## File S1: Sample code for linear mixed models

The linear mixed models employed were all variations on the following general model:

$$Y = X\beta + \sum_{j=1}^{5} Z_j \gamma_j + \epsilon$$

where:

*Y* is an  $n \times 1$  vector of responses.

X is a fixed effects design matrix which can accommodates sex and treatment (and the interaction thereof), the pre-treatment phenotype value, as well an intercept.

 $\beta$  is a vector of fixed-effect parameters associated with *X*.

 $Z_i$  is an  $n \times q_i$  random effect design matrix.

 $\gamma_i$  is the  $q_i \times 1$  random effect vector associated with the *j*th random effect.

Our models of interest include up to five random effects: a batch effect ( $\gamma_1$ ), parental strain effect ( $\gamma_2$ ), a parental strain-by-treatment interaction effect ( $\gamma_3$ ), a sex-by-strain effect ( $\gamma_4$ ), and sex-by-strain-by-treatment interaction effect ( $\gamma_5$ ). The associated random design matrices are constructed as follows:

- Each row of Z<sub>1</sub> has a single nonzero element, which is a 1 in the column corresponding to mouse's batch.
- Each row of  $Z_2$  has two nonzero elements, which are 1's in the columns corresponding to the parental strains.
- $Z_3$  is constructed from  $Z_2$  by switching the 1's to -1's for mice that are treated with placebo.
- $Z_4$  and  $Z_5$  are constructed from  $Z_2$  and  $Z_3$ , respectively, by switching the signs of the two elements in each row corresponding to female mice.

We assume that the  $\gamma_j$ 's are mutually independent and  $\gamma_j \sim N(0, \sigma_j^2 I_{q_j \times q_j})$ . Further, the error term  $\epsilon \sim N(0, \sigma_\epsilon^2 * I_{n \times n})$ , independent of the random effects (*n* denotes the total sample size for the phenotype being studied).

All our models were fit with the SAS code below, where &depvar and &indvars are macro variables that contain the dependent and relevant independent variables, respectively, for the phenotype being modeled, and &numbatch and &numparent correspond to the number of batches and number of parental strains represented in the dataset.

```
proc mixed data=dataset;
model &depvar. = &indvars. / s;
random batch1-batch&numbatch. / type = TOEP(1);
random addint1-addint&numparent. / type = TOEP(1);
random addtmt1-addtmt&numparent. / type = TOEP(1);
random addsex1-addsex&numparent. / type = TOEP(1);
random addsextmt1-addsextmt&numparent. / type = TOEP(1);
run;
```