

Table S1. Description of the different filtering schemes applied to the data set. The order of rows indicates the sequential filters applied to the data. minDP – include only genotypes greater or equal to the value; minQ – include sites with quality above the value; mac – include sites with minor allele count greater or equal to the value; geno – retain sites that have been successfully genotyped in the given proportion of individuals (max-missing filtering option in vcftools); imiss – retain individuals with a proportion of missing data smaller than the value.

FILTER	CHINESE <i>S. MISCANTHI</i> SAMPLES	ENGLISH <i>S. AVENAE</i> SAMPLES
MISSING DATA	max-missing 75	max-missing 50
LOW-CONFIDENCE SNP CALL	minDP 3 mac 3 minQ 30	mac 3 minQ 30 minDP 3
MISSING DATA	remove-indels	max-missing 50 imiss > 50% max-missing 75 remove-indels
INFO FILTERS	thin 2000	thin 2000
MISSING DATA	max-missing 0.90	
INFO FILTERS	thin 5000	
ALL SAMPLES SNPS	14520	846
ALL SAMPLES INDIVIDUALS	100	98

Initial dataset of 100 individuals and 564295 SNPs for Chinese *S. miscanthi*.

Initial dataset of 119 individuals; 2248285 SNPs for English *S. avenae*.

Table S2. Geographic distances between the different locations sampled in Chin. The distances are in kilometres (Kms) and have been estimated in straight lines in Google maps.

	Yinchuan	Langfang	Pingliang	Qingdao	Tai'an	Taigu	Kunming	Mianyang	Suzhou	Wuhan
Yinchuan	0									
Langfang	934	0								
Pingliang	348	980	0							
Qingdao	1279	508	1242	0						
Tai'an	990	390	947	300	0					
Taigu	564	450	550	704	426	0				
Kunming	1546	2120	1287	2095	1875	1668	0			
Mianyang	792	1430	534	1540	1276	980	750	0		
Suzhou	1537	980	1394	530	666	1010	1872	1507	0	
Wuhan	1156	1015	940	827	710	785	1287	925	598	0