## I. Barley panache browser tutorials

1. The barley panache browser can be accessed using the following link

http://database.barleypangenome.com/barley\_panache/

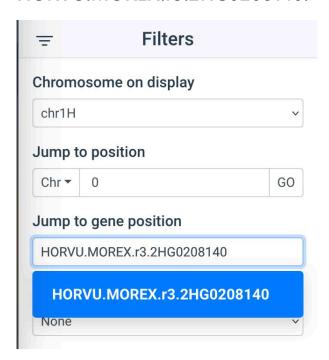
2. Additional documentation on Panache can be found here

Wiki home: https://github.com/SouthGreenPlatform/panache/wiki

Functionality: https://github.com/SouthGreenPlatform/panache/wiki/Functionalitiestour

PAV Sorting: https://github.com/SouthGreenPlatform/panache/wiki/Sorting-options

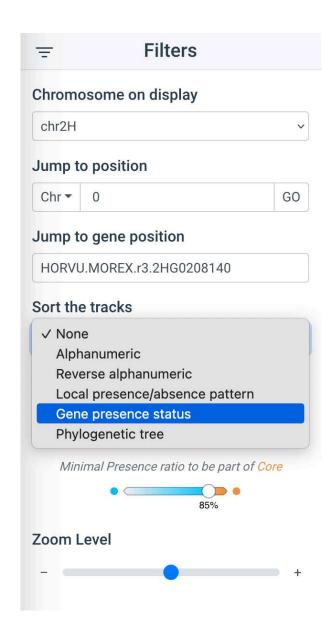
- 3. Open Barley Panache and wait for the tracks to load in (can take a while depending on server load and data size).
- 4. Using the gene HTP2 as a use case, from the menu go to 'Jump to gene position' and load up the HPT2 gene using gene ID HORVU.MOREX.r3.2HG0208140:



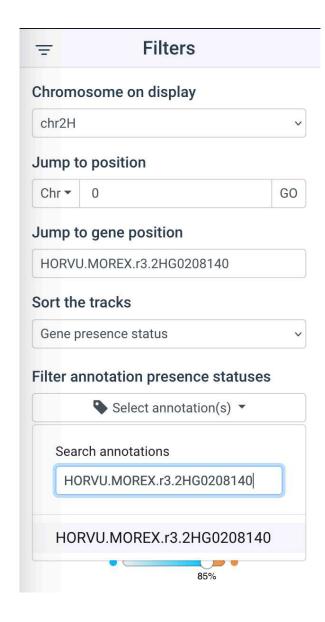
5. Locate the HPT2 gene.



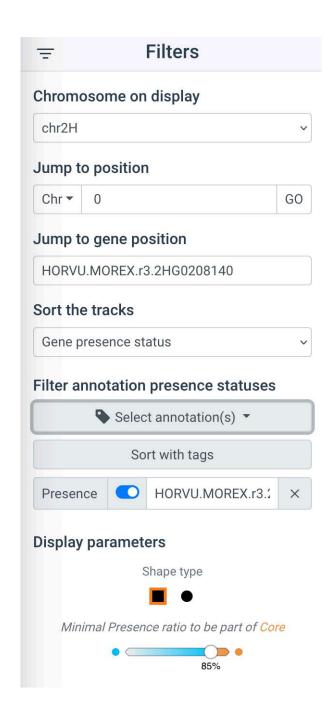
6. From the menu select 'gene presence status'. Note: if selecting 'Phylogenetic tree' the genomes are sorted based on the phylogenetic tree, as determined by mashtree (mash distance).



7. Put the HTP2 gene ID into the annotation search (multiple genes can be added).



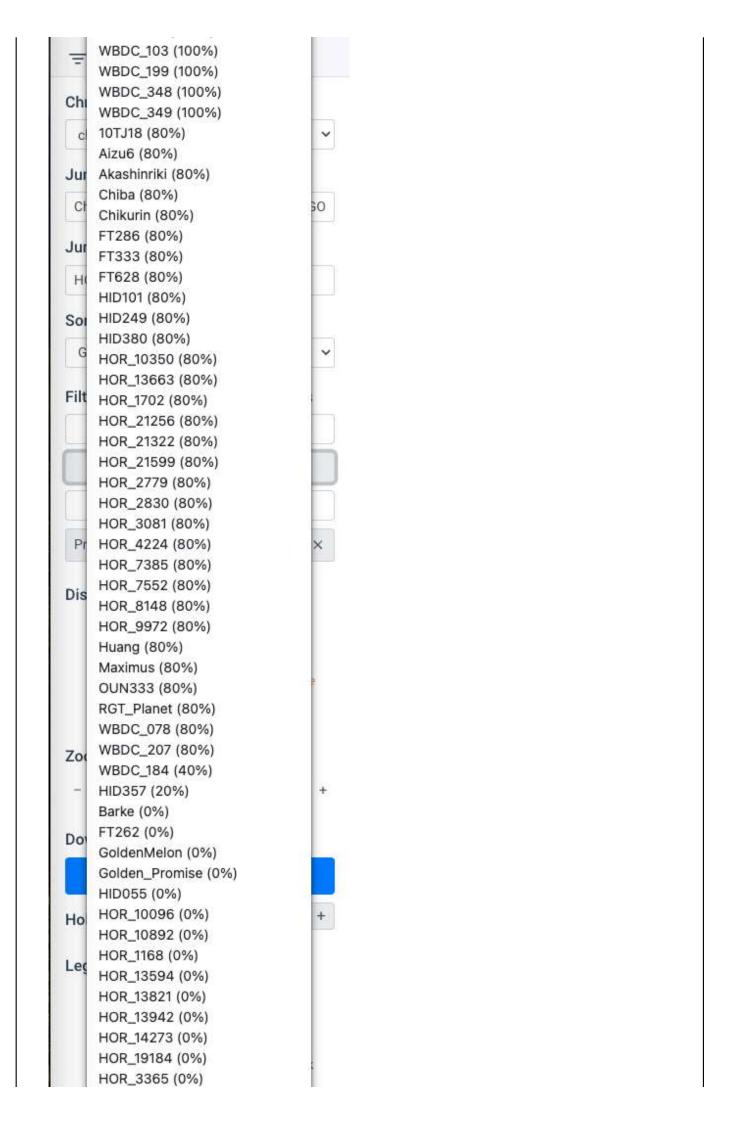
8. From the menu select 'Sort with tags'



9. The genomes are now sorted by the HPT2 gene's presence/absence status



10. The percentage of presence/absence of HPT2 across each genome is calculated and displayed



Mo	HOR_3474 (0%)	
Ch	HOR_495 (0%)	
	HOR_6220 (0%)	
	HOR_8117 (0%)	
	HOR_9043 (0%)	
	Igri (0%)	
	WBDC_133 (0%)	
	WBDC_237 (0%)	