CREDITS AND DATA ACCESS:
Under the leadership of Mingcheng Luo and Jan Dvorak (UC Davis, CA, USA) and with funding from the US National Science Foundation, an improved version of the reference wheat genome has been completed and is being released in advance of publication to the scientific community **under the terms of [Toronto agreement](#)** which affords the data producers the right to publish the first whole genome analyses of the data.

The genome assembly of *Triticum aestivum* cv. *Chinese Spring* (IWGSC RefSeq v1.0; [IWGSC, 2018](#)) was improved using whole genome optical maps and contigs assembled from whole-genome-shotgun (WGS) PacBio SMRT reads ([Zimin et al. 2017](#)). Optical maps were used to detect and resolve chimeric scaffolds, anchor unassigned scaffolds, correct ambiguities in positions and orientations of scaffolds, create super-scaffolds, and estimate gap sizes more accurately. PacBio contigs were used for gap closing. Pseudomolecules of the Chinese Spring 21 chromosomes were re-constructed to develop a new reference sequence, IWGSC RefSeq v2.0. All revisions involved approximately 10% sequence length of the IWGSC RefSeq v1.0.

Importantly, please note that this version has yet to be annotated. The IWGSC annotation team will be performing targeted annotation and QC of IWGSC RefSeq v2.0. In addition, all manually curated genes submitted to the IWGSC by the end of August 2019 (see [call for contributions](#)) will be integrated into IWGSC RefSeq v2.0, annotation v2.0. The IWGSC aims to release the annotation v2.0 in January 2020.

PLEASE NOTE:
MD5 checksums are provided to ensure complete data transfer of files, please make sure that the MD5 checksum of your copy corresponds to the one provided with the files.

QUESTIONS:
In case of questions please contact Michael Alaux from URGI in the first instance at:
urgi-support@inra.fr

Unplaced scaffolds

The unplaced scaffolds can be found on the following files:
- iwgsc_refseqv2.0_chrUn.fa.zip
It is a "fake" chromosome with all the unplaced scaffolds randomly ordered and separated by 100 Ns.
- iwgsc_refseqv2.0_unplaced_scaffolds.fa.zip
It is a multi fasta file with all unanchored scaffolds as individual sequences.