

Legends to Supplemental Material Files

Figure S1: The IGHD genes identified in IGHA locus. At the top, a detailed structure of IGHD located at the C μ -C δ region. The transmembrane (TM) exons are also indicated. A correspondence between C δ exons found in *Salmo salar* (blue boxes) and rainbow trout genome assemblies is shown using dashed lines. At the bottom, the schematic representations of additional IGHD genes (IGHD1 and IGHD2) found in IGHA locus of Arlee genome assembly. The IGHD1 and IGHD2 are upstream of C μ -C δ region.

Figure S2: Phylogenetic analysis of the C δ exons annotated at the IGHM-IGHD region of locus IGHA. A phylogenetic tree obtained from the alignment of the C δ nucleotide sequences from rainbow trout Arlee genome assembly (▲) with those of *Salmo salar* (■) and rainbow trout Swanson (●) genome assemblies. The identification of C δ exons is based on the nomenclature used in *Salmo salar* and shown in different colors.

Figure S3. The amino acid alignment of known rainbow trout secreted IgD sequence and the deduced amino acid sequences from the 10 C δ exons identified at the IGHM- IGHD region of rainbow trout IGHA locus (Arlee genome assembly). Over the lines the corresponding exons are indicated, following the feature of teleost IgD that it is a hybrid of C μ 1 domain linked to different number of C δ domains.

Figure S4: Phylogenetic analysis of the C δ exons identified IGHD1 and IGHD2 genes of locus IGHA. The phylogenetic tree obtained from the alignment of the C δ nucleotide sequences from rainbow trout Arlee genome assembly (▲) with those of *Salmo salar* (■). The identification of C δ exons is based on the nomenclature used in *Salmo salar* and shown in different colours.

Figure S5: A) The alignment of rainbow trout IgT aminoacid sequences deduced from the functional IGHT genes identified in Arlee genome assembly. Over the lines the corresponding exons are indicated. Consensus sequences, with a threshold >70%, is shown in bold. B) Percentage identity of the amino acid sequence deduced from functional IGHT genes identified in Arlee genome assembly and the three rainbow trout IgT subclasses previously identified (GenBank accession numbers are indicated).

Supplementary Files:

Supplementary File 1: Repeat sequence library generated from the genome sequence.

Supplementary File 2: A Perl script that was used to convert the standard blast tabular outputs into the input format of dot plots.

Supplementary File 3: List of the Hi-C assembly scaffolds.

Supplementary File 4: Graphic presentation of the Hi-C contact map.

Supplementary File 5: Summary statistics of the 32 major scaffolds in the Arlee genome assembly.

Supplementary File 6: Number of scaffolds, contigs and gaps per chromosome in the genome assembly.

Supplementary File 7: SNP haplotypes of the Omy05 double inversion in the 12 WSU doubled haploid lines.

Supplementary File 8: List of small inversions detected between the Swanson and Arlee lines genome assemblies.