



Supplementary Figure S1. Read alignments to the *S. eubayanus* reference genome.

Samples correspond to four haploid spores of CL216.1, a diploid CL216.1 sequenced with short reads (Illumina sequencing), and a diploid CL216.1 sequenced with long reads (Nanopore sequencing).

A potentially novel heterozygous site (A/G) is shown in diploid CL216.1 strain (Nanopore) which segregates in a 2:2 proportion among the four CL216.1 spores.