## Justification for focus of allelic data over genotypic data

For the purposes of this paper, reference refers to the allele listed in the mm10 genome build and alternative refers to the common nucleotide that does not match the reference (GRCm38/mm10). This differs from Xu and Garland (2017) who used 0 to represent the most common allele and 1 for the minor allele (prior to culling mice for analysis)

The genotypic data are organized such that for every locus a mouse has a single data point:

0 = homozygous reference (H0)

0.5 = heterozygous (Het)

1 = homozygous alternative (H1)

The allelic data are organized such that for every locus a mouse has two data points representing the two alleles, with either a 0 for the reference allele or 1 for the alternative.

Since the genotypic data is a single number for each locus and mouse, within-mouse variance cannot be calculated. This is not true for the allelic data. This creates potential problems in the accurately estimating the variance for calculation of F statistics. Below is an example from the MegaMUGA data (UNC010516347, chr1:6,010,860).

**Table S7 Distribution of genotypes in each line for marker UNC010516347**

|  |  |  |  |
| --- | --- | --- | --- |
| Line | H0 | Het | H1 |
| C1 | 2 | 8 | 0 |
| C2 | 1 | 8 | 0 |
| C4 | 2 | 8 | 0 |
| C5 | 0 | 10 | 0 |
| HR3 | 0 | 8 | 0 |
| HR6 | 0 | 9 | 0 |
| HR7 | 0 | 10 | 0 |
| HR8 | 0 | 7 | 0 |

At a glance, this marker should not be differentiated between the HR and C lines. However, the genotypic data produces a p-value of 0.0677 (suggestive before multiple testing correction). Alternatively, the allelic analysis of the same marker produces a p-value of 0.5819 (Xu and Garland, 2017). Although examples such as this marker should be rare, markers with allele distributions like this are better analyzed with the allelic data.