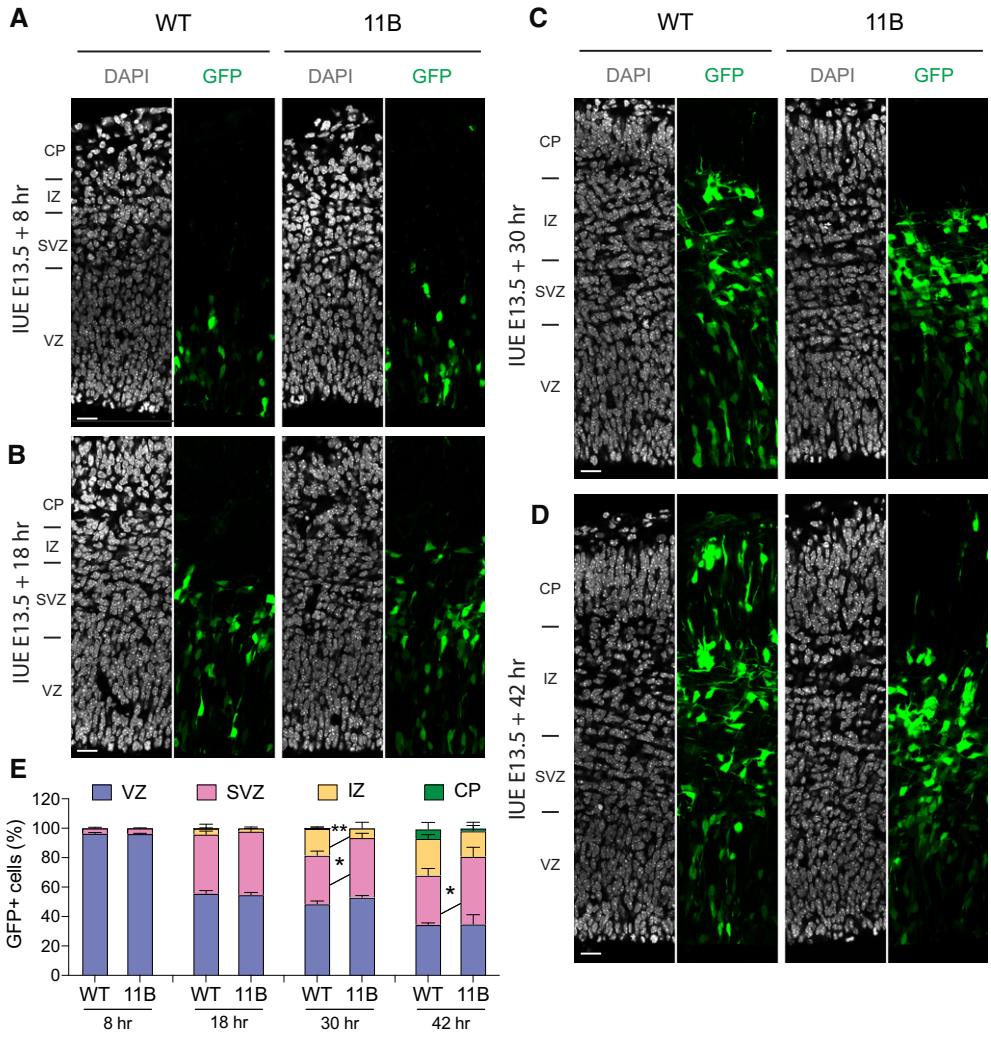

Figure EV2. Increased BP abundance results from BP self-amplification.

E13.5 wild-type and 11B mouse neocortex were subjected to IUE with a plasmid encoding GFP, followed by analyses at 8, 18, 30 and 42 h post-IUE.

A–D Representative immunofluorescence for GFP (green), combined with DAPI staining (white), of wild-type (WT) and 11B mouse dorsolateral neocortex rostrally at 8 h (A), 18 h (B), 30 h (C) and 42 h (D) post-IUE. Images are single optical sections. Scale bars, 20 μm.

E Distribution of GFP^+ cells across the indicated zones of the neocortical wall, expressed as percentage of the total number of GFP^+ cells in a 200 μm-wide segment of the entire cortical wall, of WT and 11B mouse dorsolateral neocortex, using immunostained cryosections obtained as in (A–D). Data are the mean of 3–5 (WT) and 3–5 (11B) littermate embryos, which were derived from 3 to 4 separate litters at each time point analysed. Error bars indicate SD, two-way ANOVA, followed by Bonferroni's multiple comparisons test, $^*P < 0.05$, $^{**}P < 0.01$. $P = 0.0231$ (30 h, SVZ); $P = 0.0086$ (30 h, IZ); $P = 0.0466$ (42 h, SVZ).

Figure EV3. Analysis of the dendritic and spine morphology of upper-layer neurons in the adult WT and 11B mouse neocortex.

A, B Examples of a Golgi-Cox stained upper-layer pyramidal neuron (A) and dendritic spines of an upper-layer neuron (B) in layers II + III of the somatosensory cortex of the rostral neocortex of P56 adult wild-type (WT) mice. Images are a Z-stack projection of five optical sections (A) and a single optical section (B). Scale bars, 10 μm (A); 5 μm (B).

C Representative Sholl analysis image showing the dendritic morphology of an adult mouse neocortical upper-layer neuron. The cell mask was drawn using Fiji to represent the shape of the upper-layer neuron. Concentric circles, with 10-μm intervals, were placed on the upper-layer neuron cell mask using the Sholl analysis plug-in in Fiji. Intersections with the concentric circles are indicated by the dots.

D–G Quantification of the numbers of apical (D), basal (E) and total (F) dendritic intersections with the concentric circles and the total dendritic length (G) of adult WT (white) and 11B (black) mouse neocortical upper-layer neurons, using Golgi-Cox stained vibratome sections obtained as in (A). Data are the mean of 3 (WT) and 3 (11B) adult male mice. Error bars indicate SD. Two-tailed unpaired Student's *t*-test.

H, I Quantification of spine number in a 10 μm-long dendrite (H) and of the percentage of each spine morphotype (I) of P56 adult WT (white) and 11B (black) mouse neocortical upper-layer neurons, using Golgi-Cox stained vibratome sections obtained as in (B). Data are the mean of 3 (WT) and 3 (11B) adult male mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

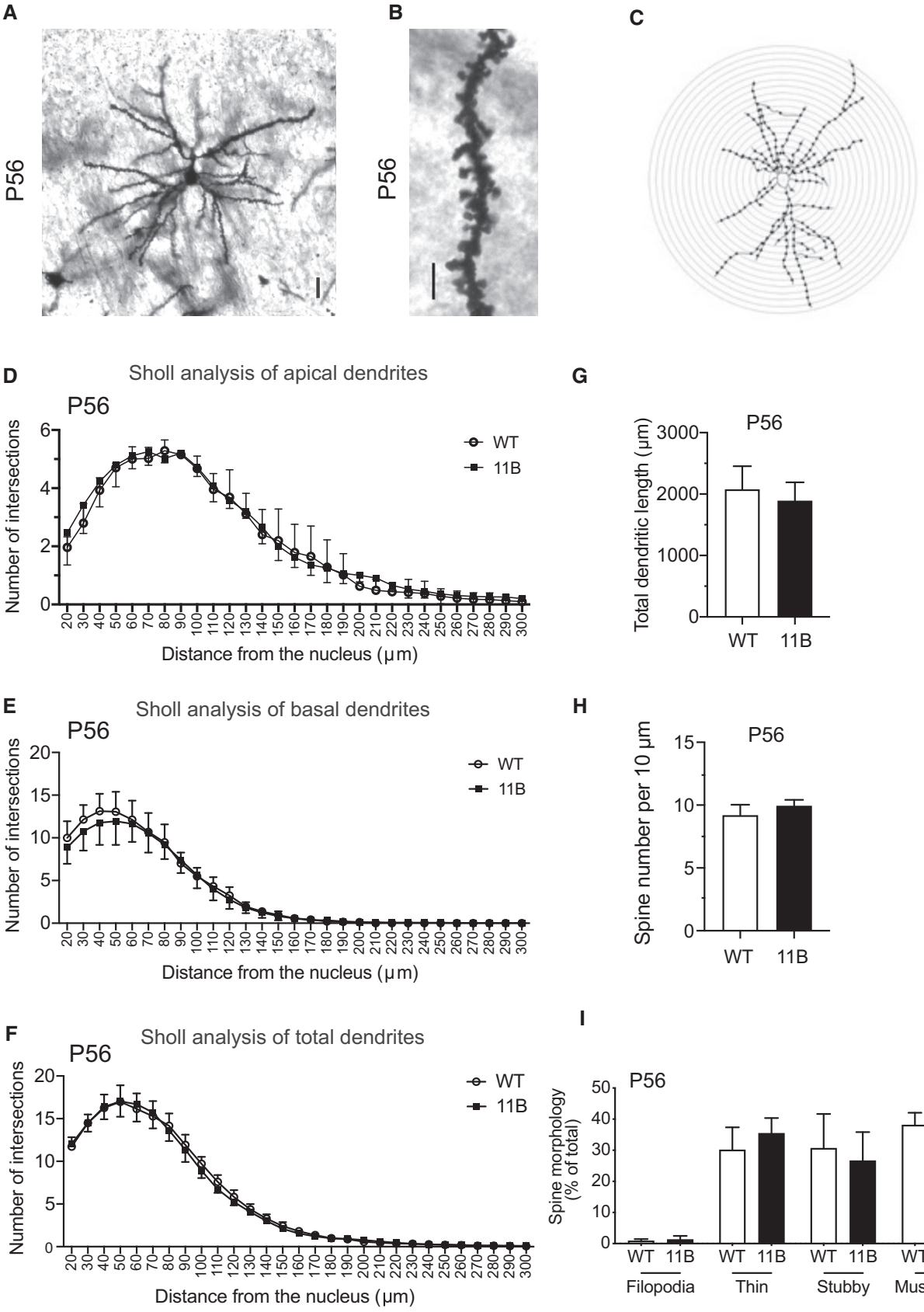

Figure EV3.

Figure EV4. Learning and memory analyses of 11B mice.

A–F Quantification of the primary distance (A–C) and primary error number (D–F) before reaching the target escape box during training sessions of adult wild-type (WT) and 11B male (A, D) and female (B, E) mice in the Barnes Maze. Quantification of primary distance (C) and primary error number (F) before reaching the target hole during the probe test one day after the training sessions of adult WT and 11B male and female mice in the Barnes maze. Data are the mean of 12 male (WT), 12 male (11B), 12 female (WT) and 12 female (11B) mice. Error bars indicate SD. Two-way ANOVA and two-tailed unpaired Student's *t*-test.

G–I Quantification of track length (G), average velocity (H) and % spontaneous alteration (I) of adult WT and 11B mice in the Y maze. Data are the mean of 7 male (WT), 11 male (11B), 8 female (WT) and 9 female (11B) mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

J, K Quantification of freezing time of adult WT and 11B male (G) and female (H) mice in the fear conditioning test. Data are the mean of 7 male (WT), 12 male (11B), 8 female (WT) and 9 female (11B) mice. Error bars indicate SD, two-way ANOVA.

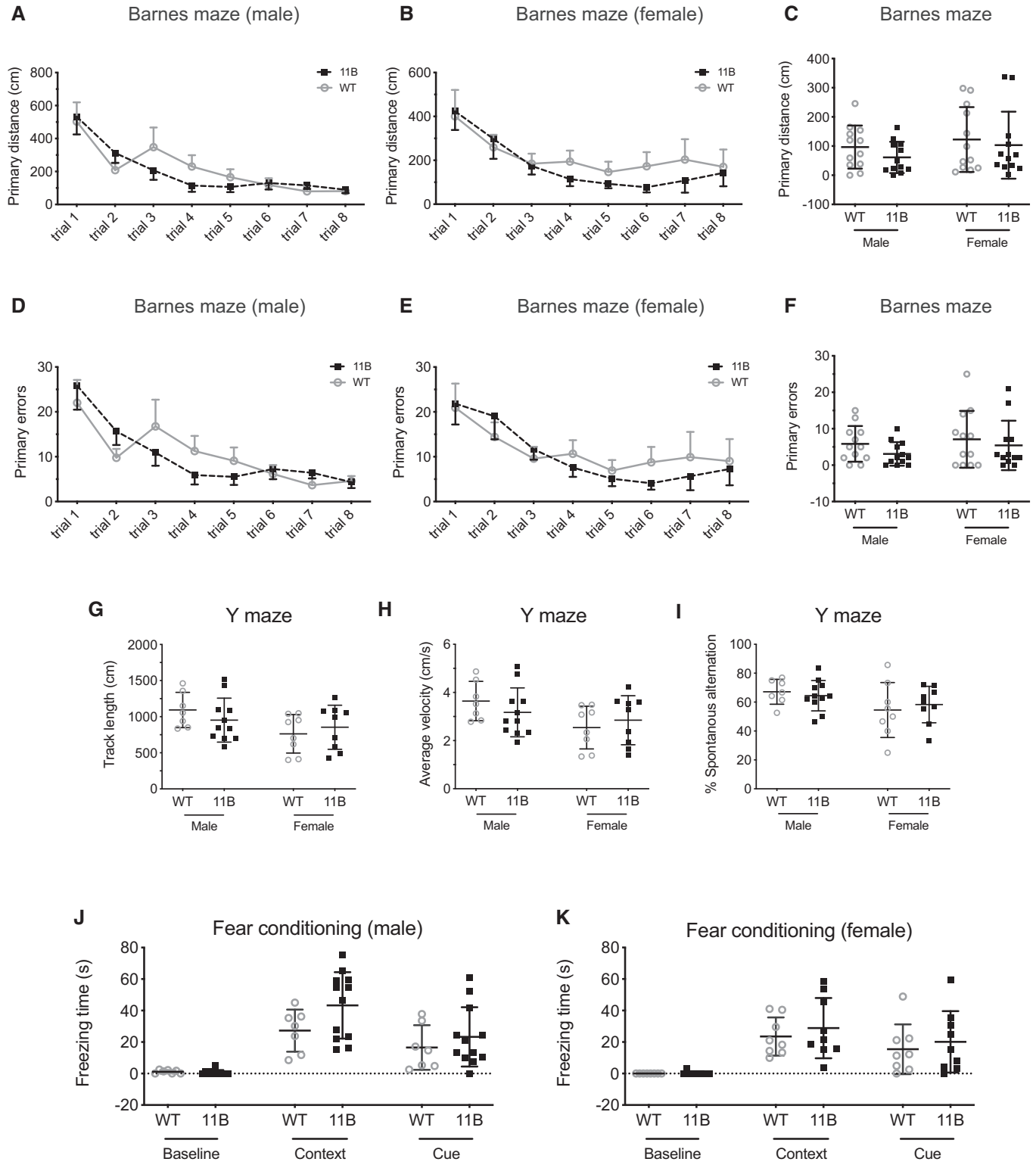

Figure EV4.

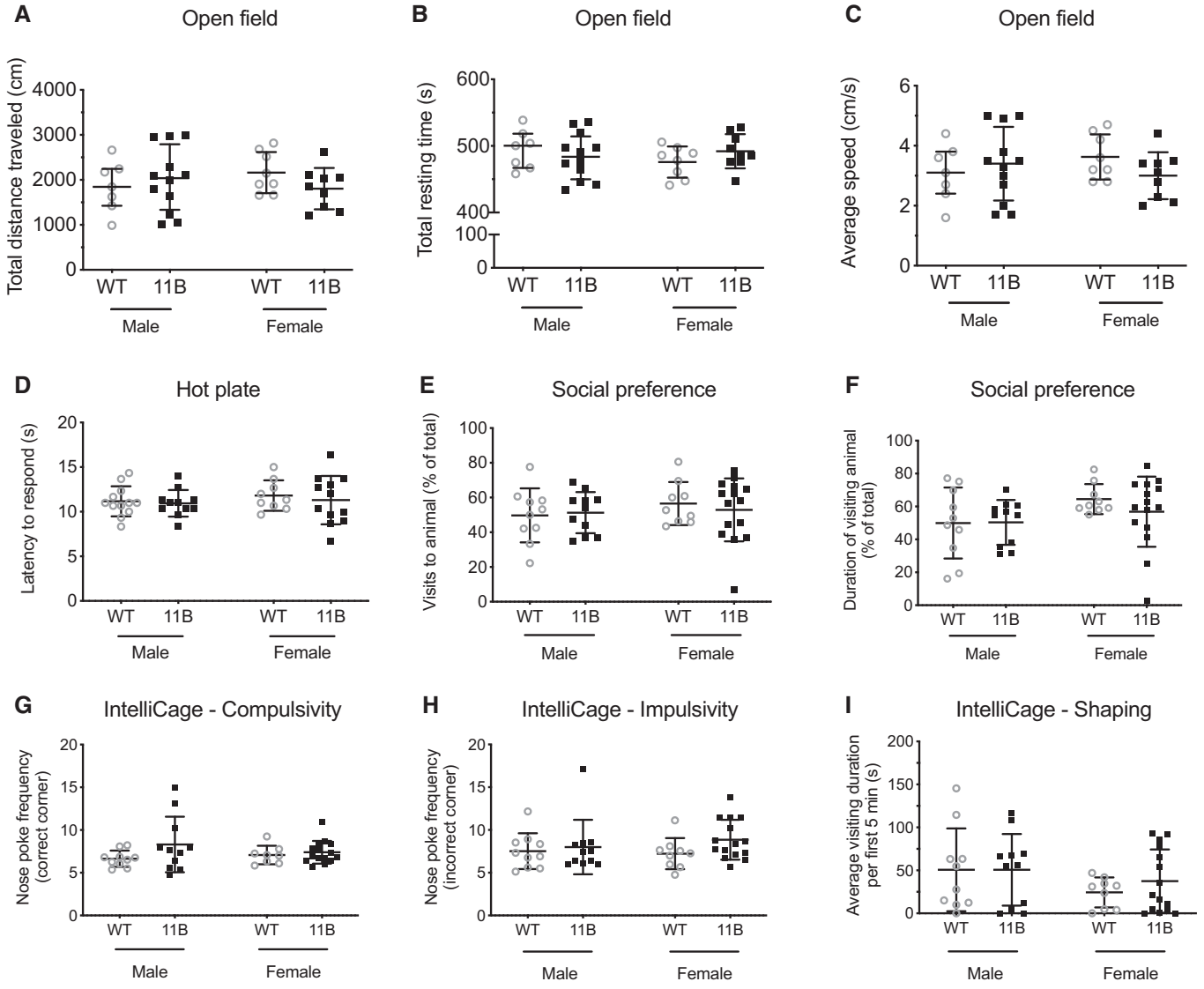

Figure EV5. Behavioural analyses of male and female adult 11B mice.

A–C Quantification of the total distance travelled (A), total resting time (B) and average speed (C) of adult wild-type (WT) and 11B mice in open field. Data are the mean of 7 male (WT), 12 male (11B), 8 female (WT) and 9 female (11B) mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

D Quantification of the latency of adult WT and 11B mice to respond in the hot plate test. Data are the mean of 12 male (WT), 12 male (11B), 9 female (WT) and 12 female (11B) mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

E, F Quantification of the percentage of visits (E) and of the visiting duration (F) to the target animal of adult WT and 11B mice in the social preference test. Data are the mean of 10 male (WT), 11 male (11B), 9 female (WT) and 15 female (11B) mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

G, H Quantification of the nose-poke frequency in IntelliCage for compulsivity (G) and impulsivity (H) of adult WT and 11B mice. Data are the mean of 10 male (WT), 11 male (11B), 8 female (WT) and 15 female (11B) mice. Error bars indicate SD, two-tailed unpaired Student's *t*-test.

I Quantification of the average visiting duration within the 5 min after water is accessible in IntelliCage for competitive dominance behaviour of adult WT and 11B mice. Data are the mean of 10 male (WT), 11 male (11B), 9 female (WT) and 15 female (11B) mice. Error bars indicate SD, Mann–Whitney test.