

SGSC Conference Call  
February 18, 2008  
Draft Minutes

- I. Present:** A. Archibald, M. Caccamo, P. Chardon, C. Churcher, K. Eversole, R. Green, D. Hamernik, and L. Schook.  
**Apologies:** R. Clark and D. Milan

**II. Action Items:**

- 1) Schook and Archibald will draft a plan for prioritizing chromosomes for 6X coverage and they will distribute the plan to the group for input.
- 2) Schook will advertize the Pig Genome Annotation Jamboree on email listservs as soon as the Sanger website has been updated with registration information.
- 3) Schook will talk to Illumina to see if they will coordinate contracts and purchase orders at Illumina.

- II. Sequence Update:** Churcher briefly described the two graphs of sequencing progress distributed by Clark on February 15, 2008. To date, about 12,780 clones have been selected and sent for sequencing. This covers about 80% of the map. A total of 1,319 Mb of sequence has been generated from 7,970 clones. About 3,778 clones have been improved/finished that has generated about 54 Mb of sequence. Churcher stated that the number of clones in the pipeline meets the previously agreed to rate. She asked the group for input regarding which chromosomes should be selected for the next round of priority finishing. Sanger would like a decision by March 1, 2008 so as to make maximal use of their sequencing pipelines. This issue was also discussed at the SGSC meeting in Paris in October, 2007. Archibald suggested making gene-rich chromosomes the next priority. Gene-rich chromosomes could be identified by CpG islands or from Humphray's mapping paper. Archibald reminded the group that SSC 4, 7, and 14 were the first priorities because funding was in place to take these chromosomes to a 6X coverage. Schook and Archibald will draft a plan for prioritizing chromosomes for 6X coverage and they will distribute the plan to the group for input. Schook thanked the Sanger sequencing staff for their excellent progress on the swine project.

- III. Annotation Update:** Caccamo reported that the Hinxtton Pig Genome Annotation Jamboree will be held Wednesday through Friday, July 16-18, 2008. These dates should facilitate participation by those attending ISAG in the Netherlands. There will be a social on Thursday afternoon. The meeting will be organized by the Wellcome Trust Sanger Institute. Archibald has obtained ~\$12,000 for on-site costs. If SABRE funding can also be secured, this could be used to provide small travel grants to international participants. Schook encouraged the use of a small registration fee (~\$100) to prevent participants from not attending. Caccamo pre-booked 20 sleeping rooms on the Hinxtton campus. There is room for a maximum of 40 participants. Based on previous experience, 30 participants would be a target number of participants. Many staff from the Sanger Institute will assist with the training so that almost every participant will have their own tutor. Participants can bring their own laptop computer or they can use computers at Sanger. Participants will learn how to perform actual annotations on actual pig sequence. The Sanger website will be updated by February 22, 2008 to contain information on registering

for the Jamboree as well as software that should be downloaded on laptops prior to the Jamboree. Caccamo asked Schook to advertize the Jamboree soon. If annotators want to annotate specific regions of the genome that have not yet been sequenced, staff at Sanger will work to get these regions into their sequencing pipeline. Schook thanked Caccamo for all of his work to organize the Jamboree.

**IV. SNP Chip Update:** Schook described the Illumina pricing structure that he received on Friday, February 15, 2008. The pricing structure is for a 60K chip and is based on total price related to the scale of synthesis. There are three “tiers” of pricing. Tier A = \$2 million, Tier B = \$3 million or \$120/sample x 25,000 samples, and Tier C = \$4 million or \$100/sample x 42,000 samples. Schook said that about 40,000 samples have been committed from the international swine genomics community; thus, they should be able to achieve the desired price of ~\$100/sample. Orders need to be committed by July 2008 so that chips can be obtained and assays completed by the end of 2008. Dollars will be due when the agreements are signed in June or July. There was some discussion as to who will organize the contracts and purchase orders. Green suggested use of a third party (independent from USDA or academic institutions) such as Eversole’s Alliance for Animal Genomics. Eversole was interested in assisting with this process and asked for a quick decision from the group. Since no money will actually change hands (e.g., only purchase orders need to be prepared for Illumina), Schook will also ask Illumina if they would be willing to coordinate the contracts and purchase orders at Illumina. Green reminded the group that Illumina uses a two-tier system for pricing: 1) chips only or 2) chips and genotyping services. Thus, if an investigator plans to spend less than \$25,000, it is probably more cost effective to have Illumina provide the genotyping service.

Schook also reported that Tim Smith (USDA-ARS-MARC, Clay Center, NE) had been working on some reduced representation and Solexa sequencing on a pool of DNA assembled by Schook, Martien Gronen, Gary Rohrer and Jon Beever. This work is supported by Schook’s NRI grant. Christian Bendixen is also interested in playing an active role with the selective sequencing. Schook thanked Archibald for his efforts to encourage Bendixen to participate with this phase of the project.

**V. Other:** Schook and Churcher discussed procedures for communicating invoices. Invoices should be sent directly to Schook by email. Schook will copy Churcher on correspondence at his institution regarding invoices. Schook will also send a letter to Hamernik (NRI) describing the changes in personnel at Sanger.

**VI. Next Conference Call:** Monday, March 17 at 8:00 am (Eastern; US).