

## CerealsDB FAQ

The CerealsDB site has been designed to be intuitive and simple to navigate. Different areas of the site can be accessed via the top menu bar:



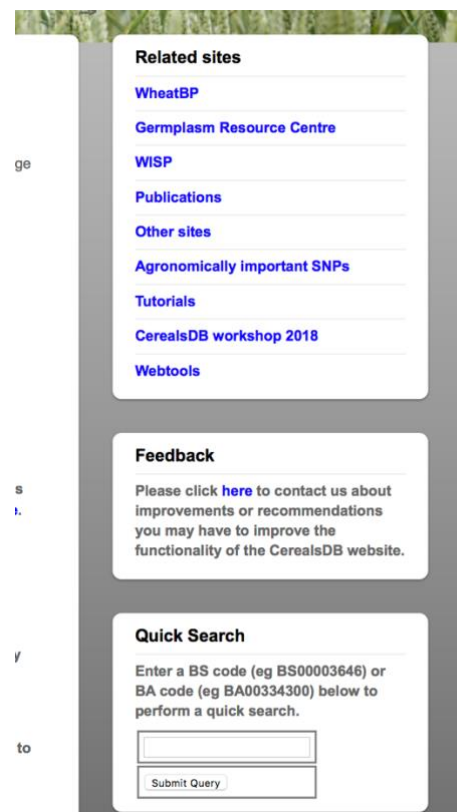
This links through to specific markers that have been developed for wheat SNPs, including KASP, Axiom, iSelect, Taqman and SNPs developed for targeted genotyping by sequencing (TGbyS). There is also a link to a BLAST site where users can input nucleotide sequences and search local BLAST databases hosted on our servers. There is also a link to information on the web services available for high throughput programmatic access to the underlying database.

An additional navigation menu is also available on the right-hand side of the web pages and differs for each section of the site. The menu contains links to various webtools that allow users to interrogate and visualize the data in CerealsDB. There is also a 'Quick search' field that users can specify a particular BS or BA SNP code and quickly access information related to that SNP.

We have also included a Feedback box to allow users to inform us of problems with the site along with improvements or recommendations they may have to improve the functionality and user experience.

If we begin by entering a SNP code such as the example given in the 'Quick search' field (BS00003646), we can retrieve information that is displayed on a new page describing which genotyping platforms that SNP is available, along with the contig sequence that the SNP is located in and the SNP highlighted in red. If genetic mapping data is available, it will also be displayed along with any KASP primers that may be associated with the SNP.

The majority of SNPs in CerealsDB are hosted in the Axiom array section of the site and this is where most users will want to concentrate their searches, however the KASP section is also an important part of the site for plant breeders and researchers.



Clicking on the KASP section in the top menu bar links to a page providing statistics for KASP markers. Clicking on the numbers for an individual chromosome links out to tables of SNPs for that particular chromosome.

Users can search for genetic maps for a wheat chromosome by clicking on the ‘Select primers’ link in the right-hand menu bar, which provides ideograms of each chromosome, and clicking on a chromosome links out to a genetic map.

Users can then search for KASP primers for a particular SNP on the map or download and excel spreadsheet containing information on ALL of the primers on the genetic map.

Similarly, users can select the ‘Obtain haplotypes’ link in the right-hand menu bar to list all the wheat chromosomes and clicking on a specific chromosome will download ALL the haplotypes available for that chromosome. Users can also align SNPs to *Brachypodium*, search for putative varietal SNPs and download core marker sets.

### KASP SNPs Summary Statistics

Total number of varietal SNPs in SNP database: **99,945**  
 Markers for which assays have been developed: **8,700**  
 Marker assays that have been validated: **7,228**  
 Markers that have been mapped: **5,033**

The work behind this study was undertaken to mine the UK wheat germplasm for varietal SNPs. We used both the available wheat expressed sequence tags (ESTs) that are deposited in the public databases and next-generation sequencing (NGS), together with a novel sequence alignment and assembly approach to identify varietal SNPs in lines of interest to European wheat breeders (23 wheat varieties were used in the initial study). We then investigated whether these SNPs could be validated by the LGC Genomics (formerly KBioscience) high-throughput genotyping procedure, Competitive Allele-Specific polymerase chain reaction (KASP) assay. Finally, we made use of the existing Avalon X Cadenza mapping population to examine whether the validated SNPs could be efficiently placed onto the existing linkage groups identified within this doubled haploid population. The details of this work are available in the article [Transcript-specific, single-nucleotide polymorphism discovery and linkage analysis in hexaploid bread wheat \(\*Triticum aestivum\* L.\)](#).

Number of SNPs mapped to each chromosome; (expected values are shown in brackets).

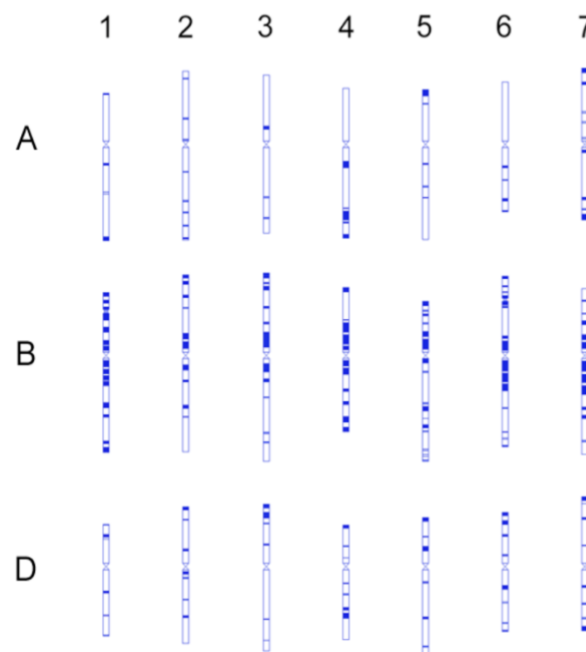
	1	2	3	4	5	6	7	Total
A	236 (236)	286 (266)	239 (244)	130 (253)	267 (244)	269 (212)	248 (240)	1675 (1695)
B	428 (251)	369 (274)	290 (293)	156 (242)	374 (257)	253 (268)	116 (266)	1986 (1851)
D	438 (178)	240 (215)	53 (227)	69 (191)	256 (221)	141 (187)	134 (215)	1331 (1434)
Total	1102	895	582	355	897	663	498	4992

Table showing the number of KASP SNPs that have been mapped to each of the 21 wheat chromosomes; the expected number, given the relative lengths\* of each chromosome and the total number of mapped SNPs (4,992), is shown in parentheses. These data clearly show that far fewer SNPs have been mapped to the D genome than would be expected were the SNPs to be evenly distributed across the genome.

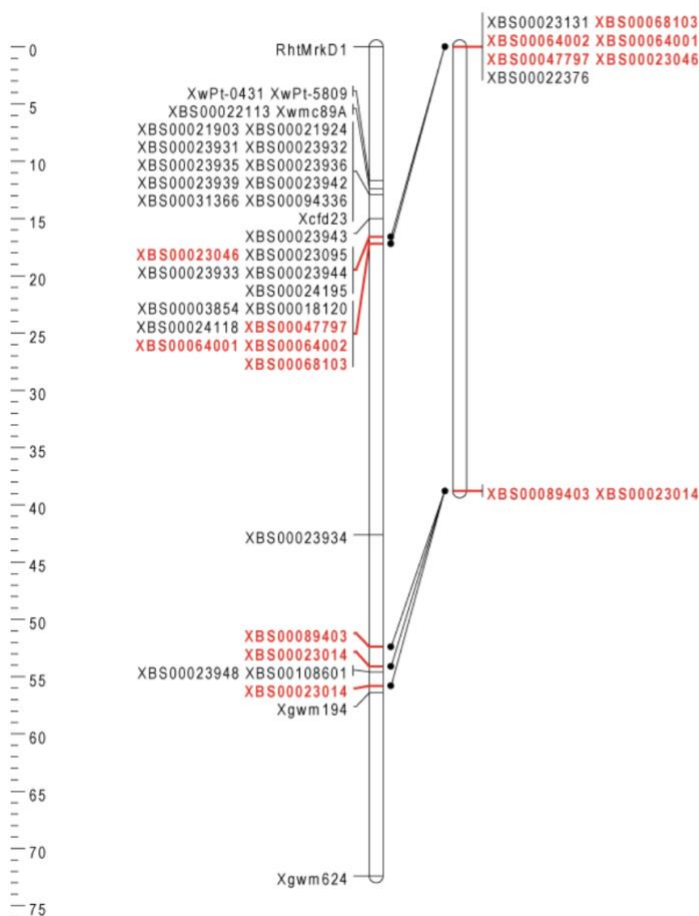
\*The total length of the wheat genome (234.4 µm) and the percentage length of each chromosome and genome (A = 34.0%, B = 37.2%, C = 28.8%) were taken from Gill, B.S., Friebe, B. and Endo, T.R. (1991) *Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat, Genome 34: 830-839*; this paper reports on the relative length in the variety Chinese Spring, which may differ from that for the varieties used in this study.

### Clickable map for selecting KASP primers

The ideogram below gives access to a list of all the SNP markers on any particular chromosome: click on the image of the chromosome for which you wish to obtain KASP primers.



Select all SNPs on chromosome 4D



To download an Excel file containing the KASP primers for all the SNP markers on chromosome 4D please [Click here](#)

The population of doubled-haploid (DH) individuals, derived from F1 progeny of a cross between cvs Avalon and Cadenza, was developed by Clare Ellerbrook, Liz Sayers and the late Tony Worland (John Innes Centre), as part of a Defra funded project led by ADAS. The parents were originally chosen (to contrast for canopy architecture traits) by Steve Parker (CSL), Tony Worland and Darren Lovell (Rothamsted Research). All marker data for non BS-coded markers was made available by the [Wheat Genetic Improvement Network](#).

The axiom pages host the majority of the SNPs on CerealsDB and can be accessed via the top menu bar. The Axiom® 820K array is a high-density array containing 819,571 exome-captured SNP sequences derived from hexaploid wheat accessions, including both elite and landrace accessions, diploid and tetraploid progenitor accessions and wheat relatives. The Axiom® wheat HD Genotyping Array is designed to characterise a range of wheat-related species, and in particular to identify and track introgressions in hexaploid wheat.

The Breeders' 35K Axiom® array (Affymetrix product ID 550524) contains 35,143 SNPs selected to be informative across a wide range of hexaploid wheat accessions. This 384-sample format array is a cost effective and efficient system for screening large numbers of lines. The array has been used to screen a large global collection of elite and landrace varieties including hexaploid and tetraploid accessions and the publicly available dataset (below) is regularly updated.

**Axiom® Menu**

- [Download 820K and 35K data](#)
- [Search with term or SNP name](#)
- [Publications](#)
- [Putative KASP primers for Axiom SNPs](#)
- [Axiom® Array presentation](#)
- [Introgression Plotter](#)
- [Create flapjack files](#)
- [Functional SNPs](#)
- [Extract genotypes](#)
- [Extract genotype for a specific SNP](#)
- [Search varietal information](#)
- [Extract probes](#)
- [820K dendrogram](#)
- [35K dendrogram](#)
- [Link SNP to related species](#)

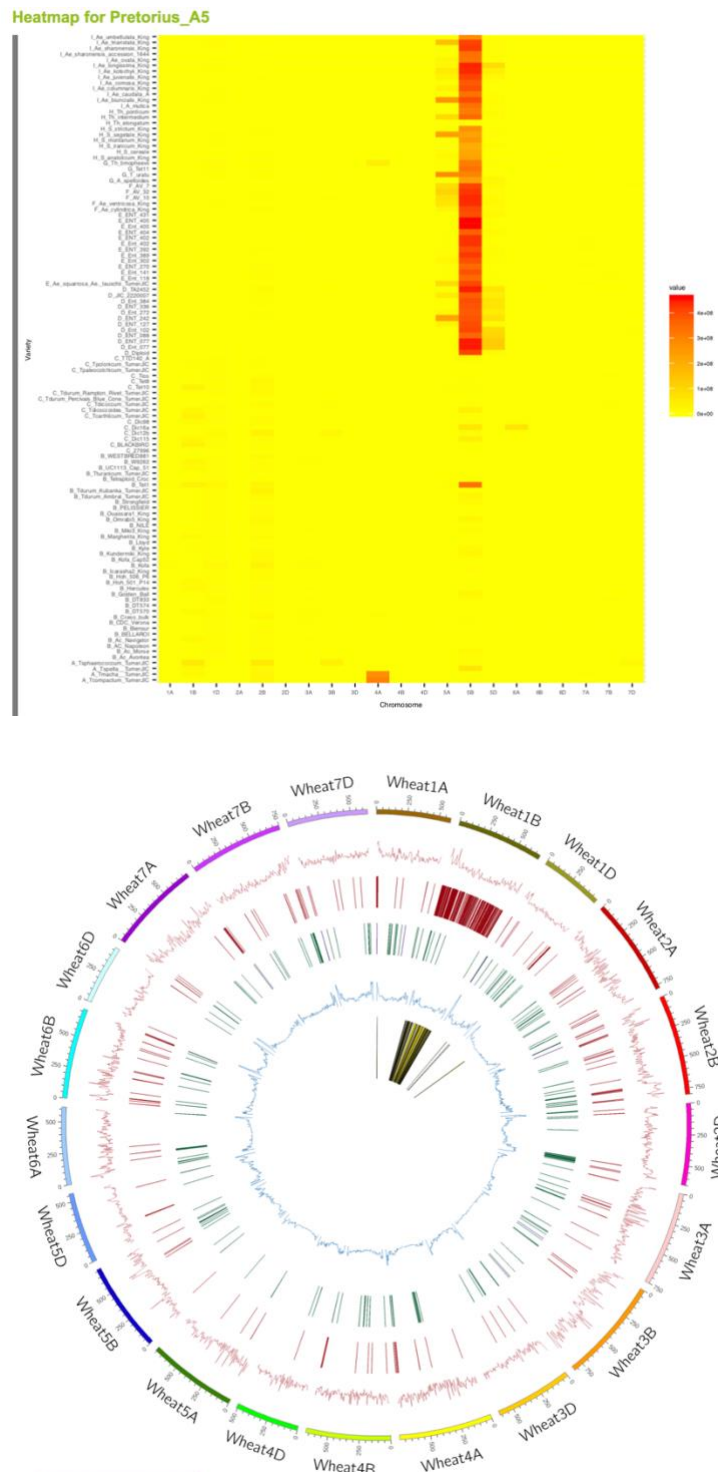
The right-hand menu bar lists a range of options for downloading and visualising the SNP data and also includes webtools for locating introgressions, creating flapjack files for haplotype analysis, a functional SNP database, extraction of genotypes, searching for varietal information, extraction of adjacent SNPs and exploring varietal relationships via online dendrograms.

The **introgression plotter** allows users to search for introgressions in elite wheat varieties that are predicted to be derived from wheat relative and progenitor species. Users can input a wheat variety and then specify percentage match cutoff for specificity and can also choose to exclude small introgressions.

This will generate a heatmap showing the presence of introgressions from wheat relative and progenitor species for each chromosome. The darker the red colour the larger the introgression. A table of introgressions is also produced which can be ordered by clicking on the table headers such as number of introgressions or size of the introgressions. Clicking on a particular relative links out to a circos plot.

In the circos plot, the innermost track is Track 1.

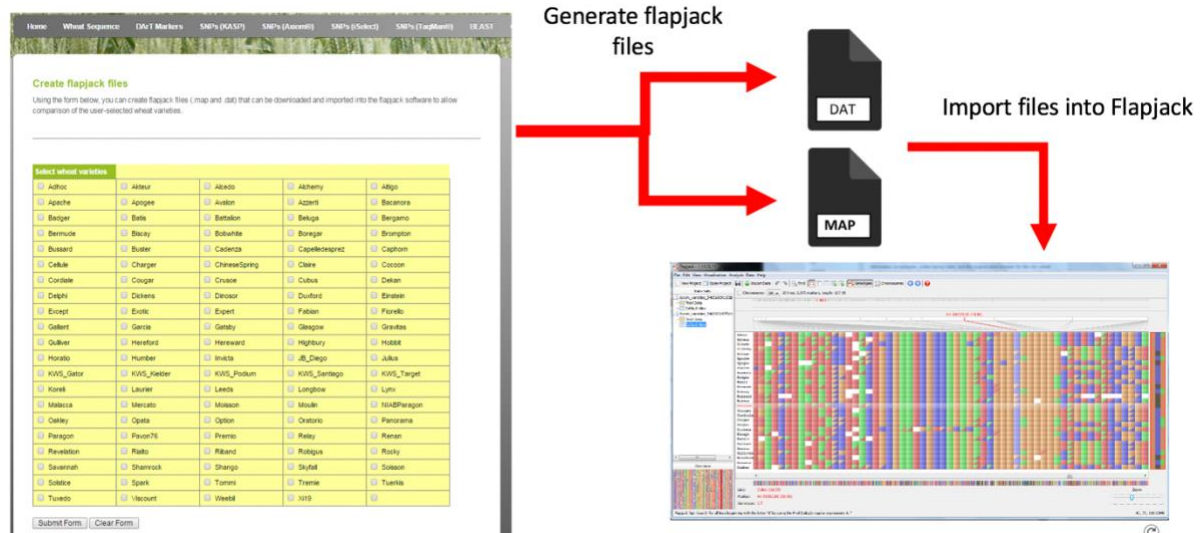
- **Track 1** - shows introgressed regions.
- **Track 2** (blue) - shows SNP density for each wheat chromosome.
- **Track 3** (green) - shows CNV gain.
- **Track 4** (red) - shows CNV loss.
- **Track 5** (red) - shows minor allele frequency for each chromosome.



The outermost track represents the wheat chromosomes with scales added ie 500 equals 500 million base pairs.



**Creation of flapjack files** is a useful tool that allows users to create flapjack files (.map and .dat) that can be downloaded and imported into the flapjack software to allow comparison of the user-selected wheat varieties. The flapjack software is a multi-platform application providing interactive visualizations of high-throughput genotype data, allowing for rapid navigation and comparisons between lines, markers and chromosomes and has been developed by the James Hutton Institute.



The **Functional SNPs** tool, allows users to search for SNPs that produce a non-synonymous (missense) mutation and obtain information on the sequence surrounding the SNP, the amino acid sequence and annotations.

A non-synonymous mutation is a point mutation in which a single nucleotide change results in a codon that codes for a different amino acid. These mutations can render the resulting protein non-functional, however the amino acid substitution with another amino acid with similar chemical properties can result in a neutral mutation and the protein will function normally.

Functional SNPs are non-synonymous SNPs that have a deleterious effect on protein function. The fSNPs in CerealsDB have been characterised using the FATHMM pipeline and annotated with BLAST against a non-redundant embryophyta database.

Functional SNPs are defined as SNPs with a FATHMM score less than -3.0 or greater than 3.0.

**CerealsDB**  
Tools for the analysis of the wheat genome

Home Wheat Sequence DArT Markers SNPs (KASP) SNPs (Axiom) SNPs (iSelect) SNPs (TagMant) BLAST

**Obtain information on non-synonymous (nsSNPs) and functional SNPs (fSNPs)**

From this page you can search for SNPs that produce a non-synonymous (missense) mutation and obtain information on the sequence surrounding the SNP, the amino acid sequence and annotations.

A non-synonymous mutation is a point mutation in which a single nucleotide change results in a codon that codes for a different amino acid. These mutations can render the resulting protein non-functional, however the amino acid substitution with another amino acid with similar chemical properties can result in a neutral mutation and the protein will function normally.

Functional SNPs are non-synonymous SNPs that have a deleterious effect on protein function. The fSNPs in CerealsDB have been characterised using the FATHMM pipeline (Shihab et al.) and annotated with BLAST against a non-redundant embryophyta database.

Functional SNPs are defined as SNPs with a FATHMM score less than -3.0 or greater than 3.0.

Using the input fields below you can access fSNP information in several different ways:

- 1) Enter a SNP name (a 10 character alphanumeric beginning with 'BS' or 'BA'; e.g., BS00010624 or BA0033400) to find the contig to which it maps and all other putative SNPs, validated or not, that have been mapped to it. SNP names (IDs) may take different forms depending on the platform on which the assay was developed:

KASP assays	BS00003890
Axiom array	BA00809142

SNP names with 'BS' codes may have an extension (e.g., '1', '2'). These should not be added when performing a search; if they are added they will be removed by the program before the search is performed.

- 2) Enter a search term (e.g., disease) in order to obtain a list of contigs that when BLASTed against the NCBI database returned a hit containing the chosen term.
- 3) Set a threshold for the FATHMM score (e.g. -3 will return all SNPs with a FATHMM score less than -3.0)
- 4) Set a threshold for the FATHMM score (e.g. 3.0 will return all SNPs with a FATHMM score greater than 3.0)

1) SNP_id (e.g. BS00003890 or BA00809142)	
2) Search term (e.g., 'disease', 'glutenin')	
3) FATHMM score LESS THAN (e.g. '-3')	
4) FATHMM score GREATER THAN (e.g. '3.0')	1.5
<input type="button" value="Submit Query"/>	

Users can search for functional SNPs, by entering a Bristol SNP code, a generic search term such as ‘gliadin’ or by FATHMM score, to retrieve all functional SNPs that match the criteria specified in the search. This produces the amino acid sequence surrounding the SNP with the amino acid change highlighted and links out to Uniprot if available.

1) SNP_id (e.g. BS00003643(.1) or BA00334300)	
2) Search term (e.g., 'disease', 'glutenin')	disease
3) FATHMM score (e.g., '-3' or '3')	
<input type="button" value="Submit Query"/>	

Enter a search term, for Example "disease"

**CerealsDB**  
Search for the analysis of cereal genomes

Home Wheat Sequence DArT Markers SNPs (KASP) SNPs (Axiom) SNPs (Select) SNPs (TagMulti) BLAST

The non-synonymous SNPs containing the search term **disease** are listed below. There are 360 contigs in the list.

1. BS00028451 is located on contig BC000013481 - There are No mapped KASP SNPs on this contig.

The SNP has the following annotation: Eval = 4e-57

glt475617979glt[EMT30296.1:Putative\_disease\_resistance\_RPP13-like\_protein\_1\_[Aegilops\_tauschii]

MLEDQFLAKCQGLPLAKVINGLLOKEXTRDWDQVNDQIVSVQMSKELNAYLEYDGLSPYKQGLFHSUKPKTVND(TGSE)  
VSMAYGESVSGDITYSRNLEEDQWYKELVRLIEVDTDDPGLFONKHQVRSFAGPARGETLY

To search for the EMT30296 accession on Uniprot, please click the button on the right.

The FATHMM score for this SNP was 8.562881 which suggests it has a **negligible** effect on protein function.

**Extraction of genotypes** can be performed for a particular variety or for a particular SNP. The genotyping data is available for the 820K array, 35K breeders array and 35K wheat relatives array. We also have genotyping data available for a large number of mapping populations. Users can select a specific array or mapping population and download ALL genotypes for a specific variety or SNP.

Select an array or mapping population	
<input type="radio"/> 820K_array	<input type="radio"/> 35K_breeders_array
<input type="radio"/> 35K_relatives_array	<input type="radio"/> AvalonxCadenzaDH
<input type="radio"/> ApogeeXParagonf5	<input type="radio"/> Boden_tilling_samples
<input type="radio"/> CadenzaXAvalonf5	<input type="radio"/> Chinese_Spring_Deletions
<input type="radio"/> Doonan_sphaerococcumxCapelle	<input type="radio"/> ChineseSpringxParagon
<input type="radio"/> JIC_Toolkit_3	<input type="radio"/> MalaccaxHereward
<input type="radio"/> NIAB_sme1	<input type="radio"/> NIAB_D_Synthetics
<input type="radio"/> OakleyxGatsby	<input type="radio"/> ParagonxBaj
<input type="radio"/> ParagonxBecard_kachu	<input type="radio"/> ParagonxCimcog47
<input type="radio"/> ParagonxCimcog49	<input type="radio"/> ParagonxExtrem
<input type="radio"/> ParagonxMisr1	<input type="radio"/> ParagonxPfau
<input type="radio"/> ParagonxStarkeshortday	<input type="radio"/> ParagonxSuper152
<input type="radio"/> ParagonxTet_syn_BC1F5	<input type="radio"/> ParagonxTetraploid_BC1F5
<input type="radio"/> ParagonxWatkinsNEW	<input type="radio"/> ParagonxWatkins_305
<input type="radio"/> ParagonxWatkins912	<input type="radio"/> ParagonxWaxwing
<input type="radio"/> ParagonxWyalkatchem	<input type="radio"/> ShamrockxShango
<input type="radio"/> TetxHex_synth_NAM_population	<input type="radio"/> WeebilxCimcog03
<input type="radio"/> WeebilxCimcog32	<input type="radio"/> WeebilxCimcog56
<input type="radio"/> Yumai34xClaire	<input type="radio"/> Yumai34xUkrainka
<input type="radio"/> Yumai_34xValoris	<input type="radio"/> Zinc_content_ParagonxWatkins

You can download this data as a text file by clicking on the download icon below (Right Click -> 'Save Link as'):



Variety	Axiom probe	Genotyping call	Chromosome	Converted
A24_PxMISR1_48	AX-94618000	2	chr1A	BB
A24_PxMISR1_48	AX-95198379	2	chr1A	BB
A24_PxMISR1_48	AX-95112378	0	chr1A	AA
A24_PxMISR1_48	AX-94742787	9	chr1A	NoCall
A24_PxMISR1_48	AX-95102830	2	chr1A	BB
A24_PxMISR1_48	AX-94722894	9	chr1A	NoCall
A24_PxMISR1_48	AX-94761084	2	chr1A	BB
A24_PxMISR1_48	AX-94436763	0	chr1A	AA
A24_PxMISR1_48	AX-95194884	2	chr1A	BB
A24_PxMISR1_48	AX-95144698	2	chr1A	BB
A24_PxMISR1_48	AX-94562727	2	chr1A	BB
A24_PxMISR1_48	AX-94637020	1	chr1A	AB
A24_PxMISR1_48	AX-94972660	2	chr1A	BB
A24_PxMISR1_48	AX-95143266	0	chr1A	AA
A24_PxMISR1_48	AX-94383913	2	chr1A	BB
A24_PxMISR1_48	AX-94894053	2	chr1A	BB
A24_PxMISR1_48	AX-94813118	2	chr1A	BB
A24_PxMISR1_48	AX-94785197	0	chr1A	AA

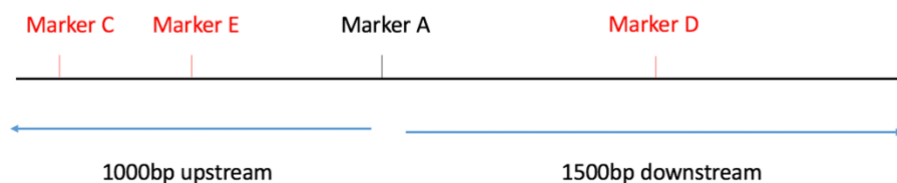
Users can also search **Varietal information** on CerealsDB and can select information on a particular wheat variety that has been included on the 35K or 820K axion arrays. You should specify which array you want to extract data from (820K or 35K) and then type the varietal name (this will autocomplete if it is in our list of varieties). Alternatively you can look for varieties using a general search term, such as country of origin (eg UK) or the source of the variety (eg University of Bristol).

There is also a webtool that allows users to **select all axion probes between two specified probes**. You can provide two axion probes (eg AX-94597091 and AX-94829239) that are located on the same chromosome in the IWGSC v1 assembly and extract all probes that lie in between these probes. If you only have a single axion probe it is also possible to search a specified distance upstream or downstream of your probe to retrieve all axion probes within this range.

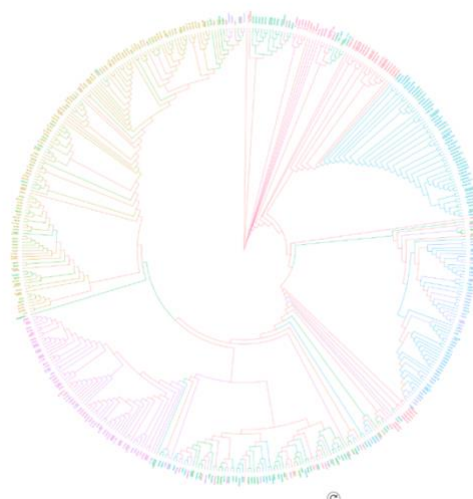
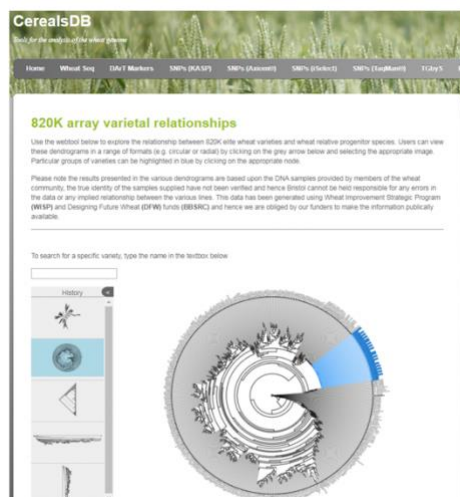
Scenario 1: Locate all markers between two known marker sites



Scenario 2: Locate all markers a specified distance either side of a known marker site



Interactive **online dendrograms** generated using genotyping data from the 820K array and 35K breeders array are available to explore the relationship between elite wheat varieties and wheat relative progenitor species. Users can view these dendrograms in a range of formats (e.g. circular or radial) by clicking on the grey arrow below and selecting the appropriate image. Particular groups of varieties can be highlighted in blue by clicking on the appropriate node. Users can also download a high quality .png image of the dendrogram.



Finally, there is a tool that facilitates the **search for SNPs that align to related species**. Given a known SNP\_id, users can find other SNPs containing sequences that align to the same region in other species including rice(*Oryza sativa*), *Brachypodium* and Sorghum.

Other genotyping platforms such as iSelect, Taqman and Targeted Genotyping by Sequencing (TGbyS) are also represented on CerealsDB and information on these markers can also be downloaded similar to the KASP and axiom platforms.

### iSelect SNPs Summary Statistics

Total number of markers on array: **81,587**

Markers that have been mapped: **43,999**

Markers that have been unambiguously mapped: **41,704**

The design of the wheat 90K iSelect assay and a consensus genetic map are available for download from [Kansas State University](#).

The description of assay design, accuracy of genotype calling using the polyploid version of GenomeStudio, development of cluster files and genetic maps will be provided in the manuscript [Characterization of polyploid wheat genomic diversity using a high-density 90,000 SNP array](#). (2014) *Plant Biotechnology Journal*.

Number of SNPs mapped to each chromosome; (expected values are shown in brackets).

	1	2	3	4	5	6	7	Total
A	2306 (1974)	2059 (2224)	1920 (2045)	1769 (2117)	2556 (2045)	2135 (1779)	2597 (2010)	15342 (14194)
B	3697 (2099)	5865 (2294)	2548 (2455)	1438 (2028)	2862 (2152)	2438 (2241)	2318 (2224)	21166 (15493)
D	553 (1494)	1310 (1797)	272 (1903)	320 (1601)	1056 (1850)	511 (1565)	1174 (1797)	5196 (12007)
Total	6556	9234	4740	3527	6474	5084	6089	41704

### TaqMan® SNPs Summary Statistics

Total number of markers available: **4,800**

Mapped markers available: **4,735**

TaqMan® Assays are a gold standard in qPCR applications and the technology is based on 5' nuclease chemistry using specific fluorescent probes to discriminate SNP variants. These assays come as single tube, pre-formulated primer and probe sets which can be used right out of the box requiring no optimization or laborious setup. Assays are available in three sizes or in other high throughput formats from [Life Technologies](#) – custom 96- and 384-well plates, microfluidic cards and OpenArray® plates.

Number of SNPs mapped to each chromosome (expected values are shown in brackets).

	1	2	3	4	5	6	7	Total
A	227 (224)	278 (252)	232 (232)	128 (240)	262 (232)	265 (201)	243 (228)	1635 (1609)
B	414 (238)	356 (260)	281 (278)	156 (230)	362 (244)	249 (254)	113 (252)	1931 (1756)
D	386 (169)	207 (204)	46 (216)	66 (181)	227 (210)	117 (177)	120 (204)	1169 (1361)
Total	1027	841	559	350	851	631	476	4735



## Search TGbyS probes

Using the form, users can search the sequence capture probes that were designed for use with the MyBait system. First select a probe category - users can select:

All probes

Co-dominant probes (the most useful set for breeding purposes)

Dominant probes

Partially co-dominant probes.

Once a category has been selected, users should also select a probeset - there are three available:

All: This set consists of all 15,167 probes.

Cross Platform: This set consists of 3,256 probes that showed greater than 95% similarity between the Axiom and NextSeq genotyping platforms.

Cross Platform (All): This set consists of the 782 probes that were common to the KASP, Axiom and NextSeq genotyping platforms.

Once a probeset has been selected, you can then select probes from specific chromosomes (or click on the "Select All" box to highlight all chromosomes).

### Search sequence capture probes

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Cross Platform (All): This set consists of the 782 probes that were common to the KASP, Axiom and NextSeq genotyping platforms.

Once a probeset has been selected, you can then select probes from specific chromosomes (or click on the "Select All" box to highlight all chromosomes).

The number of probes designed for each chromosome is displayed in the table below:

	1	2	3	4	5	6	7	Total
A	864	710	720	597	885	885	865	5526
B	1370	1651	1070	529	1034	1107	841	7602
D	470	261	426	89	326	206	261	2039
Total	2704	2622	2216	1215	2245	2198	1967	15167

The entire set of 15,167 probe sequences and associated information can also be downloaded in excel spreadsheet format [here](#).

### Selected Probe Sequences

The number of probes that match your query is: 864.

The following set of probes can be viewed in FASTA format by clicking the "Display fasta" button at the bottom of this page.

Some of the probes have a SNP position that is not located centrally at 61 base pairs and in these instances the SNP position is highlighted in blue.

Bait name	SNP pos	Sequence	Chr
AX-94405728_108_Dominant_pos-61_v1	61	CTGAAGACTGTTTCTGTATCTAAGTTTGTATCCAGAGG	1A
AX-94409545_225_Partially_pos-61_v1	61	ATATACACTATTCTCCCTGTAGGCAAGCACTGGCCCTTT	1A
AX-94449086_64_Co-dominant_pos-61_v1	61	CAGTGGTATCAACGCAGAGTATTATGATTTCGACTTAAGA	1A
AX-94496430_155_Partially_pos-61_v1	61	CGAAGCTAAATAAGGCAGATAAACGGGAAGAAGATGA	1A
AX-94506140_421_Co-dominant_pos-61_v1	61	GTGCTTTACATCAAAATTAGCCAAAGAGGCCATTAGCT	1A
AX-94569456_378_Dominant_pos-61_v1	61	TCTAGACCATGCAAGCTTCTCCAAAGGAACCTCATGTGGA	1A
AX-94569525_443_Dominant_pos-61_v1	61	AACCGATTAATGAAGAGGATGTCCAGCCATGCCAACAT	1A
AX-94747031_583_Dominant_pos-61_v1	61	TATCCTTACAAGTGACGTGCAGAGCAAGGTCAGTGAT	1A
AX-94778893_192_Dominant_pos-61_v1	61	CTGGCCTAGCAACAGCTCGATTGGCTTATTGTGCGCTT	1A
AX-95009086_254_Dominant_pos-61_v1	61	TCGACGAGCTGGCGCACACCATCATGCTGGTGTCTCACG	1A
AX-95153822_411_Partially_pos-61_v1	61	TCTGGTGTGCGCAGATGACCTGAACATCCATCGCCA	1A
AX-95161614_192_Dominant_pos-61_v1	61	TGACCGCGAACAACAGAACTCTCTGGTCTGAGTCAC	1A
AX-95170683_281_Dominant_pos-61_v1	61	AGGCGGTGCTAGTGGGTTCTTTTATAGAAAGATCTGCT	1A
AX-94422082_36_Co-dominant_pos-36_v1	36	GAAGATCCTTCCCTGATCAATATAAATCAGTTTGG	1A
AX-94733072_41_Co-dominant_pos-41_v1	41	TGCTCCGTGACTTTACCGGCAAGCGCGGGGACAAGAA	1A
AX-95004364_43_Partially_pos-43_v1	43	ATCAGATGCTCCCTGTCTCGCACTGCCAGGGGAAGTA	1A
AX-94607341_44_Co-dominant_pos-44_v1	44	TGACTGCACAATGGTCTCTTGTTCCTCCGCAAGGCAAGC	1A

The detailed MyBait probe capture protocols are also available, so users can replicate perform their own sequence capture experiments using the probes we have designed.

## CerealsDB web services overview

Web services have been developed for CerealsDB to allow bioinformaticians to access CerealsDB data (currently SNPs, contigs and search terms for our KASP genotyping platform).

The CerealsDB webservices have been developed in collaboration with the Data Infrastructure & Algorithms group at the Earlham Institute and we would like to thank Rob Davey, Simon Tyrell and Xingdong Bian for their help setting up these services.

This part of the site has been written with software developers in mind and may therefore appear rather esoteric to some of our users. If you aren't familiar with command lines and writing code, you may find yourself out of your depth, but I hope this page will at least impress upon users the power of web services for data integration and standardisation, which is a pressing need in the wheat community where information is stored on disparate databases around the world.

We have created a web service based on REST Architecture (RESTful web services). A web service is a collection of open protocols and standards that are used to exchange data between applications or systems. Software applications written in a variety of programming languages and running on various platforms can use web services to exchange data over computer networks such as the Internet. This interoperability (e.g., between Java and Python, or Windows and Linux applications) is due to the use of open standards such as JSON.

The CerealsDB web services use HTTP methods to implement the concept of REST architecture. A RESTful web service usually defines a URI, Uniform Resource Identifier a service, provides resource representation such as JSON and a set of HTTP Methods.

