**Predictions**

Heterochiasmy (what traits are sexually dimorphic?)

1. **SC length**
2. **SC length will be sexually dimorphic**
3. **(density will be sexually dimorphic, log regression of SC ~ chrm class will be less sig in females)**

**2) Normalized CO positions**

**A. 1CO normalized positions will be sexually dimorphic**

**B. Sis-co-ten (sister cohesin tension) will also be sexually dimorphic:** (because it reflects the overall uniform vs telomere pattern)

**C. centromere and telomere distances: this will be sexually dimorphic**; males having more telomere positioned COs

**3) IFD**

**A. no predicted difference across sexes**

Y = subsp \* sex + random(strain)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Traits** | Fixed Effects | | | Random Effect | Predictions met |
| **subsp** | **sex** | **Subsp\*sex** | **Strain** |
| SC length  Long.biv | X | Highly  Highly Sig | X | Slightly significant | Yes, female bivalents are longer (still need to test XX adjustment) |
| (logistic regres, SC ~ CO Class) |  |  |  |  |
| IFD.raw | X | Barely sig,  P=.04 | X | X | No, there is a sex effect for IFD |
| IFD.per | X | =.007 | X | p=0.0548 |
| Nrm.CO.pos | X | p=0 | X | p=0 | Yes |
| Sis.co.ten | X | p=0 | p=0.005 | p=0.0018 |
| Telomere.dist | X | p=0 | X | p=0.0021 |
| Cent.dost | X | X | p=0.0009 | X |

**Male polymorphism (which traits distinguish high and low recombining males in Musc strains?)**

1. **SC length**
   1. **SC length will be longer**
   2. **(density – more dense in high (despite longer chrms)?**
2. **Normalized CO positions**
   1. **1CO norm**
   2. **Sis-co-ten: General pattern, higher in High rec strains because there are more 2COs, --- but what about sis-co-ten when compared by chrm class? (no prediction)**
   3. **centromere and telomere distances**
3. **IFD**
   1. **Shorter IFD in higher rec strains – denser packing of COs**

**Logistic regression (can a trait significantly predict the Rec group, (**High Musc male | Low Musc male **)**

1. Logistic regression Rec Group ~ trait -- (implies groups sig differ by that trait)
2. T.tests (high vs low) -- (implies 1 group is significantly different)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Traits** | **Log regression** | | **t.tests** | | Predictions met |
| **^all bivs** | **Mouse average** | **Single bivalent** | **Mouse average** | **Single**  **bivalent** |  |
| ^SC length | 0.0237 \* | <2e-16 \*\*\* | 0.001567 | < 2.2e-16 | Yes |
| 2CO\_IFD.raw | 0.0366 \* | 9.98e-05 \*\*\* | 0.009133 | 3.595701e-05 | (check the coeffec |
| 2CO\_IFD.PER | 0.1143 | 0.0443 \* | 0.06068 | 1.304e-07 |
| Nrm.1CO.pos | 0.942 | 0.355 | 0.0001753 | 0.3529 |  |
| ^Sis.co.ten | 0.00725 \*\* | <2e-16 \*\*\* | 8.823e-12 | 4.74e-16 |
| ^Telomere.dist | 0.0555 . | 0.00902 \*\* | 0.0007462 | 0.007452 |
| ^Telo.Dist\_PER |  | 1.32e-05 \*\*\* |  | 5.425e-06 |
| ^Cent.dist | 0.00368 \*\* | 5.21e-09 \*\*\* | 0.7848 | 3.658e-09 |
| ^Cent.Dist\_PER |  | 6.74e-16 \*\*\* |  | 4.52e-16 |  |

\*Check the mouse averages for F1 levels, maybe there is an outlier

Consider running the cent and telomere distances with PER

- No difference between the Musc strains in single biv telomere distance…

\*The distinction between the normalized 1CO positions and the sis.co.ten tests is likely due to --- SC space (sis.co.ten measured in physical SC units)…?

that (normalized 1CO positions

**-Do any of these traits predict / increase predictive power for gwRR?**

**SC Length**

Main figures – (scatter plot with nester boxplots

HetC

MM