

2019-06-19 Meeting notes

Date

19 Jun 2019

Attendees

- [Clayton L Birkett](#)

Goals

Discussion items

Time	Item	Who	Notes
	GrainGenes	Taner	update
	Knetminer		new release?
	PolyMarker		updated primer design file
	gVCF files		filtering heterozygous SNPs QUAL - Phred-scaled quality score DP - depth GQ - genotype quality MQ - mapping quality filtering: 75% of data present and only biallelic snps. We removed heterozygous sites and kept only those singletons that had depth of coverage of 10+.
	PHG		Practical Haplotype Graph <ul style="list-style-type: none">• new CreateConsensi script• new scripts for findpath.sh using minmap2

Action items

- ☐ [Clayton L Birkett](#) - put gVCF on public drive
- ☐ [Clayton L Birkett](#) - is read depth higher for homozygous snps?
- ☐ [Clayton L Birkett](#) - vcf to hapmap for flapjack
- ☐ [Clayton L Birkett](#) - ask Gina if she can select wheatcap lines