SGSC Conference Call
November 17, 2008
Draft Minutes

I. Present: K. Eversole, D. Hamernik, K-T, Lee, D. Milan, C. Rogel-Gaillard, L. Schook, and B-S, Yang.
Apologies: A. Archibald, C. Churcher, R. Clark, Lucy Matthews, and others from Sanger

II. Action Items:

1) The group would like Sanger to provide an update regarding plans for incorporating fosmid sequence into the assembly. The update can be provided by email or at the PAG meeting in San Diego, CA in January.
2) Archibald or Caccamo are encouraged to join the call in February 2009 to discuss some problems with downloading software updates/revisions on local platforms.
3) The teleconference originally scheduled for December 15 has been cancelled due to the holidays. The SGSC workshop at PAG will be held from 10:20 a.m. - 12:30 p.m. on Sunday, January 11, 2009.
4) Monthly conference calls will resume on the third Monday of the month beginning in February 2009.

III. Sequence Update: The Sanger team was not on the call due to a holiday. Prior to the call, however, Clark distributed an update to the group. A total of 15,266 clones have been selected for sequencing and sent to the pipeline. This covers about 94.1% of the physical map. There are 2,323 Mb of total sequence (63.6 Mb of finished quality) from 15,697 clones. About 7,734 clones have been sequenced to the "improved/finished" stage. She estimated that about 79.53% of the physical map had been sequenced. They are averaging about 550 clones per month. Schook thanked the entire Sanger staff for their excellent progress and for their dedication during the transition in leadership of this project (about 1.5 years ago). He also acknowledged Mike Stratton for living up to their commitment to provide a high quality draft swine genome sequence.

Milan asked if fosmids were being sequenced to fill in the gaps from the BACs. Schook was not sure how to answer this question. He thinks that some fosmids have been sequenced but the updates provided by Clark are based entirely on BAC sequence. The group was impressed that this level of finishing was obtained with only the BAC sequences. Schook acknowledged the high quality physical map for this accomplishment. The group would like Sanger to provide an update regarding plans for incorporating fosmid sequence into the assembly. The update can be provided by email or at the PAG meeting in San Diego, CA in January.

IV. Annotation Update: No update at this time. Rogel-Gaillard said that members of her laboratory have had some problems installing updates or different versions of the software from Sanger on their local platforms. She asked if anyone else had these problems. No one on the call has had experience with this issue.

V. SNP Chip Update: Schook stated that letters from universities and companies were due to Illumina on Friday, November 14 stating that all of the SNP on the 60K chip were in the public domain and that there were no intellectual property issues associated with any of the 60K SNP. He also stated that about 2,000 SNP were found to have bad synthesis scores which are likely due to a production problem (e.g., an assembly problem or another SNP nearby). The consortium identified another 3,000 – 4,000 SNP to replace these problematic SNP and serve as back-ups.

Schook also described the ~590 samples that were selected for the HapMap and allele frequency studies. About 50 unrelated animals from 5 breeds were selected for allele frequency studies. The 5 breeds used for SNP discovery include: Landrace, Pietrain, Duroc, Hampshire, and Large White/Yorkshire. Samples will also be included from trios (sire, dam, offspring) from each of the major breeds. The trios samples will be used to determine haplotypes. Most of the trios samples came from private companies.

Schook acknowledged the tremendous effort of the international swine SNP consortium to complete this project in ~6 months. The project was initiated de novo in March 2008 and the final list of SNP sequences was submitted to Illumina in August 2006. This is a tremendous accomplishment!

VI. Other: The group briefly discussed the need for additional funding for this project. Churcher recently distributed an estimate of $5 million to "finish" sequencing all chromosomes. Schook recently gave an update on the sequencing project to the National Pork Board and National Pork Producers Council. He does not think that the National Pork Board will contribute more funding for sequencing. However, the National Pork Board may try to lobby the National Pork Producers Council to contribute more funding ($100,000 – 200,000) to the sequencing project. They would also like to develop and conduct more education programs for pork producers.

Regarding Genome Canada, Graham Plastow indicated to Schook that their animal/aquaculture genomics preproposal was well received. However, it is not clear how much effort in this proposal will involve swine genome sequencing. Also, it will be at least another 12 months before the call for full proposals will go out and another ~6 months for funds to be released. There is minimal leadership from the Canadian swine industry for support of genome sequencing. In contrast, the beef and aquaculture industries are well organized and involved with genome sequencing. There may be a Genome Canada swine workshop at PAG (organized by David Bailey) but it is not clear what will happen. Landmark Genetics (part of BASF in Montreal) is interested in genotyping pigs in Canada and has purchased many Illumina 60K SNP chips through the consortium.

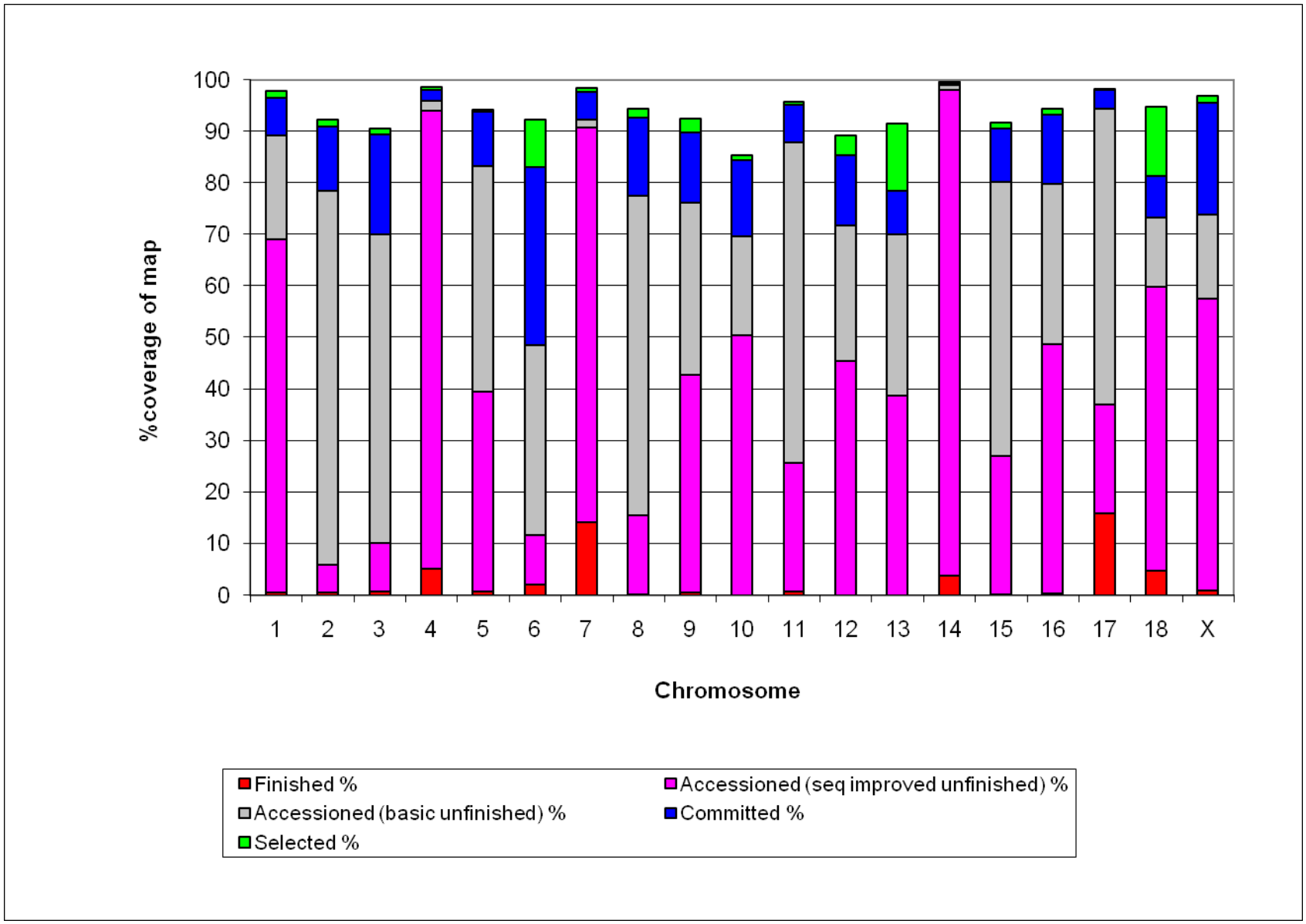
Schook said that he had a conversation with Stratton regarding additional sequencing of the swine genome at Sanger. Stratton did not make any commitment to future swine projects. However, he was potentially interested in using some of the new resequencing technologies on pools of different BAC complexities to improve the swine genome sequence and test the process at the same time.

Eversole said that the BBSRC plans a call for proposals for genome sequencing and this may be another option for funding. Hamernik said that the USDA AFRI Animal Genome Tools & Reagents program will accept proposals on genome sequencing and improving genome assemblies in FY2009. The FY2009 AFRI Program Announcement with program priorities and application deadlines will be available on the CSREES website (www.csrees.usda.gov) by the end of November 2008.

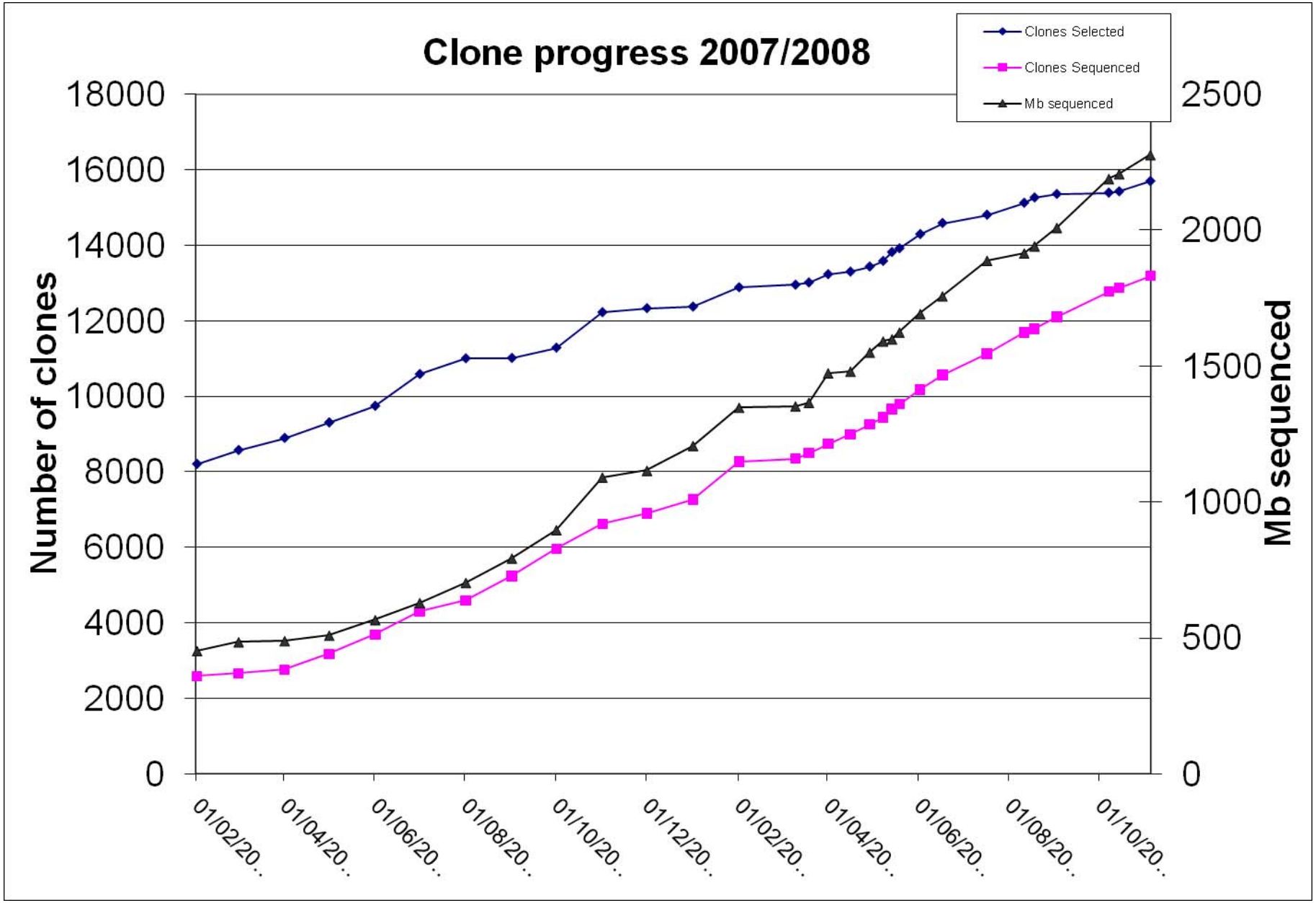
VII. Next Conference Call: The teleconference originally scheduled for December 15 has been cancelled due to the holidays. The SGSC workshop at PAG will be held from 10:20 a.m. - 12:30 p.m. on Sunday, January 11, 2009.

Monthly conference calls will resume on the third Monday of the month beginning in February 2009.

Sequence clone progress 17/11/08



Clones selected and sent for sequencing cover 94.1% of the physical map.
Clones sequenced cover 79.53% of the physical map.



15266 clones selected and sent for sequencing.
Total sequence = 2323 Mb (63.6 Mb Finished quality) from 15697 sequenced clones with 7734 at Improved status.