Figure S2. — Expected heterozygosity, divergence and HKAI on the chr2R for the North American (RAL), African (MW) and simulans (SIM) samples. The (blue) expected heterozygosity, \( \pi \) at the midpoint of 150 kbp windows (incremented every 10 kbp, minimum coverage = 0.25 and Q30 sequence). The (red) lineage specific, average Q30 divergence in 150 kbp windows (incremented every 10 kbp and minimum coverage of 0.25). A preliminary application of HKAI on the Q30 data in windows of 4096 contiguous polymorphic or divergent sites identified centromere- and telomere-proximal regions (orange bars) in which the each window exhibited a deficiency of polymorphic sites relative to the chromosome-arm arm average. Then HKAI was applied again on the Q30 data in windows of 512 contiguous polymorphic or divergent sites (excluding these centromere-and telomere-proximal regions from calculation of the chromosome-arm-wide expected proportions, \( p \), and \( d \)). The (olive) \( \chi^2 \log[p_{calc}] \) is the log of the p-value associated with HKAI plotted with the sign of the difference between the observed number and the expected number of polymorphic sites in the window.