

Figure 1. Schematic overview of the methods used to identify the Z-chromosome in a genome assembled only to scaffold level. The golden eagle genome referred to in the dark grey box represents the reference in which we are attempting to identify scaffolds belonging to the Z-chromosome. The golden eagle genome in the black bar is the genome with known chromosomes, used to identify which scaffolds in the dark grey boxed genome probably belong to Z-chromosome (and autosomes) – to use as a reference. The light grey boxes are the four approaches we tested to find the scaffolds belonging to the Z-chromosome: 1) Depth: analysis of difference in sequencing depth between scaffolds in a high depth whole genome sequenced white-tailed eagle female. 2) Heterozygosity: analysis of the difference in heterozygosity per scaffold a high depth whole genome sequenced white-tailed eagle male and female. 3) LASTZ: mapping of the golden eagle reference genome to the chicken genome using LASTZ. 4) SNP-loadings: analysis of SNP-loadings for principal components splitting the sexes, in 133 RADseq white-tailed eagle individuals.