

SGSC Pig Genome Manuscript Newsletter

Welcome and Update. You are receiving this Newsletter due to your participation at either the Pig Genome III meeting recently held at the Sanger Institute or the 2010 Swine Genome Sequencing Workshop at the PAG Meeting in San Diego. The SGSC Genome Manuscript Steering Committee that was established following the Pig Genome III Conference to coordinate activities associated with developing an assembly incorporating all sequence information to date and to create a manuscript based on the assembled and annotated pig genome. The Steering Committee is also providing coordination for related companion manuscripts. With support from the USDA, the Steering Committee is holding teleconferences every two weeks to discuss issues related to developing manuscripts related to the pig genome project. It is the intent of the Steering Committee to be fully inclusive and invite full participation of the broader community. Due to the logistics and costs of including every one of the calls, we do invite you to forward questions and comments to our attention so they can be added to the Teleconference Agenda. Please forward comments or questions to the attention of either Alan Archibald or Larry Schook. Also, feel free to contact any one on the Steering Committee regarding specific topical issues.

Sscrofa10 Assembly. The Sanger Institute and The Genome Analysis Center (TGAC) are working on the release of the pig genome assembly (Sscrofa10) that will provide the basis for the pig genome and companion manuscripts. Our aim is to release an early version of this assembly to the working groups for their analyses in early April. We will distribute the files through an FTP site together with information on those regions that changed with respect to the current assembly (Sscrofa9). This early release will allow us to incorporate corrections identified by the analyses of the working groups before the submission of the assembly Sscrofa10 to the Ensembl group for annotation. This assembly will be based on the latest physical map and will incorporate:

- all the sequenced clones sequenced to date
- gap-fillers and gap-extensions from the BGI Illumina contigs and the WGS reads generated by NLRI (Korea)
- corrections provided by Denis Milan's group (Toulouse) from the comparison study between the Sscrofa9 and pig radiation hybrid maps.

We encourage the community to contact us if you have information about any issues in the current Sscrofa9 assembly. With the early release of Sscrofa10 in April we will set up an FTP site that can be used to exchange data within the analyses group working on the manuscript. To request access via the FTP site please contact Mario Caccamo.

Participation and Exchange of Data. It is anticipated that there will be a need for reducing overlap of analyses and the exchange of data between topic groups (see current list of topic groups below). On several fronts, collaborations have already been initiated between topic groups and we wish to further encourage such interactions. In order to provide full access and distribution, data exchange to all interested parties Mario Caccamo will provide coordination of data exchange. Thus, individuals and groups participating in this Pig Genome Sequencing project must agree to share their analyses and agree to the proposed authorship guidelines provided below. Statement of rules and policies governing all participants will be published soon (Archibald et al.). A copy of the draft manuscript will be provided by February 15, 2010.

Guideline for Pig Genome Sequencing Manuscript Authorship. Authorship is provided to those individuals who intellectually contribute to the analyses and development of the pig genome manuscript as defined by the included topical areas. Manual annotation of pig genes submitted to Ensembl is not in and of itself sufficient for inclusion as an author. The **SGSC**

Genome Manuscript Steering Committee is charged with the responsibility to recognize scholarly contributions related to authorship. Thus, all participants working with Topic Leaders will be considered as co-authors. As for citation of authors, the SGSC Genome Manuscript Steering Committee has made the following decision. The list of authors will consist of the Steering Committee followed by authors (alphabetically). Specific responsibilities of each author will be noted (e.g. Leader of Manual Annotation, contribution to Genome Diversity). Authorship for related companion manuscripts is at the discretion of the collaborating individuals.

Companion Manuscripts. The Steering Committee encourages topic groups as well as others to develop companion manuscripts. The Steering Committee would request that groups forward their intent to develop a companion manuscript (including a tentative title) to their attention (either Larry Schook or Alan Archibald) in order to coordinate data exchange and to ensure no overlaps or competing efforts. Also, developing a list of potential companion manuscripts will permit the Steering Committee to negotiate with journals for a dedicated issue focused on the pig genome project. Also, please forward your ideas as to potential journal(s) for the Steering Committee to contact. Submission of companion manuscripts has a target date of September 1, 2010.

The current Topic List (see below) was developed by Alan Archibald through discussions at both the Sanger and PAG meetings. It is not meant to be exclusive or exhaustive. If you and colleagues wish to propose an additional topic(s) and are prepared to provide leadership please contact Alan Archibald immediately.

SGSC Genome Manuscript Steering Committee

Alan Archibald, Roslin Institute, UK (alan.archibald@roslin.ed.ac.uk)

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Hirohide Uenishi, (huenishi@affrc.go.jp)

Current Topic Groups

Assembly: Alan Archibald (leader), Tim Hubbard, Mario Caccamo, BGI, Denis Milan

Repetitive DNA, transposable elements: Geoff Faulkner (leader)

Gene builds: Steve Searle (leader), Alan Archibald, Jim Reecy, Jen Harrow

HapMap: Hendrik-Jan Megens

Protein interactions, systems biology and metabolism: Soren Brunak (leader)

Segmental duplication, structural and copy number variation: Christian Bendixen (leader), Max Rothschild, Alan Archibald

Transcriptomes, splicing: Henrik Hornshøj

Manual annotation: Jim Reecy (leader), Jen Harrow, Alan Archibald (Gene prediction and consensus gene set)

EST Sequencing: Hirohide Uenishi (leader), Merete Fredholm, Christian Bendixen, Martien Groenen

Speciation and Domestication: Lawrence B. Schook (leader), Greger Larson, Martien Groenen, Richard Crooijmans, Massimo Scandura, Hendrik-Jan Megens, Ning Li, Jian Ma, Miguel Perez Enciso, Alan Archibald

Comparative and evolutionary analysis: Leif Andersson (leader), Lawrence Schook, Harris Lewin, Denis Larkin, Chris Ponting

Physical and genetic mapping: Denis Milan (leader), Gary Rohrer, Jonathon Beever, Patrick Chardon, Craig Beattie, Wansheng Liu, Alan Archibald

PERV and retrotransposable elements: Yasu Takeuchi

Genomic Variation: Martien Groenen (lead), Christian Bendixen, Alan Archibald, BGI

Sex chromosomes: Carole Sargent

Immune response: Chris Tuggle (Leader), Claire Rogel-Gaillard (leader), Anna Anselmo, Alan Archibald, John Butler, Harry Dawson, Elisabetta Giuffra, David Hume, Ronan Kapetanovic, Joan Lunney, Dennis Prickett, Jim Reecy, Hirohide Uenishi, Shuhong Zhao

Gene regulation including miRNA and non-coding RNA: Jan Gorodkin (lead)

Biological Insights

Behavior

Olfactory – Chankyu Park

Biomedical Models: Randall Prather (lead), Lawrence Schook, Merete Fredholm

Transgenic

Naturally occurring

Anti-xenobiotic mechanisms – Bill Beck (leader)

Agricultural Insights: Max Rothschild (lead), Gary Rohrer, Christian Bendixen, Martien Groenen

Reproduction – Max Rothschild, Randy Prather

Fat/obesity – Max Rothschild, Romi Pena, Roberta Davoli