1. **Background** / research question for aim 3 // comparison of meiotic features

CO number and position (basics for aim 3) (I plan to extend these analysis to more strains and females.

2. Integrate sexual dimorphism patterns / Canonical landscape patterns

Genome-wide

Lower

Bivalent

Telomere biased / non-uniform distribution

3.Hypothesis for PWD – KAZ comparison

Hypotheses and models are MLH1 driven (are based on MLH1 patterns)

1. 2 Musc strains with divergent MLH1 counts
2. Male pattern

Some are already established / some not so much

**Data / basics of analyses**

1. Curation step
2. The new data set
3. For creating bins, I need to supplement with manual measures

~4 mice

X cells, X bivalents,

X automated, (~X missing biv measures from auto (incomplete cells)

X hand measures,

**Hypotheses**

Based on MLH1 pattern

PWD – longer SC (more MLH1)

PWD, more telomeric 1CO position (natural bias for telomere then fit centromere

(PWD weaker centromere bias?)

PWD, shorter IFD-normalized (weaker interference)

**How are these distinguished?**

**Results**

**PWD Longer SC**

1. **Total SC**
2. **SC in bins**
3. **SC lengths by bivalent classes**

**More 2COs**

-X percent more 2CO in PWD than KAZ

-What are the IFD distributions? (raw and normalized)

-

**Interference**

Stronger interference in KAZ (

**Position**

Stronger telomereic in PWD

**Extensions**

Heterochiasmy

Evolution