Tomato genotyping library

The LGC, Biosearch Technologies[™] tomato genotyping library offers convenient access to functionally validated <u>KASP[™] genotyping assays</u>. The SolCAP consortium, in collaboration with Biosearch Technologies, have generated a validated panel of 384 carefully selected KASP SNP markers for cultivated tomato, plus ~7000 additional KASP SNP markers.

Tomato KASP SNP markers

The Solanaceae Coordinated Agricultural Project (SolCAP) was supported by the Agriculture and Food Research Initiative Applied Plant Genomics CAP Program of USDA's National Institute of Food and Agriculture.

The project linked together people from public institutions, private institutions and industries dedicated to the improvement of the Solanaceae crops: potato and tomato.

Working with the SolCAP team of academic bioinformatics experts, tomato breeders and LGC, we have generated a 'Core Marker Set' for cultivated tomato. This core set of 384 KASP assays have been selected from validated SNPs. The markers have been selected to maximise polymorphic information content based on 110 large-fruited elite fresh-market tomato varieties. The SNPs were further selected to be evenly distributed across the genome, based on both genetic and physical maps.

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Other collaborators in this study were the Department of Plant Biology, Michigan State University, and the Seed Biotechnology Center, University of California Davis.

All information from the study is available to view and download from http://solcap.msu.edu/index.shtml.

These KASP genotyping assays are easy to run, robust, accurate and highly cost-effective. The reagents for KASP genotyping can be delivered to you so that you can run the assays in your own laboratory; KASP can be read on most qPCR instruments and FRET-capable plate readers.

Alternatively, we can run the entire project for you in our genotyping service laboratories, including DNA extraction from your samples if required.

Advantages of the tomato assays:

- Panel includes 384 functionally validated SNP assays
- Pick and choose the assays relevant to your research from our tomato assay lists
- Assays can be either:
 a) run in your
 own laboratory
 b) run through our
 genotyping service
 laboratories
- Proven KASP
 technology delivers
 superior genotyping
 performance









Figure 1. Typical SNP genotyping results using a prevalidated Tomato KASP Assay on 1536-well plate with SNPline instrumentation. The data was normalised with ROX and plotted using KlusterCaller™ software.

Additional genotyping panels

Biosearch Technologies has been providing genotyping solutions for over 15 years to a global customer base. Libraries of pre-validated KASP genotyping assays have been developed for a wide range of species, in collaboration with scientific partners who have substantial experience of working with their respective organisms.

Also available are rice, lentil, maize and wheat <u>genotyping</u><u>libraries</u>.

Ordering inf	ormation
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Cat no.	Size	Description
KBS-2500-002	(2500 × 10 μL reactions)	Tomato KASP Assay Mix
KBS-1050-101	500 × 10 µL reactions (2.5 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (2.5 mL)*
KBS-1050-102	5000 × 10 μL reactions (25 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (25 mL)*
KBS-1050-103	50000 × 10 μL reactions (250 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (250 mL) (10 x 25 mL)*

* Alternative master mixes with high ROX and low ROX are also available. Please ensure that you are using the optimal version of KASP-TF Master Mix for your instrument.

References

Single nucleotide polymorphism discovery in cultivated tomato via sequencing by Synthesis. Hamilton, J. P., Sim, S. C., Stoffel, K., Van Deynze, A., Buell, C. R., Francis, D. M. (2012). The Plant Genome. Vol. 5, 17-29.

Generation of the extensive SolCAP database of transcript sequences and > 60,000 non-redundant SNPs to aid tomato genetics and breeding projects. The study used data from six tomato accessions spanning different cultivated classes; utility of the SNPs for assessing genetic variation within cultivated and wild populations was demonstrated.

High-density SNP genotyping of tomato (Solanum lycopersicum L.) reveals patterns of genetic variation due to breeding. Sim, S-C., Van Deynze, A., Stoffel, K., Douches, D.S., Zarka, D., Ganal, M.W. ... & Francis, D.M. (2012). PLoS ONE 7(9): e45520.

In order to investigate genetic variation on the tomato genome due to contemporary breeding, Sim et al. used an array of 7,720 of the SolCAP SNPs to genotype 426 accessions representing different market classes of cultivated tomato

and closely related wild species.

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