



Figure S1. Flowchart used to detect rye genes not expressed in triticales.

RNA-seq workflow was performed to characterize the expression of 23,503 rye reference contig assemblies. Rye and triticales transcripts were aligned to their corresponding rye reference assemblies using BWA-SW algorithm of BWA. About 465 reference sequences were found to be expressed in at least one rye tissue and were not found in any of the eight triticales libraries used in the study. Out of these, 112 rye reference sequences were found to be not expressed in all triticales tissues. The depth of each library (the number of transcripts in each library) is written underneath each tissue.