Status of dead positives recovery

Meeting notes

Gus, Gisella, Andrea

2015-01-20 (Tuesday)

# Discussed

* Methods
  + need to be collated into one doc
* Status of LD analysis and how to choose cut-off
  + look at tryp paper and email Mark regarding this
* Status of hapFLK (haplotype analysis) and state of results
  + email to author is sent and waiting for response
  + contacting Noonan and/or Jeff Townsend regarding this
* Structure of paper
  1. Development of the base SNP set
     + a process I am not clear on at the moment
  2. Linkage Analysis
  3. Functional Annotation of filtered SNPs
  4. Discussion
     + establish the ability to do this scale of work in *G. f. fuscipes*
     + limits of the dataset as it now stands
     + Never-the-less, hypotheses can be formulated and here they are…

# Current/future plans

**Gisella:**

* [X] email Washington group about methods of Seq prep and analysis
* [X] email Aksoy group about linkage status of *G. m. morsitans*

**Andrea:**

* [ ] Re-run RAD pipeline showing Gus whats going on and writing up the pieces.
* [X] Contact Noonan and/or Townsend regarding hapFLK stuff

**Gus:**

* [X] email Mark about Tryp LD analysis in his paper
* [ ] read Tryp paper for same
* [ ] install latest Stacks version on louise and make runable by Andrea
* [ ] return hapFLK script to original code and copy altered version to new name
* [ ] Generate descriptive statistics and figures of the LD results as a whole rather than by contig where possible
* [ ] upon decision of which near-by genes are “interesting” send summary of info known about them to Aksoy group for ideas.