Table 2. Classification of scaffolds identified as Z or autosomal scaffolds based on the depth, heterozygosity, LASTZ and SNP-loading analysis. The identification was found by comparison to the genome bAquChr1.2 (GCA\_900496995.2) with known chromosomes. Results for the different methods are given in a) for total size of scaffolds (bp), and in b) for the number of scaffolds, missing is compared to the golden eagle scaffold assembly.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Depth | | Heterozygosity | | LASTZ | | SNP-loading | |
| a) |  | Z | A | Z\* | A | Z | A | Z | A |
|  | Z | 76,239,124 | 10,056,095 | - | 60,214,856 | 86,569,008 | 270,522 | 69,355,267 | 13,642,226 |
| A | 93,786 | *1,100,765,118* | - | 1,050,885,219 | 597,603 | 1,105,305,943 | 11,720,756 | 1,078,283,284 |
|  | *Total* |  | *1,187,154,123* |  | *1,159,757,217* |  | *1,192,725,744* |  | *1,173,001,533* |
|  | *Missing* |  | *5,571,621* |  | *29,104,198* |  | *0* |  | *19,714,211* |
| b) | Z | 79 | 13 | - | 34 | 110 | 58 | 28 | 12 |
| A | 14 | 512 | - | 254 | 33 | 941 | 9 | 231 |
|  | *Total* |  | 618 |  | *365* |  | *1,141* |  | *280* |
|  | *# NA* |  | *523* |  | *776* |  | *0* |  | *861* |

\*values not assigned due to lack of heterozygosity on the Z chromosome