Scenario A (less relevant right now):

1. User identifies gene of interest, e.g. through a publication on Arabidopsis.
2. User does a BLAST search with this gene against the e.g. barley genome. This returns one or more gene relevant identifiers (e.g. a barley contig number).
3. User enters a single gene identifier into the map viewer app and the gene and its homologues are visualized.
4. To be continued…..

Scenario B (most relevant currently):

1. User has 2 positions of either a barley or a rice chromosome that flank a QTL and wants to explore homologies between these and other regions on the other respective genome.
2. User selects the limits of the QTL on the target chromosome.
3. The homologies of the limits with the reference genome are displayed and these form the boundaries of the region of primary interest in the reference genome. (Q: what happens when there are no homologues for the loci demarcating the QTL on the target chromosome?).
4. Homologies between the QTL on the target chromosome and the remainder of the reference genome are also displayed (Q: how - 2D/3D?).
5. All loci in the region of interest in the reference chromosome are displayed or at least displayable on request (zooming/mouseover etc) and these should be associated with the following information: gene identifier (can be of several types/formats), gene sequence, gene description and potentially other annotation information. The display categorises loci on the basis of whether there are identifiers only or both an identifier and a sequence available.

Additional Requirements:

* Users should be able to tune the display of homologies by selecting their level of BLAST sensitivity, i.e. they should be able to have separate views on the data at the same time, where each view uses up to 3 different sets of BLAST hits (i.e. set 1 uses the top BLAST hit for each gene, set 2 uses the second best BLAST hit, set 3 uses the third best one).