

We are very pleased to inform you that a new wheat SNP array, Wheat660, is available now. It is designed by Chinese Academy of Agricultural Sciences and synthesized by Affymetrix. The Wheat660 are generated from screening four 660K SNP arrays against 192 wheat accessions including 60 worldwide modern varieties, 72 landraces, 30 wild emmer wheat and 30 *Ae tauschii*. It can detect more than 630k (630,000) SNPs in wheat. The Wheat660 has the following advantages:

- (1) **Genome specific.** All the SNPs are genome specific with clear genotypic profiles (Figure 1) which makes accurate automatic reading possible. In this regard, the Wheat660 has the characteristics of a diploid SNP array.
- (2) **High density and low cost.** It has the highest density in wheat up to now. The 630K SNP was designed in one chip, therefore the cost is much lower.
- (3) **Highly efficient.** All of the SNPs have been tested and confirmed. Further, the SNPs on subgenome D is much more than the previously arrays thus can meet the requirement for detection of D genome diversity.
- (4) **Wide range of possible application.** The Wheat660 array has wide range of possible application. More than 90% of the SNPs are polymorphic among the wheat cultivars assessed. Therefore, the array can be used for gene discovery, haplotype mapping, genomic selection and evolutionary studies.

For more information, please contact JizengJia (jaijizeng@caas.cn) or Guangyao Zhao at CAAS (Zhaoguangyao@caas.cn).

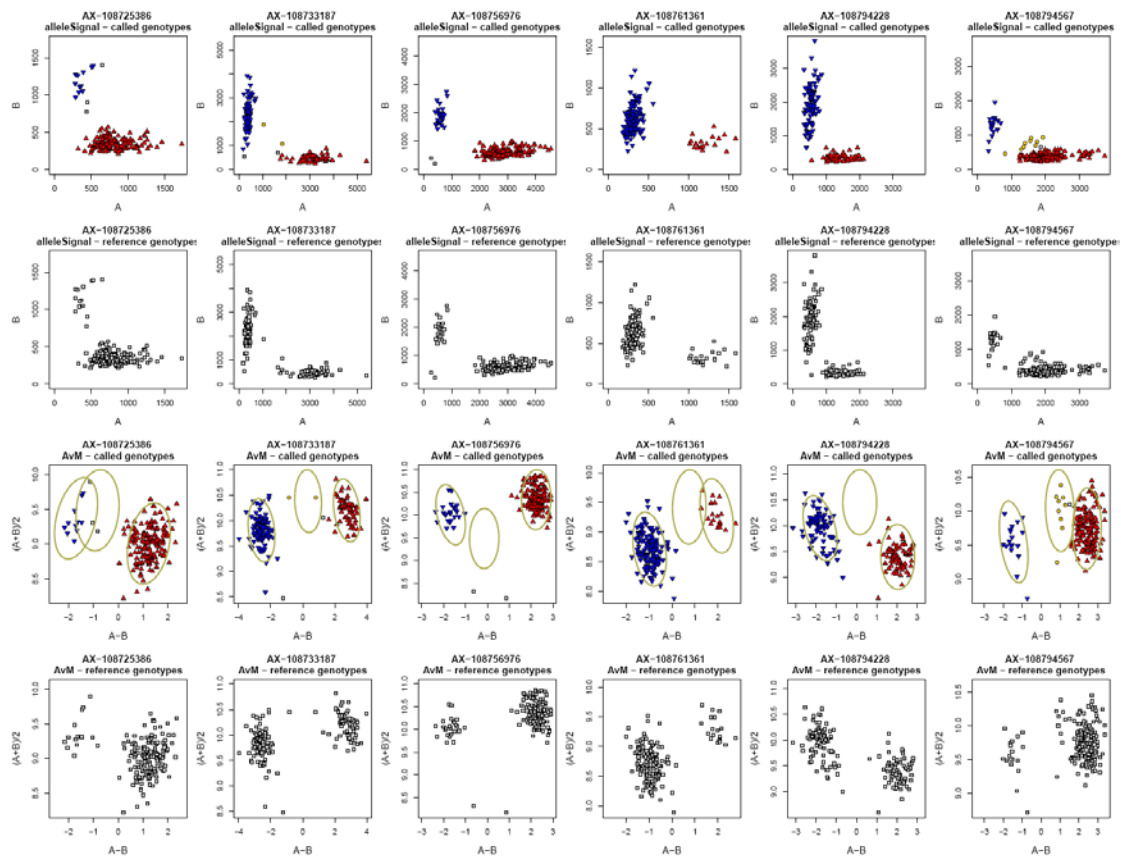


Figure 1 Visualization produces four sub-gures per probeset that is interrogating a SNP. Each column of four gures in a page corresponds to one SNP. The label above each gure is the probeset ID. The rst and second gures (rows one and two) show the scatter pattern of normalized A versus B channel intensities (A is the X axis, B is the Y axis). The third and fourth gures (rows three and four) show the scatter pattern in contrast versus size space.