

GeneChip® *Medicago* transcriptome solution

The fastest and most effective whole-transcriptome profiling approach for legume researchers who want results within a crop season

- **In a single experiment**, measure expression changes of *Medicago truncatula* reference cultivars A17 and R108, and *Medicago sativa* (alfalfa).
- **With the right results the first time**, have confidence in low-level expression data with higher reproducibility than RNA-Seq.
- **Within minutes**, analyze and visually interpret the expression of genes, exons, and transcript isoforms.

Medicago is a model organism for research into legumes such as soybean, peanut, and alfalfa. A key area of intense legume research is using whole-transcriptome profiling on genetically modified organisms (GMOs) to identify genes that allow the organism to grow successfully with minimal fertilizer. The discovery and utility of such genes can have profound implications on the global environment.

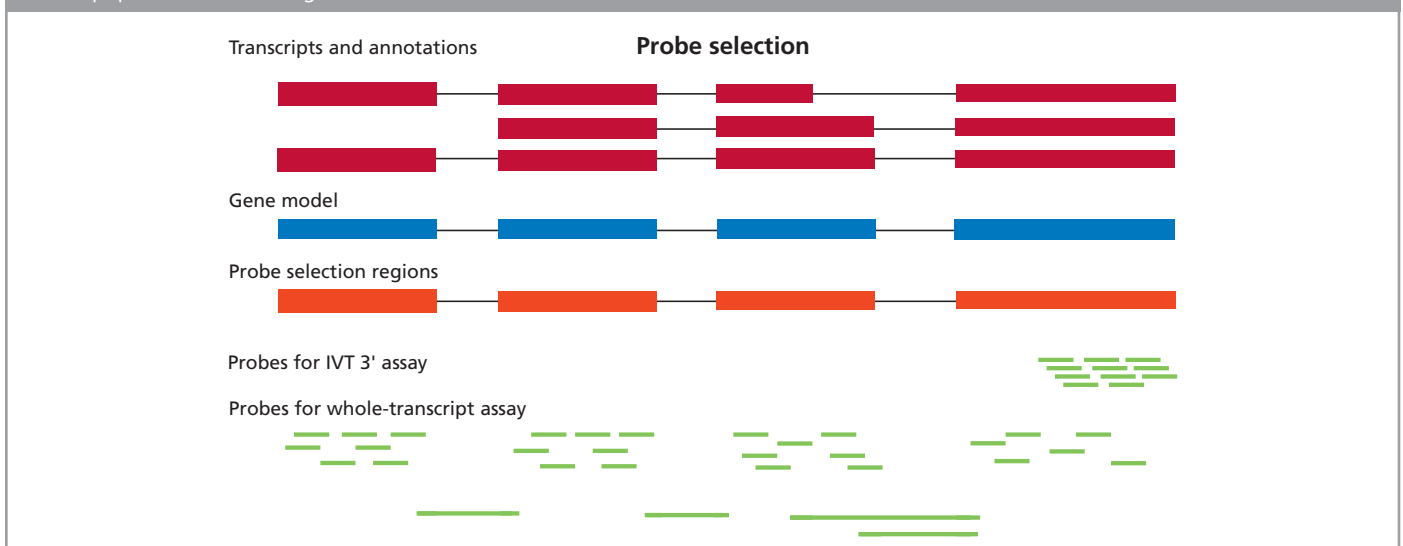


The GeneChip® *Medicago* transcriptome solution is uniquely designed to accelerate legume research, with rapid whole-transcriptome profiling of legumes for a broad range of inputs (100 pg–500 ng) and free, intuitive software for the fast statistical analysis and visualization of global expression changes necessary to make informed decisions about terminating a GMO crop within a growing season.

One experiment – multiple answers

With a single experiment, GeneChip® *Medicago* Transcriptome Assay enables analysis of the transcriptomes of two key *M. truncatula* reference cultivars, A17 and R108, and also covers the transcriptome of the *M. sativa*. The placement of detection probes across the length of each transcript provides a rich data set sufficient to decipher changes at multiple levels, ensuring important biology is not missed and avoiding the need to repeat time-critical experiments. With probes across the entire length of various transcript isoforms, whole-transcriptome designs allow for a more comprehensive view of the transcriptome and the ability to differentiate between isoforms. Probes for an IVT design are restricted to the 3' end of each gene and therefore cannot differentiate between isoforms with the same 3' end (Figure 1). Uniquely, the inclusion of exon-junction probes across the *M. truncatula* A17 transcriptome allows for confident detection of alternative splicing events in this cultivar.

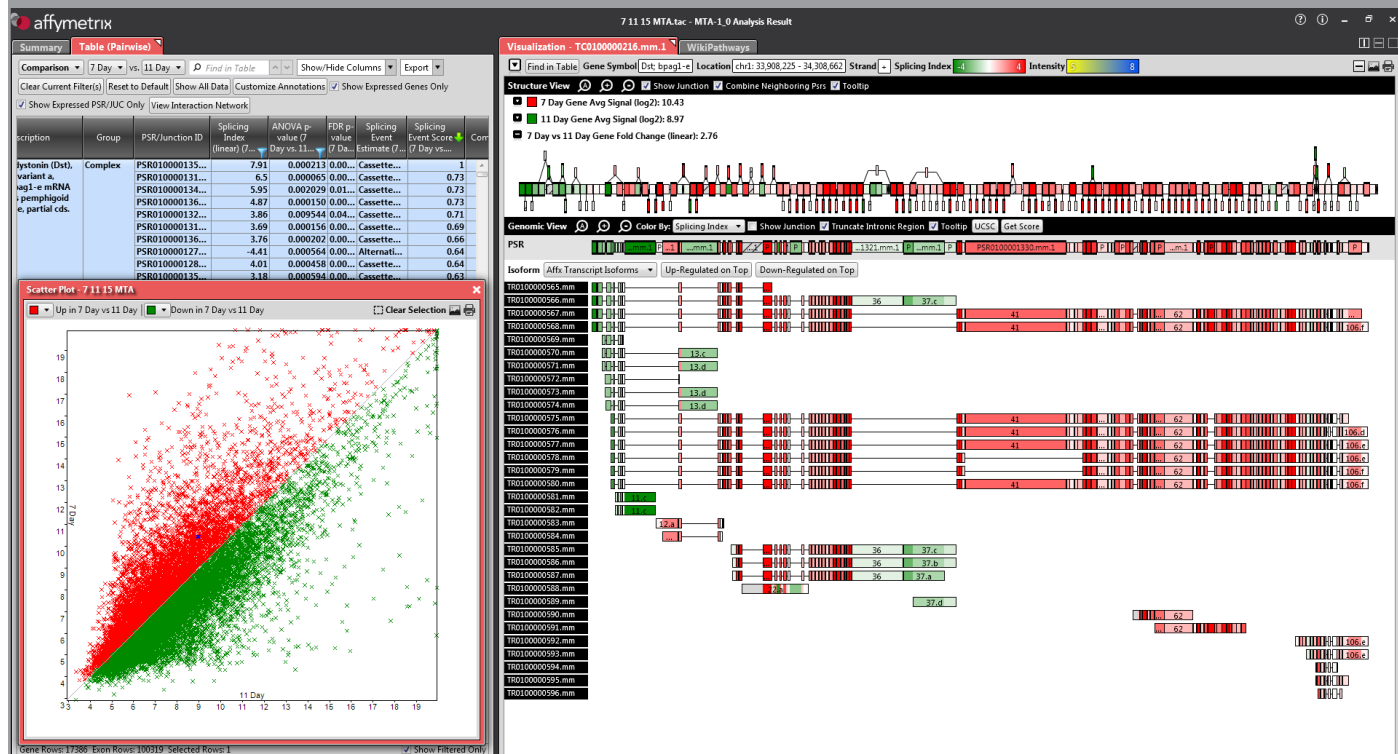
Figure 1: Whole-transcriptome assay design. Comparison of the number and location of probes selected for the classical 3' IVT-based amplification assay for traditional microarrays and a novel whole-transcriptome amplification assay. Isoform differentiation is made possible with a whole-transcript probe selection design.



A complete solution that rapidly takes you from data to insight in minutes

Obtain biological insights simply, quickly, and seamlessly, with our free, intuitive Transcriptome Analysis Console (TAC) Software, which transforms the high-quality expression data generated by the assay into biologically meaningful information in minutes.

Figure 2: Scatter plot and isoform visualizations. Visually interpret and understand multiple levels of biology of the *Medicago* transcriptome in minutes with free, intuitive TAC Software.



Array content summary

Array content	Mt4/A17	R108	<i>M. sativa</i>
Genes (transcript clusters)	>50,000	>68,000	>54,000
Transcripts	>69,000	>83,000	>71,000
Exons	>298,000	>221,000	>172,000
Exon clusters	>209,000	>221,000	>172,000

Design and annotation source summary

Design and annotation source	Mt4/A17	R108	<i>M. sativa</i>
JCVI	✓		
<i>Medicago</i> Hapmap Project		✓	
Samuel Noble Institute			✓
Controls			
ERCC probe set ^{1,2}		155	
Background probes		Antigenomic set	
Poly-A controls ²		<i>dap, lys, phe, thr</i>	
Hybridization controls		<i>bioB, bioC, bioD, creX</i>	

1. Probe sets interrogating external RNA controls present in the Ambion® ERCC RNA Spike-In Control Mixes, P/N 4456740 and 4456739 (purchased from Ambion).
2. This array contains probe sets for both ERCC and Poly-A spike-in controls. Sequence homology between the two control mixes will result in cross-hybridization of target to the control probes on the array. It is important to use only one control probe set when processing the arrays (ERCC or Poly-A controls), but not both.

Specifications

Sensitivity	≥1:100,000 (≥1.5 pM)
Correlation coefficient (intra-lot)	≥0.99
Detectable fold change	2-fold for 1:100,000 vs. 1:50,000
Dynamic range	~3 logs
Total RNA input required	50–500 ng
Probe feature size	5 μm
Probe length	25-mer
Target RNA orientation ¹	Sense target

1. The probes tiled on the array are designed in the anti-sense orientation, requiring sense-strand labeled targets to be hybridized to the array.

Array content

Organism	Genome	Annotation source	Genes ¹	Probe sets ¹	Probes/probes per gene ¹	Junction probes
<i>M. truncatula</i> A17	Mt4 by MTSC	JCVI	50,000 genes 61,000 transcripts 227,000 exons	50,000	2.6 million probes ² 50 mean per gene	Yes
<i>M. truncatula</i> R108	R108 v0.9 by the <i>Medicago</i> Hapmap Project	<i>Medicago</i> Hapmap Project	68,000 genes 68,000 transcripts 221,000 exons	68,000	1.9 million probes 28 mean per gene	No
<i>M. sativa</i>	Draft by Noble Institute	Noble Institute	54,000 genes 54,000 transcripts 172,000 exons	54,000	1.5 million probes per gene 27 mean per gene	No

1. These numbers represent mapped content only.

2. Junction probes not included in this count.

Ordering information

Part number	Description	Details
902878	GeneChip® <i>Medicago</i> Transcriptome Pico Assay (100–2,000 pg of RNA)	Sufficient for 12 samples
902879	GeneChip® <i>Medicago</i> Transcriptome Pico Assay (100–2,000 pg of RNA)	Sufficient for 30 samples
902880	GeneChip® <i>Medicago</i> Transcriptome Assay (50–500 ng of RNA)	Sufficient for 10 samples
902881	GeneChip® <i>Medicago</i> Transcriptome Assay (50–500 ng of RNA)	Sufficient for 30 samples
900720	GeneChip® Hybridization, Wash, and Stain Kit	Sufficient for 30 reactions

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