S2. Sampling information for cisco (Coregonus artedi) families collected from Lake Huron the number of individuals used. The number of offspring shown only includes those used for mapping after the removal of individuals with low sequencing coverage. The numbers of SNPs shown include those retained following quality control filtering but before inclusion in linkage mapping.

S3. Male linkage map for cisco (Coregonus artedi) containing 6340 loci. Each dot represents a locus. Lengths are in centimorgans (cM).

S4. Information for each marker on the female and male cisco (Coregonus artedi) linkage maps. Tag is the RAD tag, and marker name is the tag followed by a designation used to differentiate duplicated loci. The “Sequence P1 column” is the sequence from the single end read for each RAD tag, and the “Sequence PE” is the sequence obtained from paired-end assemblies.

S5. MAPCOMP determination of homologous chromosome arms.

S6: Probable metacentric chromosomes from the MAPCOMP analysis for coregonines.

S7. Homeologous chromosome pairs for currently available haploid linkage maps and the number of maker pairs supporting homeology (Kodama *et al.* 2014; Larson *et al.* 2015; Waples *et al.* 2016; Tarpey *et al.* 2017). Homologous chromosomes are named according to the corresponding Northern Pike linkage group Protokaryotype ID (PK).

S8. Homeologous chromosome pairs for all available salmonid genomic resources.

S9. Support for classifications from k – nearest neighbor machine learning algorithm. Cross validation indicated five nearest neighbors should be used for classification across species. The vote proportion for assignment to either putatively tetrasomic or putatively disomic categories are presented as the proportion of votes out of five at the top of each bar. Median percent similarity for each protokaryotype pair is presented as the *y* – axis and protokaryotype pairs are ranked from most similar to least (*x* – axis).