

Figure 2. Relative sequencing depth of scaffolds in a male and a female white-tailed eagle. Relative scaffold depth was estimated as mode of scaffold depth / overall genomic depth, which was 195 for the female and 181 for the male. The dots, representing scaffolds, are shaded by whether they map to the Z or autosomal (A) chromosomes in the golden eagle genome with known chromosomes. A) Relative depth in the female. B) Relative depth in the male. C) The male to female ratio (rmf) of relative scaffold depth after removing scaffolds with relative depth outside the range of 0.25-1.5 in either the male or female. D) The male to female ratio (rmf) of relative depth for all scaffolds. In A and B the dashed line represents the scaffold size threshold value of 198,789 bases (log10 5.29). In A and B, points lower than the threshold value of 198,789 bases displayed high variation for relative depth (Figure S2). Scaffolds below the threshold in A and B make up 1.1% of data, only 0.0071% is below the threshold and above a relative depth of 3. Dashed line in C and D is 1.5, which is right between expectation for autosomal (1) and Z chromosomes scaffolds (2).