



Figure S4. — Expected heterozygosity, divergence and $HKAI$ on the chr3R for the North American (RAL), African (MW) and simulans (SIM) samples. The (blue) expected heterozygosity, π 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 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_e and d_e). The (olive) $\chi[\log(p_{HKAI})]$ 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.