

Extension of PigQTLdb: Genome-wide Alignment of BAC FPC Maps and RH Maps for QTL Positional Gene Mining

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Abstract

The creation of Pig QTL database (PigQTLdb) provides a useful public tool for locating genomic regions where the best candidate genes/markers for economically important pig traits may be identified based on confirmations from multiple QTL overlaps. However, dissection of promising genomic regions for a candidate gene search still remains a challenge as the size of such regions normally spans 2 to 20 cM or millions of base pairs. The availability of the 16X complexity BAC fingerprint map and the pig-human RH comparative map have added new opportunities to search for underlying genes of a QTL. We have performed a genome-wide alignment of the pig QTL maps with the Sanger BAC FPC maps, in an attempt to create a QTL interval-mining pipeline for end users. To date, we have produced 89 anchor points to link the two maps for 18 out of 19 pig chromosomes based on sequence blast matches, and we are in the process of adding more anchor sites on a few chromosomes to improve alignment quality. We have also aligned the QTL locations to the UIUC RH map that is further linked to human genome locations. Tools were also created for end-users to search with QTL location information (cM) for underlying BAC clones, and further to obtain the sequences and their corresponding human gene information. The map alignments will be further refined as more sequences become available from the porcine genome-sequencing project.

Introduction

The PigQTLdb has provided a useful tool to confirm promising genomic regions that harbor a QTL (Hu et al., 2005). The further dissection of the genomic region for useful candidate genes requires comparative information to be mapped and sequences available for further analysis.

Recently, Meyers et al (2005) developed a high-density porcine radiation hybrid (RH) map composed of 2,272 markers, and aligned the map to the human genome. We have successfully incorporated the comparative mapping information into the PigQTLdb, and allowed relating pig QTL information to human genome through web functions. Humphray et al (2005) has developed a highly contiguous, integrated BAC physical map of the porcine genome. This resource allows the selection of a minimally overlapping tilepath of BAC clones covering the entire genome as well as specific QTL regions. Based on sequence blast results, we were able to identify matches of porcine markers to the BAC end sequences, and subsequently to determine anchor markers between pig linkage map and the BAC fingerprinted clone (FPC) maps.

We have extended the PigQTL database to include the porcine RH-human map and the porcine BAC FPC map data, and developed tools and web portal to enable the information retrieval.

Results

The MySQL database structure within the PigQTLdb was modified to house the pig RH - human comparative mapping data and the pig BAC FPC map data. On this basis, we tools are added to extend the PigQTLdb functions for comparative information traverse.

982 pig linkage map marker sequences were blasted against 577,151 BAC end sequences. The blast-identified chromosome locations of the BAC clones were compared to that obtain by BAC-RH mapping results. 90 anchor markers were confirmed (Table 1).

- Pop-up menu (Figure 1, in red circles) are added in the PigQTLdb "chromosome view" to link from a QTL region to the RH-human comparative maps
- A form (Figure 1, in red circles) are added in the PigQTLdb "chromosome view" to link from a QTL region to the RH-human comparative maps

- Comparative maps of the pig linkage map to either human map (Figure 2), or to pig BAC FPC map (Figure 4), can be brought up from either the pop-up menu or the link form.

- The human chromosome locations on the pig RH-human comparative maps (Figure 2) are linked to human detailed map information hosted at NCBI (Figure 3) by a simple click.

Table 1

Number of anchored markers between the pig linkage map and the BAC FPC map based on blast evidence.

Chromosome	Number of anchor markers
1	8
2	7
3	11
5	6
6	6
7	7
8	11
9	4
10	2
11	3
12	1
13	7
14	7
15	5
16	3
17	1
18	1

Figure 1.

Pop-up menus and forms (in red circles) are added in the PigQTLdb "chromosome view" to link from a QTL region to the RH-human comparative maps (Figure 2).

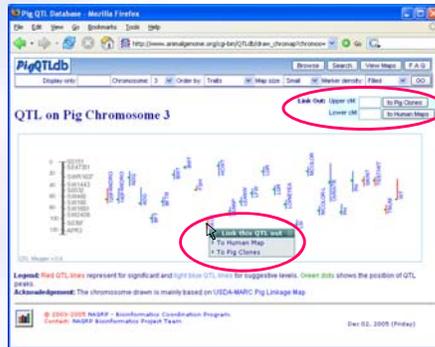


Figure 2.

The linked RH-human map showing that part of the human chromosome 2 is corresponding to pig chromosome 3 that are harboring a QTL for pig Basal Glucose Levels (BGL). Note the interested QTL region is highlighted.

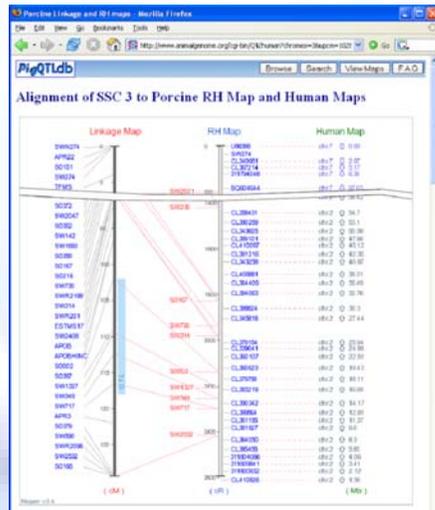


Figure 3.

The human chromosome locations on the pig RH-human comparative maps are linked to human detailed map information hosted at NCBI by a simple click.

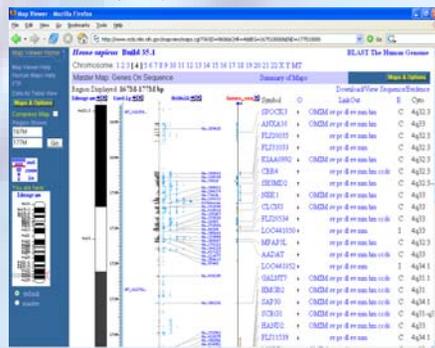
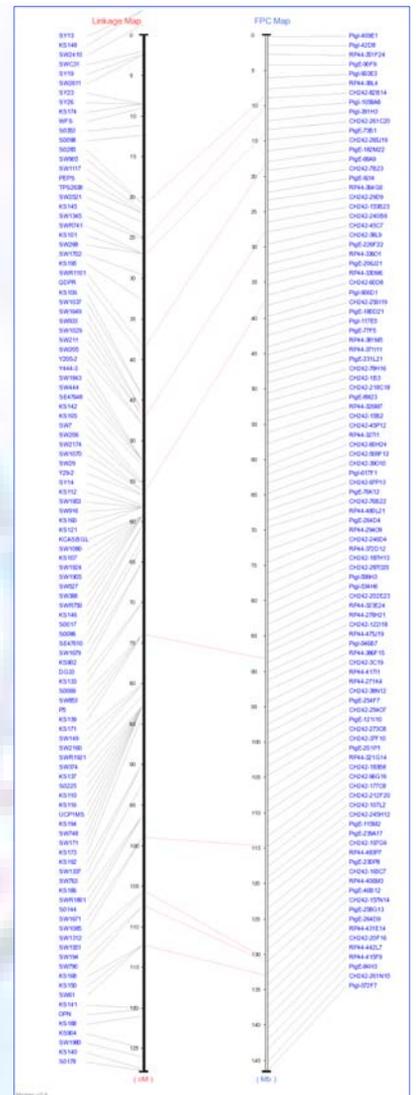


Figure 4.

The alignment between pig chromosome and BAC FPC map. Shown in the example is pig chromosome 8.



References

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