

Using genomics to study tanoak's past, present, and future

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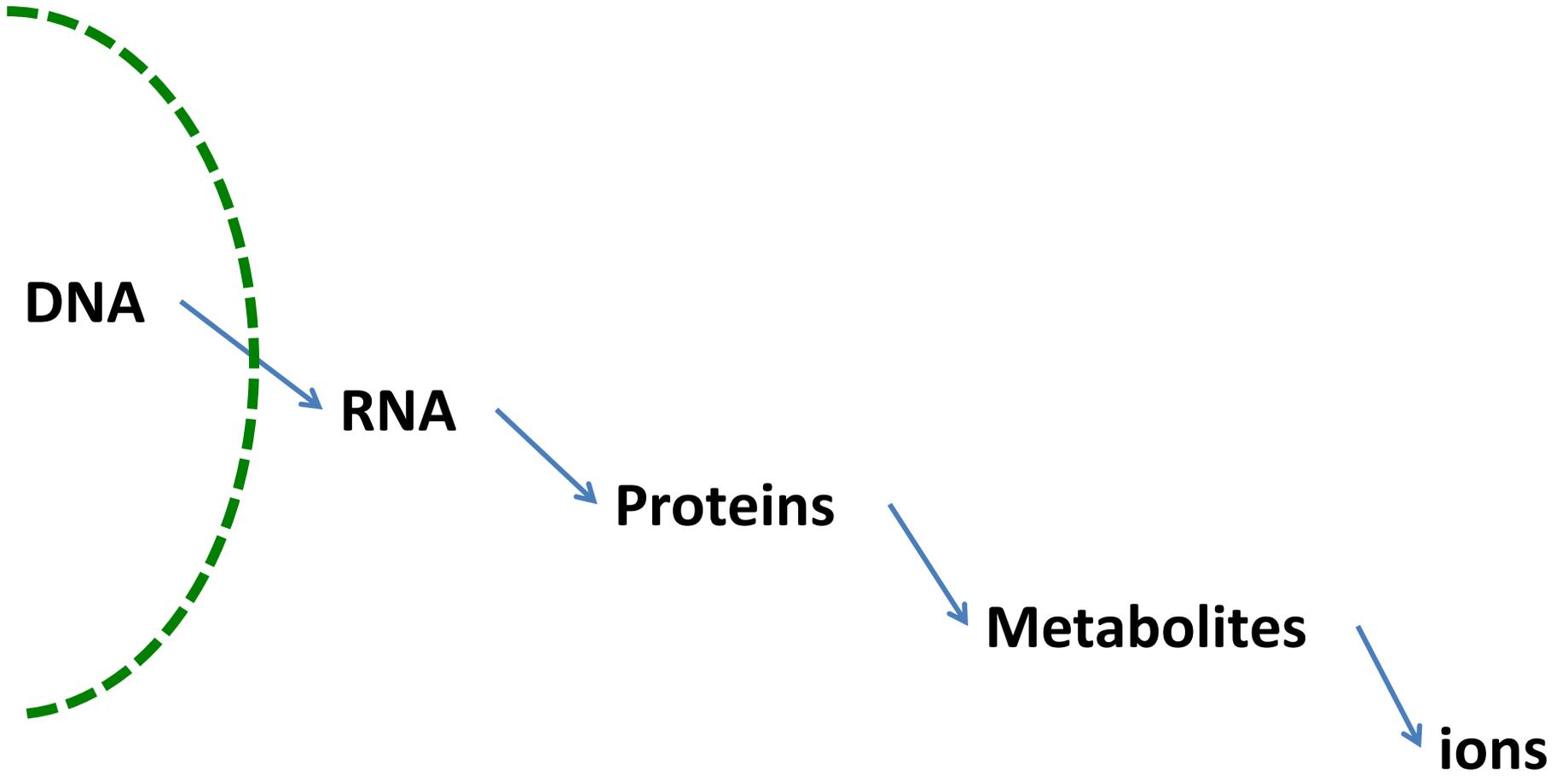


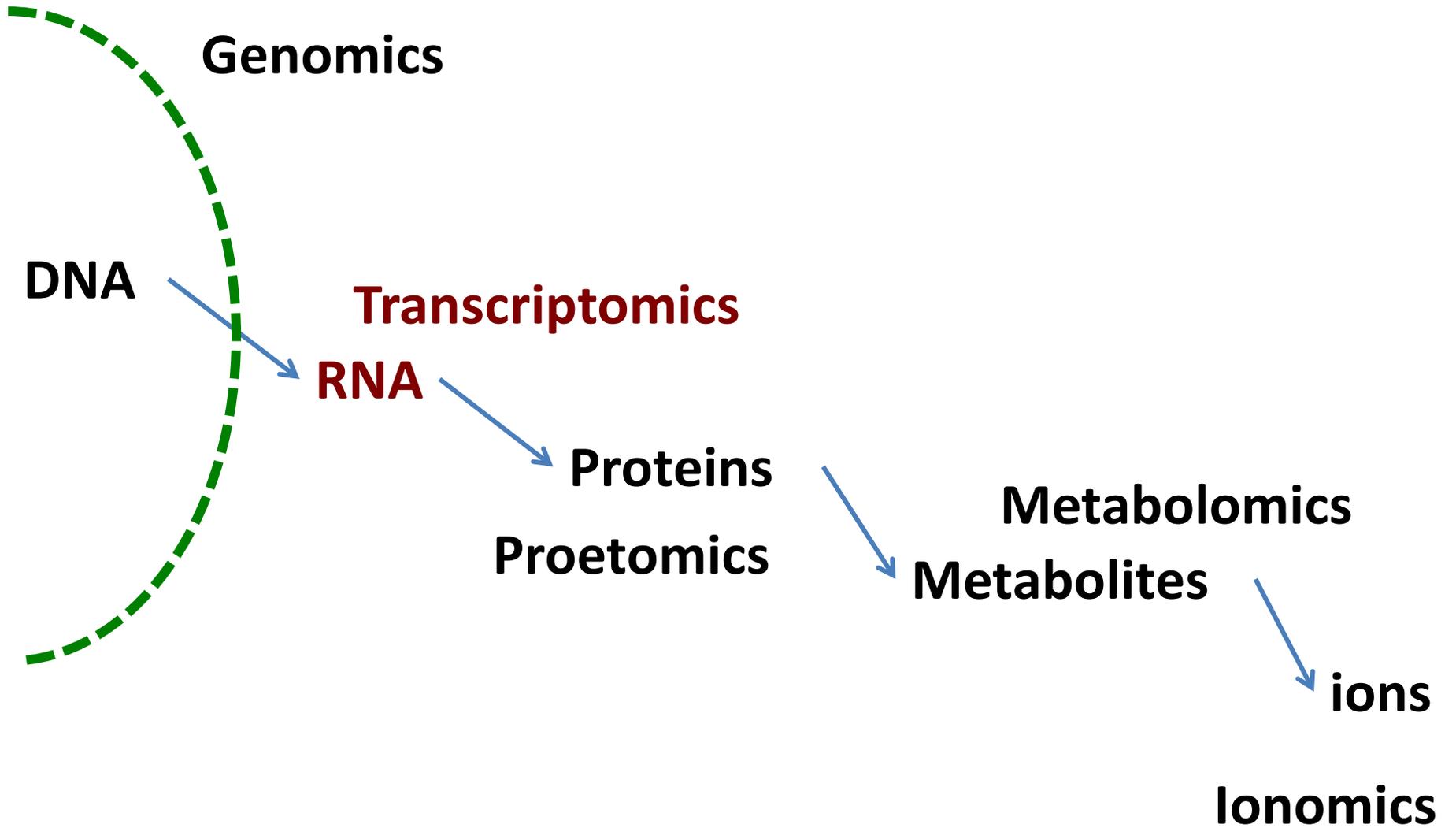
Current Knowledge

- Partition of neutral genetic diversity
 - Range-wide
- Contribution of clonality to stand genetic diversity
 - Within a stand
- Pollination and outcrossing to parentage
 - Within a tree
- Contribution of gene expression to phenotype
 - Within a genotype

Family BL-1





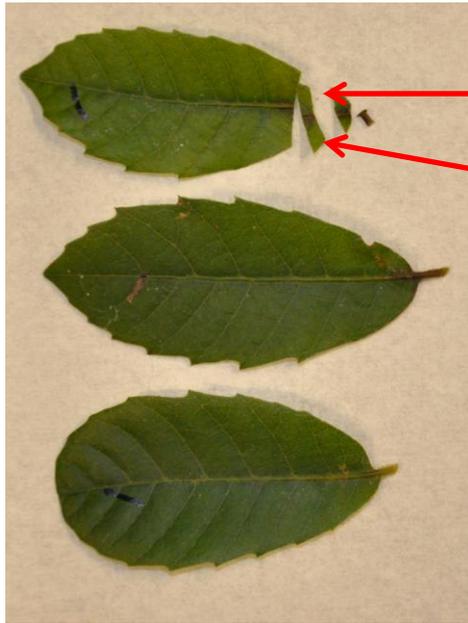


The present

First experiment

- One tree genotype
- One pathogen genotype
- One mock-inoculation control
- 2 time intervals from inoculation

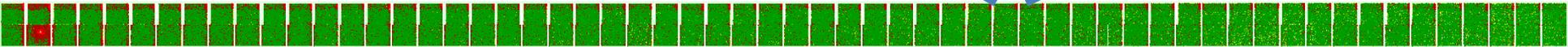
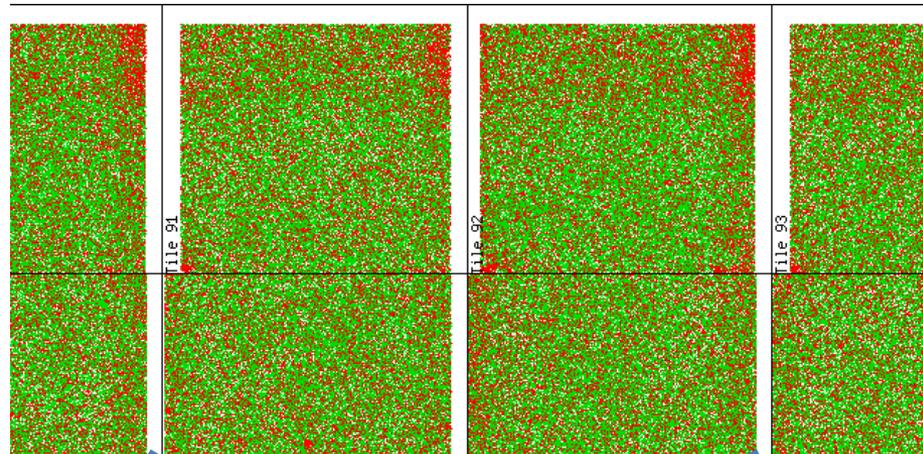




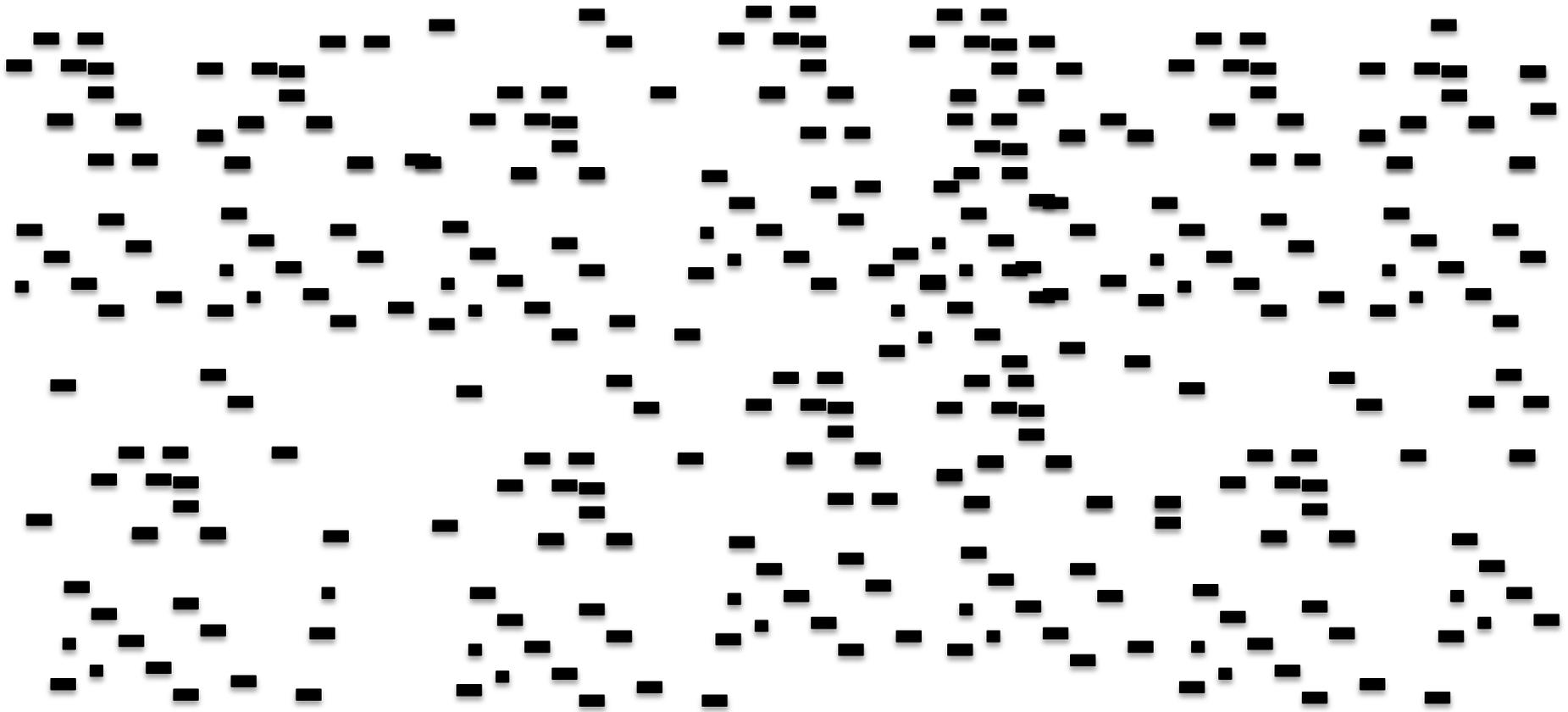
Tanoak mRNA

P. ramorum mRNA

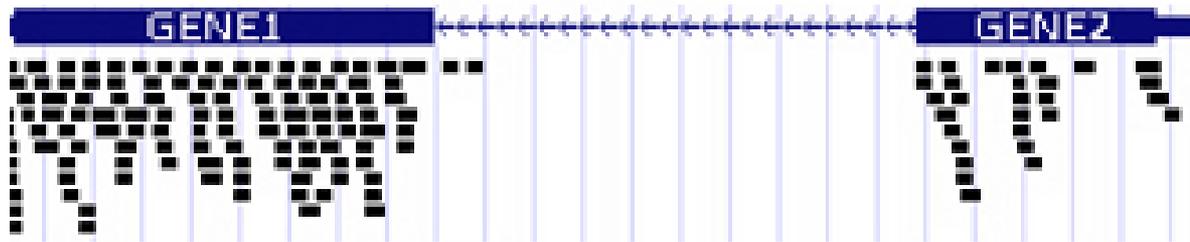
RNAseq
Illumina GAI



5.2 Gbp, in 64 M 80bp fragments



Align to the *P. ramorum* reference to
subtract pathogen sequences



Reference genome: Tyler et al. 2006.
Science 313: 1261-66

Align to the *P. ramorum* reference to subtract pathogen sequences

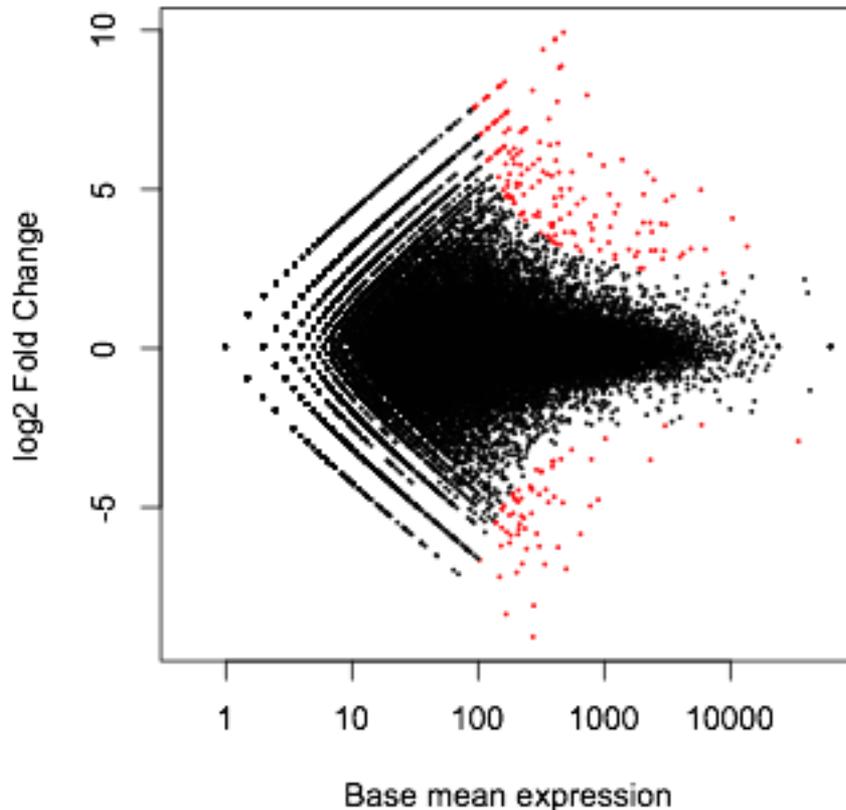
	% match <i>P. ramorum</i>
1 day inoculated	1.2%
1 day control	1.4%
5 day inoculated	4.5%
5 day control	0.9%

5 day inoculated

Pathogen sequence type	Transcripts matched
<i>P. ramorum</i> and <i>P. sojae</i> avirulence homologs (Jiang et al. 2008)	41
<i>P. ramorum</i> cellulose-binding, elicitor, lectin-like, and necrosis-inducing proteins (assembled from Tyler et al. 2006)	63
<i>P. infestans</i> CBEL, CRN, and necrosis-suppressing genes (Sierra et al. 2010)	16
Additional BLAST annotation <input type="text"/>	1893

Differential expression , 5 days post-inoculation

Treated vs control at 5 days



844 genes up- or down-regulated

- 102 match disease-related genes in Chestnut (A. Barakat, NC State)

- 47 R-genes

- Others annotated from published genomes, NCBI databases, and GO annotations

The future

We have

- Pipeline for inoculation, sequencing, and analysis
- The first tanoak transcriptome reference
- A first look at what is different in infected tissue vs not infected
- Lots of questions unanswered-
 - Variation among trees?
 - Only 1 genotype sampled
 - Variation among pathogen genotypes?
 - Only 1 genotype sampled
 - Confirmed function of DE genes

The future

- Expand sequencing
 - Resistant and susceptible sibs from across populations
 - Integrate topics discussed here –elicitins, phenolics, transposons
 - Phosphonate-treated vs control
 - Systemic fungicide, with direct and indirect action
 - Mechanism not well-understood; may involve increases in pathogen elicitors (Grant et al. 1990)
- Reference and raw data will be freely available (dendrome)
 - For tanoak gene expression
 - For comparative genomics (better reconstruct tanoak's past)
 - For other queries
 - sequence is meaningless if we don't know what it does – each addition to the database adds to our understanding of biology

Acknowledgements

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