

The ‘WAGTAIL 90k Illumina iSelect genotypic dataset’: access conditions and data download

This dataset consists of 26,017 SNPs across 480 bread wheat (*Triticum aestivum* L.) accessions. SNP genotyping was performed using the wheat 90k Illumina iSelect SNP array (Wang *et al.*, 2014. Doi: [10.1111/pbi.12183](https://doi.org/10.1111/pbi.12183)). Genotypes were predominantly sourced from the UK, France, Germany, and the Netherlands, but also includes accessions from Belgium, Canada, Denmark, Sweden, Switzerland and the USA.

This pre-publication data are being made available under the principles of the Toronto Agreement (<http://www.nature.com/articles/461168a>) that grants NIAB and the WAGTAIL consortium (BBSRC project BB/J002542/1) the right to publish the first global analyses of the data. This includes descriptions of genome-level whole chromosome-level and pedigree-level analyses.

By accessing and downloading the data, you agree to this principle, and agree to cite the following acknowledgement when disseminating the data: ‘Wheat 90k SNP data were generated by NIAB within the Biotechnology and Biological Sciences Research Council (BBSRC) LINK project, “Wheat Association Genetics for Trait Advancement and Improvement in Lineages: WAGTAIL” (BBSRC reference BB/J002542/1), along with academic project partners at The University of Reading and the John Innes Centre and industrial collaborators at Elsoms Seeds Ltd, KWS-UK Ltd, Lantmännen SW Seed AB, Limagrain UK Ltd, RAGT, Saaten Union Biotech GmbH, Sejet Planteforædling, and Syngenta Seeds Ltd.’

On first publication of the data by NIAB and the WAGTAIL consortium, a link to the publication will be added to this webpage.

If in doubt about how you can use this data to publish, please contact keith.gardner@niab.com or james.cockram@niab.com