**Heterochiasmy Predictions**

Which bivalent level traits will be sexually dimorphic?

1. **SC length**
2. **SC length will be sexually dimorphic**

**2) Normalized CO positions**

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

**B. Sis-co-ten (sister cohesin tension) will also be sexually dimorphic:** this metric reflects the overall uniform vs telomere pattern documented in males and females.

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

**3) IFD**

**A. No predicted difference in physical distance between foci on the same foci 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 Sig | X | Slightly significant | Yes, female bivalents are longer (still need to test XX adjustment) |
| IFD.raw | X | Barely sig,  P=.04  (male, -6.55324 | X | X | **No**, the male effect coeff is  -6.5. Female IFDs are slightly longer. |
| IFD.per | X | =.007 | X | p=0.0548 |
| Nrm.CO.pos | X | p=0 | X | p=0 | Yes, the CO position (‘landscape’) traits are sexually dimorphic |
| Sis.co.ten | X | p=0 | p=0.005 | p=0.0018 |
| Telomere.dist | X | p=0 | X | p=0.0021 |
| Cent.dist | X | X | p=0.0009 | X |

-These results confirm that i) SC length/chromatin condensation and ii) differing recombination ‘landscapes’ are conserved chromosome level aspects of heterochiasmy.

-The predication for the IFD differences didn’t meet the null expectation. The IFD tests indicate that female IFD’s are generally longer compared to males.

-There might be more nuanced patterns and effects due to strains for the rec landscape and IFD. I plan to follow up these tests with post-hoc comparisons within each strain.

**Male Musc Polymorphism**

Which traits distinguish high and low recombining males in Musc strains? (High: MSM and PWD, Low: KAZ, SKIVE, MOLF).

1. **SC length**
   1. **SC length will be longer in high strains.**
2. **IFD**
   1. **Shorter IFD in high rec strains to allow denser packing of COs.**
3. **Normalized CO positions**
   1. **1CO normalized positions, will be the same (Null expectation)**
   2. **Sis-co-ten: higher in High rec strains because there are more 2COs,**

**Sis-co-ten separated by chromosome class will not be different (null expectation).**

* 1. **centromere and telomere distances, (null expectation, that there is no difference)**

Two tests were used

1. Logistic regression Rec Group ~ trait
2. T.tests (high vs low)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Traits** | **Logistic 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 |
| 1CO | 0.0973 . | 0.179 | 0.1905 | < 2.2e-16 |  |
| 2CO | 0.0176 \* | 3.01e-05 \*\*\* | 0.03376 | < 2.2e-16 | No (2CO are distinct?) |
| 3CO | 0.223 | 0.567 | 0.3661 | 9.889e-08 |  |
| 2CO\_IFD.raw | 0.0366 \* | 9.98e-05 \*\*\* | 0.009133 | 3.595701e-05 | No, High Rec groups have longer, not shorter IFDs. |
| 2CO\_IFD.PER | 0.1143 | 0.0443 \* | 0.06068 | 1.304e-07 |
| Nrm.1CO.pos | 0.942 | 0.355 | 0.2558 | 0.3529 | Yes,  Yes,  No, (follow up this pattern) |
| ^Sis.co.ten | 0.00725 \*\* | <2e-16 \*\*\* | 8.823e-12 | 4.74e-16 |
| Sis.co.ten\_1CO |  |  | 0.6619 |  |
| Sis.co.ten\_2CO |  |  | 0.1787 |  |
| Sis.co.ten\_3CO |  |  | 0.4327 |  |
| ^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 \*\*\* | 0.006659 | 3.658e-09 |
| ^Cent.Dist\_PER |  | 6.74e-16 \*\*\* |  | 4.52e-16 |  |

1. The general increase of SC length (along with more DSB meets the model of more COs come from changes early in the pathway (more SC area -> more DSB -> more COs)

2. Higher rec strains have more space between foci on the same bivalent, which goes the logic and general pattern I just outlined above. This indicates CO interference has also evolved with higher gwRR. So this pattern requires some follow up.

\* Verify with sub-sampling / permutations (account for the different proportions of chromosome classes).

\*Larger IFD/stronger interference might be act as a limit/suppressor of gwRR getting too high in the high Musc strains.

\*t-tests show no difference between the siscoten scores when separated by chromosome class. Does this indicate that the t-test of pooled sis-co-ten is due to different proportions in the high and low strains?