## 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 $X$.
$Z_{j}$ is an $n \times q_{j}$ random effect design matrix.
$\gamma_{j}$ is the $q_{j} \times 1$ random effect vector associated with the $j$ th random effect.
Our models of interest include up to five random effects: a batch effect $\left(\gamma_{1}\right)$, parental strain effect $\left(\gamma_{2}\right)$, a parental strain-by-treatment interaction effect ( $\gamma_{3}$ ), a sex-by-strain effect ( $\gamma_{4}$ ), and sex-by-strain-bytreatment interaction effect $\left(\gamma_{5}\right)$. The associated random design matrices are constructed as follows:

- Each row of $Z_{1}$ 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 $\gamma_{j} \sim N\left(0, \sigma_{j}^{2} I_{q_{j} \times q_{j}}\right)$. Further, the error term $\epsilon \sim N\left(0, \sigma_{\epsilon}^{2} * I_{n \times n}\right.$ ), 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 $=\operatorname{TOEP}(1)$;
run;

