

Supplementary Material

MAGIC-SPP: a database-driven DNA sequence processing package with associated management tools

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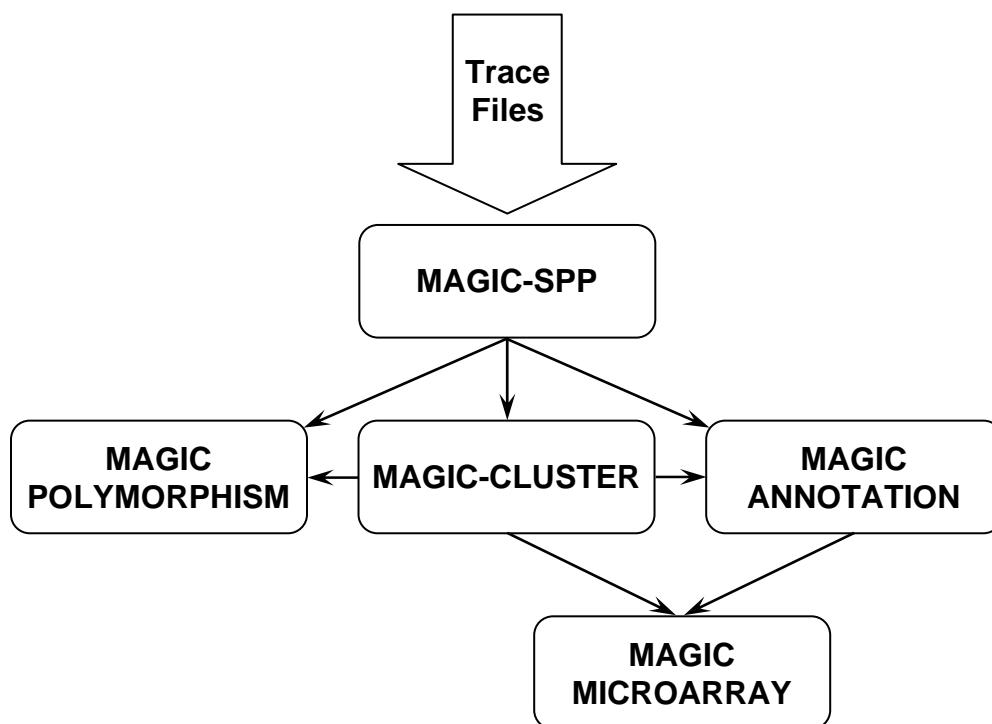


Figure 1: Relationship between MAGIC-SPP and other components of the complete MAGIC system. Information about sequence reads obtained from trace files processed through MAGIC-SPP is stored in MAGIC DB. While MAGIC-SPP can be used as a stand-alone package, it also provides input for four other major subsystems: annotation, EST clustering, detection of sequence polymorphisms, and MIAME-compliant microarrays. These downstream subsystems have been designed to benefit from features unique to MAGIC-SPP, for example the inclusion of genotype information in sequence names.

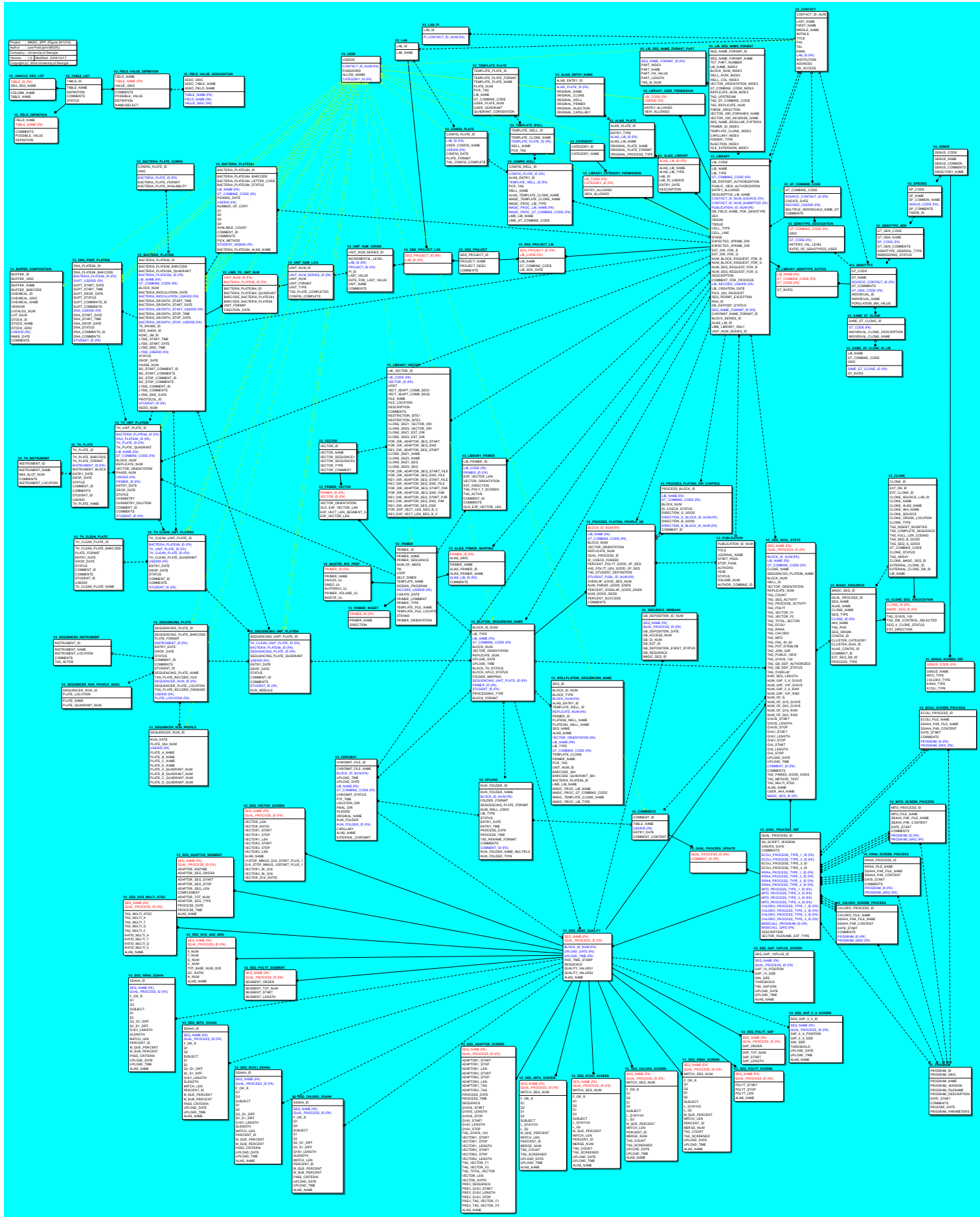


Figure 2: Entity-Relationship diagram of the MAGIC-SPP database. To see detail, use the 'Zoom To...' function in the Adobe Acrobat View menu.

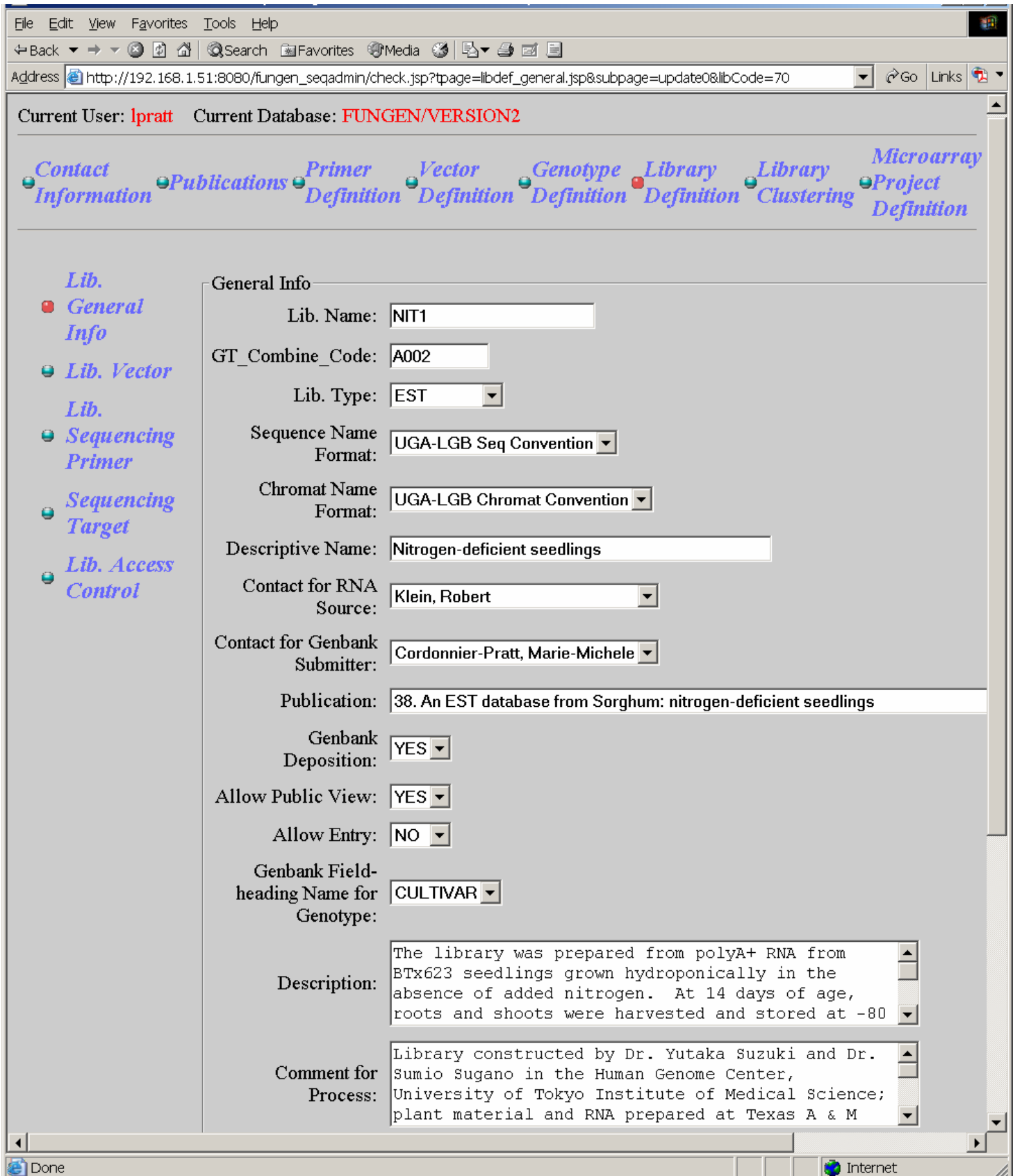


Figure 3: A screen shot of MAGIC Admin. In addition to one of the library definition screens illustrated here, note the many pages available not only for entry of contact and publication information, but also primer, vector and genotype definitions. In addition to what is shown, the sequencing primers and vector used with this library, together with all required information as described in the text, are entered using pages selected from the options along the left-hand border. These pages also permit input of target information for each sequencing project and specify user permissions with respect to both entry and viewing of data. The Contact Information page facilitates among other functions creation of user accounts.

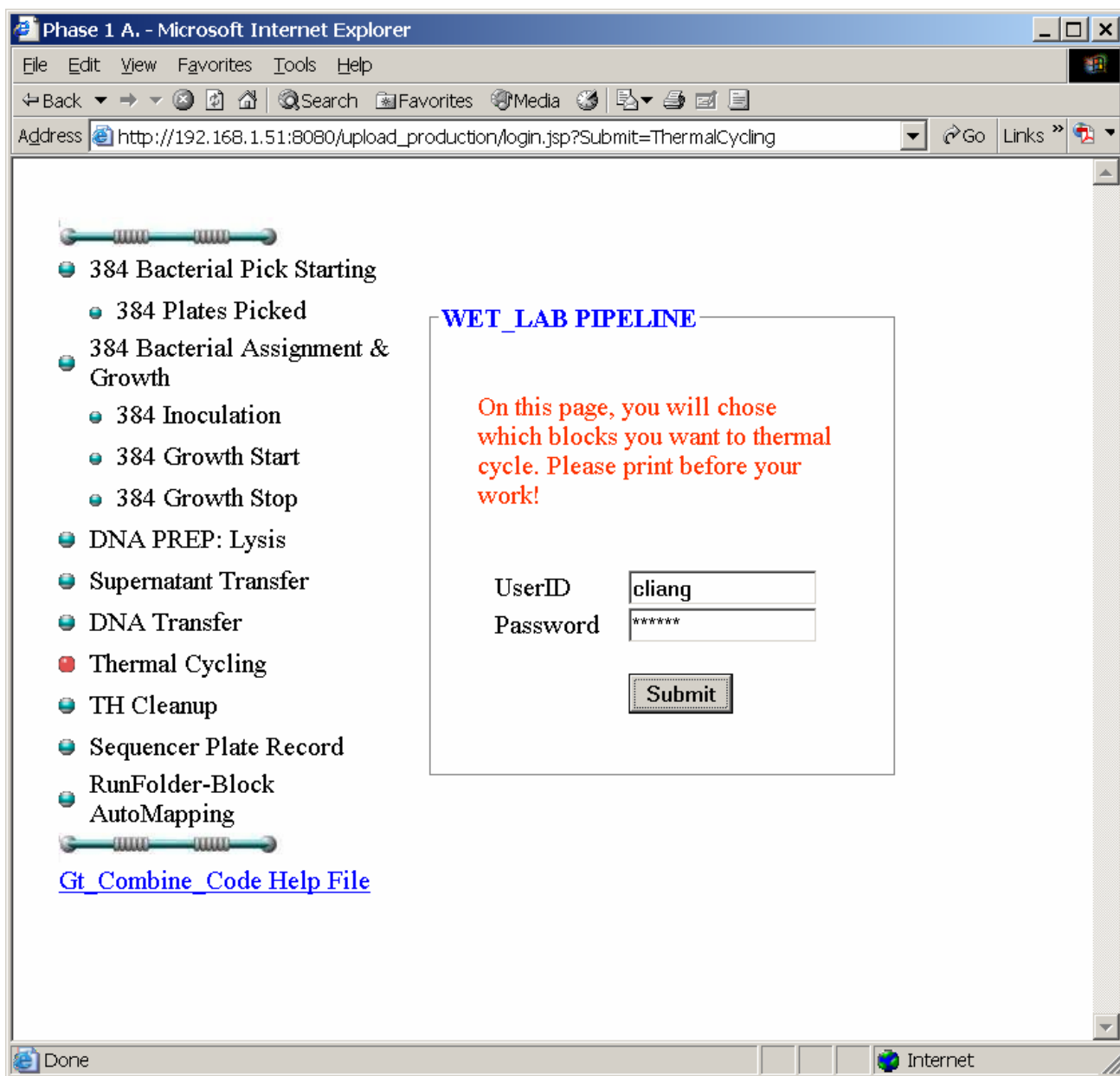


Figure 4: A screen shot of MAGIC SEQ-LIMS. This interface tracks all steps in DNA sequencing from picking of bacterial colonies to upload of trace files into the analysis server.

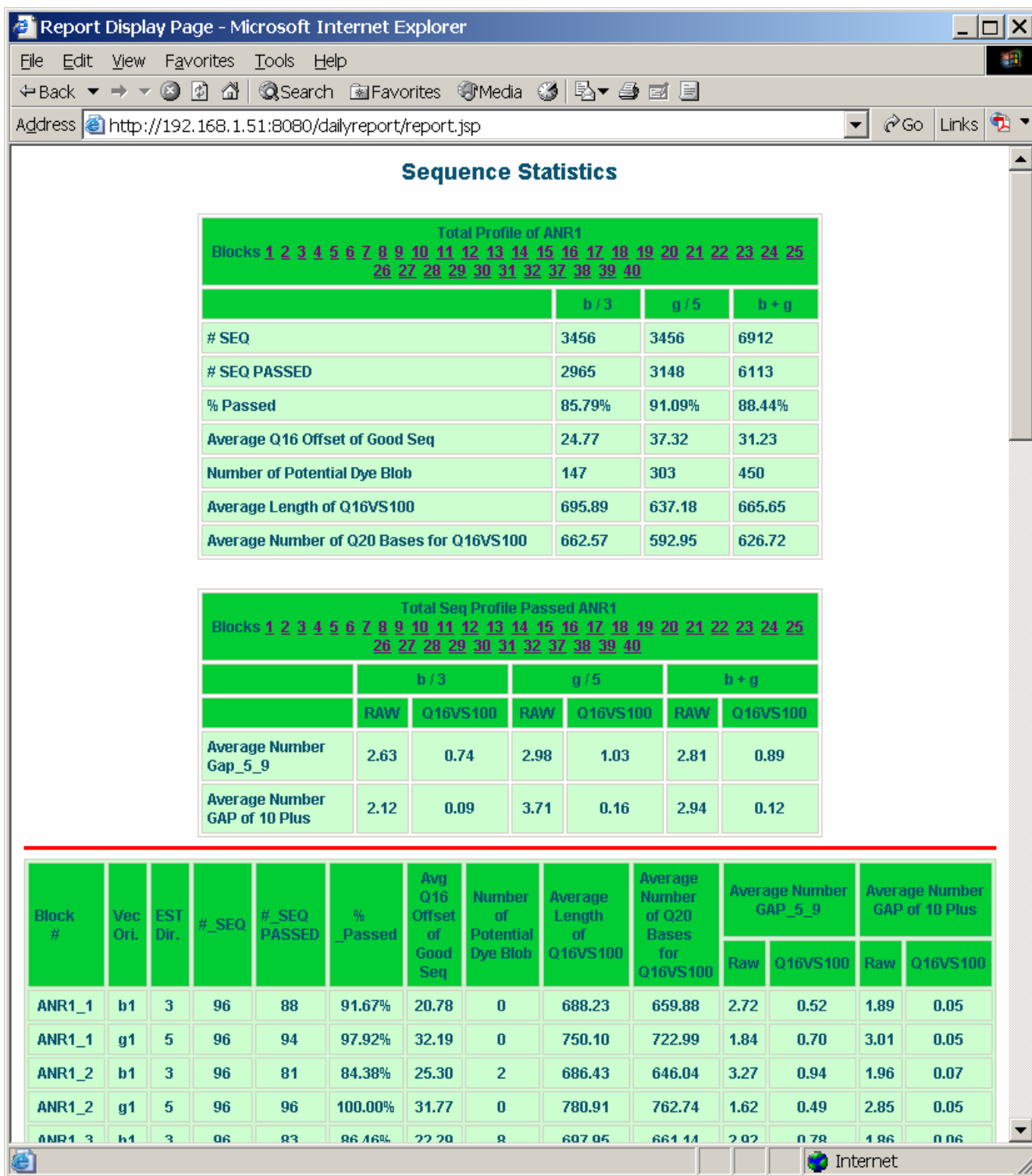


Figure 5: A screen shot of the MAGIC-SPP Sequence Statistics interface. This interface provides sequencing performance statistics for one or more plates in a selected library. In this view, all plates were selected for view both collectively (above red line) and individually (below red line).

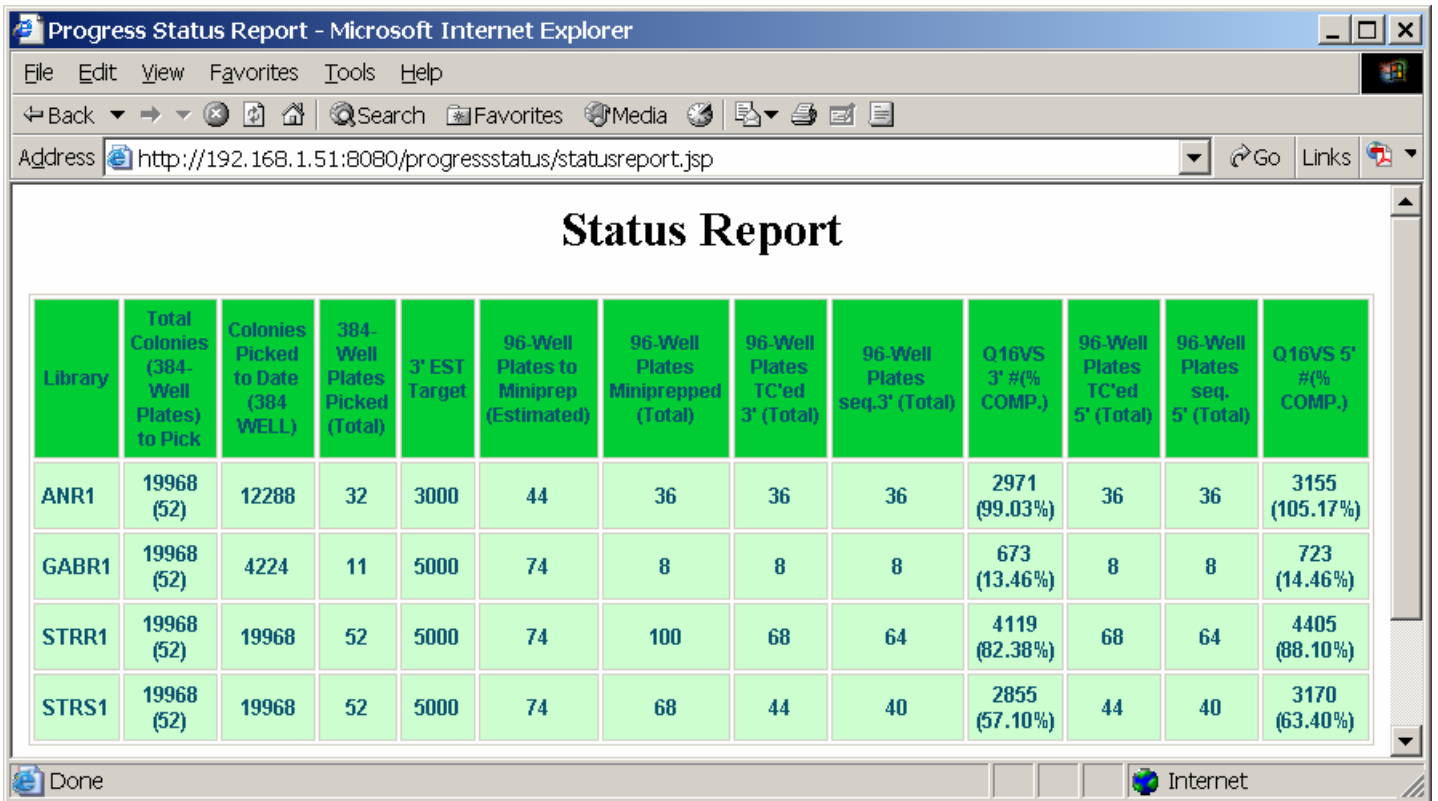


Figure 6: A screen shot of the MAGIC-SPP Status Report interface. Target information, including number of colonies to be picked and number of sequences to be obtained, is entered through MAGIC Admin (columns 1, 2, 5 and 6 from the left). Other columns report progress. The query page for this interface also permits retrieving and viewing only data entered between any two dates.



Figure 7: A screen shot of MAGIC-SPP Plate Viewer. This interface assists with troubleshooting by showing sequences from both vector directions for the same plate. For example, in this illustration wells A1, A10, A12, C11, and E10 have all failed in both forward (top) and reverse (bottom) sequencing directions indicating that these failures are most likely due to missing or poor quality template DNA. Numbers within wells represent Q16VS read lengths.