**Tables**

**Table 1**. The number of monosomies, disomies and tetrasomies seen for each MA experiment. The homozygous MA experiment had 32 events in 145 MA lines maintained for 2063 generations. The heterozygous MA experiment had 38 events in 76 MA lines maintained for 2103 generations.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **# monosomic** | | | **# trisomic** | | | **# tetrasomic** | | **total events** | |
| Chrom. # | homo | hetero | homo | | hetero | homo | | hetero | homo | hetero |
| 1 | 0 | 1 | 1 | | 3 | 0 | | 0 | 1 | 4 |
| 2 | 0 | 0 | 3 | | 0 | 0 | | 0 | 3 | 0 |
| 3 | 0 | 0 | 2 | | 0 | 0 | | 0 | 2 | 0 |
| 4 | 0 | 0 | 3 | | 0 | 0 | | 0 | 3 | 0 |
| 5 | 0 | 0 | 3 | | 4 | 0 | | 0 | 3 | 4 |
| 6 | 0 | 0 | 0 | | 0 | 0 | | 0 | 0 | 0 |
| 7 | 0 | 0 | 1 | | 5 | 0 | | 0 | 1 | 5 |
| 8 | 0 | 0 | 4 | | 0 | 0 | | 0 | 4 | 0 |
| 9 | 2 | 0 | 3 | | 2 | 0 | | 0 | 5 | 2 |
| 10 | 0 | 0 | 1 | | 1 | 0 | | 0 | 1 | 1 |
| 11 | 0 | 0 | 1 | | 0 | 0 | | 0 | 1 | 0 |
| 12 | 0 | 0 | 1 | | 7 | 0 | | 0 | 1 | 7 |
| 13 | 0 | 0 | 0 | | 0 | 0 | | 0 | 0 | 0 |
| 14 | 0 | 0 | 4 | | 2 | 0 | | 0 | 4 | 2 |
| 15 | 0 | 0 | 0 | | 1 | 0 | | 0 | 0 | 1 |
| 16 | 0 | 0 | 3 | | 10 | 0 | | 1 | 3 | 11 |

**Table 2.3**. Expected mean of gene expression in MA lines trisomic for single chromosome shown. Because more reads map to trisomic chromosome, number mapping to rest of genome will decline slightly.

|  |  |
| --- | --- |
| Trisomic Chromosome | Expected expression for trans genes |
| 1 | 0.98 |
| 2 | 0.94 |
| 3 | 0.97 |
| 4 | 0.89 |
| 5 | 0.95 |
| 6 | 0.98 |
| 7 | 0.92 |
| 8 | 0.96 |
| 9 | 0.96 |
| 10 | 0.94 |
| 11 | 0.95 |
| 12 | 0.92 |
| 13 | 0.93 |
| 14 | 0.94 |
| 15 | 0.92 |
| 16 | 0.93 |

**Table 2.2**. Number of aneuploid versus euploid MA lines in each experiment. The heterozygous ancestor strain gave rise to a substantially higher proportion of aneuploid MA lines, indicating a significantly higher mutation rate.

|  |  |  |
| --- | --- | --- |
|  | | |
|  | Heterozygous  ancestor | Homozygous  ancestor |
|  | | |
| Aneuploid  MA lines | 29 | 28 |
| Euploid  MA lines | 47 | 117 |
|  | | |

\*p<0.0001 Fisher’s exact test

**Table 2.4:** Variance comparison between aneuploid and euploid chromosomes in aneuploid versus euploid MA lines. Note: MA line 76 (Het-76) derived from the heterozygous ancestor carries a partial duplication of chromosome 14. As such, we did not examine the variance in expression for that chromosome.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| MA line | | Aneuploidy present\* | Euploid line comparison | | Aneuploid chromosomes  Levene's Statistic (p-value) | | Euploid chromosomes  Levene's Statistic (p-value) | |
| Hom-152 | 1, 7 | | Hom-1 | Chr 1: 0.21  Chr 7: 0.58 | | 4.9E-1 | |
| Hom-117 | 5 | | Hom-2 | 3.9E-11 | | 1.2E-12 | |
| Hom-123 | 5 | | Hom-3 | 3.5E-15 | | 6.5E-10 | |
| Hom-108 | 7, 9m | | Hom-4 | Chr 7: 6.0E-14  Chr 9: 4.2E-3 | | 1.1E-55 | |
| Hom-15 | 9 | | Hom-5 | 0.15 | | 2.5E-4 | |
| Hom-29 | 9m | | Hom-6 | 8.2E-1 | | 2.1E-9 | |
| Hom-88 | 9 | | Hom-7 | 4.4E-4 | | 4.6E-10 | |
| Hom-119 | 9 | | Hom-8 | 2.1E-1 | | 1.9E-1 | |
| Hom-9 | 14 | | Hom-11 | 4.1E-3 | | 7.8E-5 | |
| Hom-112 | 16 | | Hom-28 | 1.6E-5 | | 9.8E-1 | |
| Het-7 | 1 | | Het-1 | 1.6E-1 | | 6.8E-17 | |
| Het-11 | 1m, 15 | | Het-2 | Chr 1: 1.6E-1  Chr 15:1.1E-2 | | 2.2E-8 | |
| Het-18 | 1 | | Het-3 | 1.7E-4 | | 2.0E-2 | |
| Het-4 | 5 | | Het-5 | 2.3E-4 | | 1.5E-9 | |
| Het-49 | 5 | | Het-9 | 1.4E-6 | | 7.8E-2 | |
| Het-59 | 7 | | Het-69 | 3.1E-30 | | 3.8E-9 | |
| Het-61 | 7 | | Het-1 | 0.023 | | 2.4E-3 | |
| Het-76 | 9, 10p, 14 | | Het-2 | Chr 9: 8.99E-1  Chr 14: 8.8E-3 | | 4.55E-12 | |
| Het-77 | 12 | | Het-3 | 5.6E-13 | | 3.2E-3 | |
| Het-8 | 16tet | | Het-5 | 1.2E-1 | | 1.1E-16 | |

**\*** mmonosomic. ppartial duplication, tettetrasomic. All others trisomic.

**Table 2.5**. The expected expression of a gene for each expression category following trisomy (2🡪3 copies) or monosomy (2🡪1copy).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Expression Category | | | | |
| Copy number | 1 | 2 | 3 | 4 | 5 |
| 2 🡪 3 | 1.5x | 1-1.5x | 1x | <1x | > 1.5x |
| 2 🡪 1 | 0.5x | 0.5-1x | 1x | >1x | <0.5x |

**Table 2.6.** The number of genes in each expression change category across the aneuploid strains for which we have RNAseq data. 0 = unknown, 1 = no dosage compensation (DC) , 2 = partial DC, 3 = full DC , 4 = over-compensation, 5 = anti-compensation.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Category | | | | | | | | | | | |
| MA line | Aneuploidy | 0 | | 1 | | 2 | | 3 | | 4 | | 5 | | |
| Hom-152 | 1, 7  Chr 1:  Chr 7: | 52  482 | 22  9 | | 6  12 | | 0  0 | | 0  0 | | 1  0 | |
| Hom-117 | 5 | 147 | 107 | | 5 | | 0 | | 0 | | 0 | |
| Hom-123 | 5 | 209 | 50 | | 5 | | 0 | | 0 | | 1 | |
| Hom-108 | 7, 9m  Chr 7:  Chr 9: | 212  41 | 76  8 | | 129  64 | | 0  0 | | 39  84 | | 42  2 | |
| Hom-15 | 9 | 62 | 82 | | 52 | | 0 | | 0 | | 3 | |
| Hom-29 | 9m | 90 | 1 | | 107 | | 0 | | 1 | | 0 | |
| Hom-88 | 9 | 58 | 78 | | 50 | | 0 | | 0 | | 13 | |
| Hom-119 | 9 | 70 | 92 | | 37 | | 0 | | 0 | | 1 | |
| Hom-9 | 14 | 92 | 140 | | 128 | | 0 | | 0 | | 13 | |
| Hom-112 | 16 | 244 | 20 | | 0 | | 0 | | 0 | | 0 | |
| Het-7 | 1 | 51 | 29 | | 1 | | 0 | | 0 | | 0 | |
| Het-11 | 1m, 15  Chr 1:  Chr 15: | 67  413 | 0  57 | | 10  5 | | 0  0 | | 4  0 | | 0  0 | |
| Het-18 | 1 | 45 | 29 | | 6 | | 0 | | 1 | | 0 | |
| Het-4 | 5 | 165 | 71 | | 5 | | 0 | | 3 | | 21 | |
| Het-49 | 5 | 135 | 89 | | 10 | | 0 | | 0 | | 0 | |
| Het-59 | 7 | 288 | 167 | | 23 | | 0 | | 2 | | 13 | |
| Het-61 | 7 | 160 | 193 | | 20 | | 0 | | 2 | | 18 | |
| Het-76 | 9, 10, 14p  Chr 9:  Chr 10:  Chr 14: | 76  250  165 | 77  62  132 | | 43  20  81 | | 0  0  0 | | 0  0  0 | | 3  5  2 | |
| Het-77 | 12 | 145 | 184 | | 125 | | 0 | | 0 | | 11 | |
| Het-8 | 16 | 117 | 126 | | 31 | | 0 | | 16 | | 156 | |

**Table 2.7:** Example ANOVA table for chromosome I for heterozygous strain samples. Line 7, 11, and 18 are aneuploid for chromosome I (trisomic, monosomic, and trisomic, respectively).

lm(formula = y ~ Line, data = chr1DataGC)

Residuals: Min: -3.9123 1Q: -0.2504 Median: -0.0161 3Q0.1929 Max: 6.5904

|  |
| --- |
| Estimate Std. Error t value Pr(>|t|) |
| (Intercept) 0.048111 0.060519 0.795 0.427 |
| Line2 0.104434 0.085587 1.220 0.223 |
| Line3 -0.067564 0.085587 -0.789 0.430 |
| Line4 0.023977 0.085587 0.280 0.779 |
| Line5 0.062101 0.085587 0.726 0.468 |
| Line7 0.498164 0.085587 5.821 7.05e-09 \*\*\* |
| Line8 0.088339 0.085587 1.032 0.302 |
| Line9 0.055628 0.085587 0.650 0.516 |
| Line11 -0.405439 0.085587 -4.737 2.36e-06 \*\*\* |
| Line18 0.384978 0.085587 4.498 7.34e-06 \*\*\* |
| Line49 -0.023784 0.085587 -0.278 0.781 |
| Line59 -0.032118 0.085587 -0.375 0.708 |
| Line61 -0.045047 0.085587 -0.526 0.599 |
| Line69 -0.002338 0.085587 -0.027 0.978 |
| Line76 -0.066835 0.085587 -0.781 0.435 |
| Line77 0.043517 0.085587 0.508 0.611 |

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6142 on 1632 degrees of freedom

Multiple R-squared: 0.08813, Adjusted R-squared: 0.07975

F-statistic: 10.51 on 15 and 1632 DF, p-value: < 2.2e-16