

	Wheat EN K-seq	Wheat EN GBS
Samples	3	4
Reads	0.8-1.8 millions	1.6-2 millions
% sequence quality >=30 average	96.87	88.4
% mapping properly average	94.43	97.8
% mapping properly $q \ge 57$ average	36.16	56.2
n°SNPs	5047	16390
% call rate	78	85.3
Filtered SNPs (80% call rate, >10x)	655	180
Filtered SNPs % call rate	77.7	80
GBS samples:		
Neopolyploid wheat samples	Kihagen J et al. Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. Frontiers in Plant Science. 2019;10:1133	
Dichter		
Lacoue_NITA		
Jams		
Bussard		
Diploid Wheat samples	Bernhardt N, Brassac J. Genomic and phylogenetic data for the identification of ancient and recurrent hybridizations in wheat taxa [Internet]. eDAL - Plant Genomics and Phenomics Research Data Repository (PGR). Gatersleben, Seeland OT Gatersleben, Cornestraße 3, 06466, Germany; 2019. Disponible en: https://doi.org/10.59102/005/55f-a628-4166-a055-6946708201c3/7576363-dc23-4265-w	
ae_tauschi_ae056		
tr_urartu_h17521		
tr_monococcum_h11990		
tr_urartu_h15407		
tr_monococcum_h2009		
ae_spelloides_ae021		
ae_spelloides_ae517		
tr_urartu_h17148		
ae_tauschi_ae025		
tr_urartu_h17159		
tr_monococcum_h119061		
tr_monococcum_h118612		
ae_spelloides_ae684		
ae_tauschi_ae079		
ae_spelloides_ae1739		
ae_tauschi_ae527		
ae_spelloides_ae1665		
ae_spelloides_ae87238		