Supporting Information

Supplementary Materials and Methods

Tail Suspension Test. Mice were 3-5 months of age at time of test, derived from crosses between WT and *LRF*$^{+/-}$ animals. Mice were suspended by the tail for 1 minute and observed for hind limb clasping. Data was scored based on clasping during the first 30 seconds of the test (score of 2), within the 1 minute period (score of 1), or no clasping (score of 0).

Statistical Analysis

Tail Suspension. A Z-test for proportions, comparing between genotypes was used. The proportion of mice clasping in each group (determined by sex and genotype), regardless of severity, was pooled and compared against the proportion of mice that displayed no clasping.

Dark-Light Test. Duration response variables were initially converted to proportions by dividing by the length of the experiment (300 seconds). Each response variable was investigated for normality using the Box-Cox transform via the R statistical software package. Normalizing transforms (e.g., unity, log, square root, or square transforms) were selected for each variable as indicated by the Box-Cox transform. Transformed variables were subsequently analyzed using *proc GLM* and *proc Mixed* in SAS V9.1. The *repeat* statement was used in both cases to account for correlations inherent in repeated measures. In the case of *proc GLM*, a full model including main effects of genotype and sex, plus their interaction, was investigated. In the case of the *proc Mixed* analysis, models were stepwise reduced from a full model (including main effects of genotype, sex and time, plus first and second order interactions) by removing non-significant terms. Stepwise reduction began with removal of higher order interaction terms. All main effects found in any remaining interaction were left in the model regardless of significance. Reduction only occurred if removal of the non-significant term failed to significantly change the fit of the model. The reduced model was used to estimate means across days (within each genotype and gender combination), genotypes (within each gender and day combination) and gender (within each genotype and day combination).

Social Recognition Test. A similar process was used to analyze the data from social recognition test. Again, *proc GLM* and *proc Mixed* (SAS V9.1) were used. The Bonferroni and Tukey multiple comparison procedures were used (*proc GLM* with the *bon* and *tukey* option, respectively) to investigate the differences between responses from each of the experimental repeats. Based on these results, each response variable was analyzed by pooling the first 3 or 4 experimental repeats (depending on test) and comparing this to the final repeat. Finally, data were also analyzed assuming no pooling, using *proc* Mixed. Only full models were considered, which included main effects of experimental repeat, gender and genotype, plus all first and second order interactions. This model was used to estimate means across days, genotypes and gender, as well as between gender and genotypes.