

# 2018-02-14 Meeting notes

## Date

14 Feb 2018

## Attendees

- [Clayton L Birkett](#)

## Goals

## Discussion items

Time	Item	Who	Notes
	TCAP ABB mid-Atlantic material	Brian Ward	genotypic and phenotypic datasets on T3 GWAS and GS papers aligned to RefSeq_0.4 need to load 2015 GBS data
	Graingenes - T3 links		
	BrAPI notes		<ul style="list-style-type: none"><li>• Flapjack v1.18 Beta working with BrAPI</li><li>• WheatIS<ul style="list-style-type: none"><li>◦ plans for moving germplasm and phenotypes to BrAPI</li><li>◦ barley data can be loaded</li></ul></li><li>• BrAPI Apps -<ul style="list-style-type: none"><li>◦ ontology, pedigree, study comparison,</li><li>◦ R package - BMS uses this for statistical analysis</li><li>◦ HIDAP <a href="https://research.cip.cgiar.org/gtdms/hidap/">https://research.cip.cgiar.org/gtdms/hidap/</a></li><li>◦ Gigwa <a href="http://www.southgreen.fr/content/gigwa">http://www.southgreen.fr/content/gigwa</a></li></ul></li></ul>
	practical haplotype graph (PHG)		training June do we need Fasta files, who from wheat, PanGenome? can we use <a href="#">2014_HapMap_WEC</a> from Eduard? Align to refseq_v1 start with fasta/bam files

## Action items

- ☐ [Clayton L Birkett](#) - ABB experiment missing link to analysis plan
- ☐
- ☐