Goals for the Effects doc:

Outline how 5 factors /variables within my MLH1 counts (are not random or constant)

think/outline how they could affect my interpertations/inferences for mean MLH1 differences.

Cell quality

Mouse age

litter

spread / dissection month

room

Inbreeding, F1s

Human Error (how consistant is my counti) – isn’t a variable for this effects document. I’m assuming it apples uniformly across all the data and is more of an inherent factor for the data than – a technical variable to account for.

-XX is another inherent factor.

**Cell Quality**

Human assigned metric, has a bias for best cells (1) to have more MLH1 foci. I tried to keep the scoring to uniformity of staining, completeness of all the SC, lack of background noise -- but I’d score lower for more 0CO bivs, (I don’t know if 0CO bivs are true or from technical noise).

Since it’s human assigned there’s error and looking at replicate data shows that I am not always consistant in assigning scores across the same cell.

The initial purpose was to indicate which cells were kinda of crappy and should have low priority for being used in estimates. (but since not all mice have the same number of cell samples – I wanted to

(I didn’t think this quality range through very well)

Main concern:

Female and male cells have different biases in the CO count quality score relationship. (the effect isn’t equal across sexes – so I’d have to account for this when comparing across the sexes

**Mouse age**

Males

Age range is larger than I would prefer, (if all males could be the same age or within 4 weeks of each other that would have been perfect.

The final dataset does/will exclude old mice above a threshold, but if there are more subtle age effects

Since I was trying to breed many mice – I kept some longer before dissecting – so some strains only have old mice because I couldn’t get them to breed.

Main concern: older mice are biasing the estimated strain effect, all the different age range across the mice in my data are adding noise to the strain RR estimates.

(young and old RR age effects have been shown in previous publications)

Reassurances-

It seems unlikely that age effects – are discontinuous for the age ranges I have (i.e. there would be a window when the RR jumps up then goes back down.

Also, the general male pattern seems to be the RR is highly elevated or near the minimum. This is the main signal I’m trying to detect, --- it might be unlikely that I’d miss an elevated strain due to the age effect.

(I have at least 1 3-9 week mice for each of the strains)

(include age in MM? but it’s so unbalanced)

**Age (female)**

Getting embryos was diffecult (impossible) for some strains – also logistically impossible – so almost all of my female data came from neonates ( < 24 hours old)

I did try a few mice over 24 hours old (SPIC?) (MOLF?)

Main concerns;

**Dissection and spread (dissection date)**

(dissection month – might cause effects from humidity), (for total SC –previous Peromyscus results indicate this might be a thing)

Main concern:

**Room**

**litter**

\*age effects\* (male, maternal age)

\*litter effect\*

\*mouse room effect\* (Charmony, MSC)

\*quantification repeatability\*

\*spread batch and staining effects\*

\*power analysis on number of cells\*

\*time of year effect (on spread)\*

\*dominant effect\* (F1s)