Supplemental Figure S6: Genotype quality and recombination rate ρ **.** Black dots correspond to mean values derived from 50-kb windows sampled across the genome (top panel), at scaffold ends (second panel), near RAMs (third panel), and near crowSat1 (bottom panel) for hooded (left panels) and carrion crows (right panels). Note that, for better visibility, the range of the y-axis in all plots has been truncated (ranging from 0 – 0.6), which excludes some extreme values.

Hooded crow: Genome-wide

Carrion crow: Genome-wide

