Asante DNA Extraction
DNA extracted according to the manufacturer’s protocol, with a yeast-specific step added. Briefly, $5 \times 10^7$ yeast cells were spun down and resuspended in sterile deionized water. The cells were incubated with 20 units of zymolase for 30 minutes at 30°C (yeast specific). RNase A, proteinase K, and Binding Buffer were added, and then the cells were incubated for 30 minutes at 56°C. After incubation, a larger volume of Binding Buffer was added and vortexed thoroughly, then the cell debris was pelleted. The supernatant was passed through a Spin Column, and the bound DNA was washed and eluted in two volumes of 50 ul.

Competitor B DNA Extraction
DNA extracted according to the manufacturer’s yeast-specific protocol, with the following exceptions. Zymolase (20 units) was substituted for 200 units of Lyticase. After proteinase K digestion, RNase A was added to a final concentration of 100 ug/ml and the sample was incubated at 37°C for 10 minutes before proceeding to cell lysis.

Briefly, $5 \times 10^7$ yeast cells were spun down and resuspended in yeast lysis buffer and zymolase. After a 30 minute 30°C incubation the cells were spun down and resuspended in ATL buffer along with proteinase K. Samples were incubated for 30 minutes at 56°C, and then an RNase A digestion was performed for 10 minutes at 37°C. To lyse the cells Buffer AL and ethanol were added and the samples were immediately vortexed thoroughly. This solution was bound and washed on a Mini spin column, and a single 200 ul volume of Buffer AE was passed through the column twice to elute the DNA.

RAD-Seq Library Preparation and Illumina NGS Sequencing
DNAs from each extraction method were prepared as RAD-Seq libraries in parallel with 94 additional, non-yeast samples according to standard protocols. Briefly, 200ng of each sample was digested with SbfI, adapter-ligated, pooled, and size-extracted. The pooled DNAs were then polished and amplified. This multiplexed library containing 96 samples was sequenced on one lane of an Illumina HiSeq 2500 at the University of Oregon Genomics Core Facility using manufacturer’s protocols, reagents and methods for 1x100bp sequencing chemistry.

Results
Illumina HiSeq sequencing data from the test population was analysed using internal Floragenex programs. After demultiplexing the data by index (barcode), the Asante DNA received 2,570,287 Illumina sequence reads while the Competitor B DNA sample received 1,693,503 Illumina sequence reads. Sequence quality generated for both samples was nearly identical, with sequence data from the Asante DNA aligning uniquely against the S. banyus genome at 92.5% efficiency, in comparison to the Competitor B DNA at 92.6% efficiency.