# **2016-02-17 Meeting notes**

## Date

12 Feb 2016

## Attendees

- Clayton L Birkett
- Jean-Luc Jannink
- user-21bda
- Peter James Bradbury
- David Hane
- Gerard Lazo

## Goals

## Discussion items

Time	Item	Who	Notes
	loading oat haplotag data		wait for new hard drive installation before adding passport data need to divide genotype results into separate experiments
	QTL Mining	Clay	added gene information (CDS, 3' UTR, 5' UTR, exon, pseudogene) fixed "trial count" link
	operating system upgrade this weekend	Clay, and Dave Hane	mirror site setup for wheat, barley, and oat

## Action items

- ✓ Clayton L Birkett calculate Z-value using data from all GWAS
- ✓ Clayton L Birkett QTL Mining, look for gene function in gff3 files
- Clayton L Birkett QTL Mining, allow user to select trials, when all trials are selected display count of significant (e.g.1/8 for one out of eight trials)
- ✓ Clayton L Birkett check oat website for google analytics tracking code