This folder contains data for a diversity panel of Ethiopian wheat. The original plan was to sample Ethiopian durum wheat only, but when we started analyzing the accessions that we obtained by the Ethiopian seed bank we noticed that several genotypes were indeed hexaploid wheat. Samples were assigned a ploidy based on genotyping data, and hexaploid wheat samples were later stripped from the analysis that were eventually published. However, phenotypic and genotypic files here included contain both durum wheat and bread wheat samples

The file whoiswho.diversity.panel.txt contains information about the samples included in this study (400); it is especially relevant as matches the naming convention used in the phentoypic dataset with that used in the genotypic dataset. It reports also the species assignation on the basis of SNP markers; the species assignation is intended to be \*probable\* but not 100% certain. No cytological analysis was conducted. In the DNA code notation, the species info is reported as either a trailing D (durum) or B (bread). Some samples that were included in field experiments were not genotyped; in that case, the DNA code is reported as NA

The file Et\_diversity\_panel\_metric\_traits.txt reports phenotypes for the diversity panel. Data were collected in two locations over two subsequent years, with entries replicated in each field. The file contains the following traits:

DB, days to 50% booting (days)

DF, days to 50% flowering (days)

DM, days to full maturity (days)

SPS, number of seeds per spike (n)

SPL, spike length (cm)

PH, plant height (cm)

NET, number of effective tillers (n)

TGW, thousands grain weight (g)

BM, biomass yield (t/ha)

GY, grain yield (t/ha)

The file Et\_diversity\_panel\_farmers.txt contains farmer scores collected in the same plots of the metric traits (for one year only).In each location, 15 men and 15 women farmers scored traits in 6 gender-uniform groups of 5 people each. The farmers conducting the experiment were different across locations. Each farmer group was sided by a “leader”, that is a local person with an agronomy training. The leader was scoring independently from farmers: he was recording farmer scores, but was not sharing his scores with them. Farmers scored from 1 (bad) to 5 (good) four traits: earliness (“how much do you like the flowering time of this genotype?”), tillering (“how much do you like the tillering capacity of this genoytpe?”), spike (“how much do you like the spike morphology of this genotype?”), overall (“how much do you like this genotype?”). Farmer groups are indicated as M1 to M3 (men groups) and F1 to F3 (women groups). Within each group, farmers are indicated by numbers 1 to 5 and the leader is indicated as L (e.g.: M2\_EARLINESS\_2 is the earliness score given by farmer number 2 in the second group of male farmers). WATCH OUT: **farmer groups are different across location.**

The file diversity.panel.durum.wheat.map.hmp contains genotype calls for the diversity panel. SNPs are filtered for quality, and positions are derived from genetic positions in the durum wheat genetic map by Maccaferri et al 2016. The original cM values were multiplied by 10^6 and jittered so to avoid overlap.