**Table S5**: Number of sequence scaffolds in 18 homeologous (duplicated) chromosome arms in the new genome assembly for N.A. Atlantic salmon (SJR aquaculture strain).

|  |  |
| --- | --- |
| **Chr Arm** | **Number of Scaffolds** |
| 2p | 13 |
| 5q | 22 |
| 2q | 14 |
| 12qa | 21 |
| 3q | 15 |
| 6p | 19 |
| 4p | 11 |
| 8q | 8 |
| 7q | 7 |
| 17qb | 19 |
| 11qa | 9 |
| 26 | 19 |
| 16qb | 21 |
| 17qa | 15 |
| 9qc | 20 |
| 20qb | 21 |
| 5p | 13 |
| 9qb | 4 |

The duplicated chromosome arms and the boundaries of the chromosome arms were determined based on Figure 2 and Supplementary Table 6 from Lien et al. (2016). The average number of scaffolds in the duplicated chromosome arms in this assembly was 15 compared to the overall average of 18 for all chromosome arms in the assembly. The total number of scaffolds in chromosome sequences in this assembly was 633 and the overall average was calculated based on the number of 50 chromosome arms identified by Lien et al. (2016).