

Figure 5. Venn diagram summarizing the size of scaffolds in bases identified as Z-chromosome with the three different analysis: mapping, depth and SNP-loadings. The Z-chromosomal scaffolds were assigned by mapping the genome with scaffolds to the genome with known chromosomes. Values in parentheses represent percentage size compared to the size of the known Z-chromosome. Notice that the percentage found by mapping the golden eagle scaffold assembly to the golden eagle genome is only 98.42%.