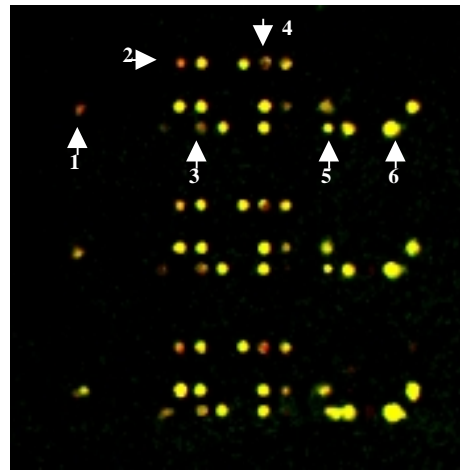


Figure 1

1. chlorophyll a/b binding protein type I
2. branched chain amino acid aminotransferase
3. agamous-like (AGL) MADS gene
4. TCTR2 (tomato CRT1-like gene)
5. farnesyl pyrophosphate synthase
6. lycopene beta-cyclase

A.

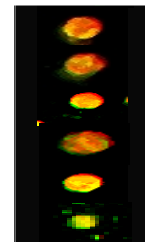
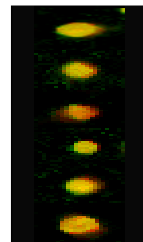


Note: Repetitive pattern is the result of all ESTs being arrayed in triplicate. Thus the top, center and lower sets of spots are the same ESTs in identical order. Similar signal ratios (color) and intensity (size) indicate the technique is fairly robust.

B.

“poor”

“good”



lycopene beta-cyclase

geranylgeranylated protein ATGP4 (*A. thaliana*)

farnesyl protein transferase subunit B

farnesyl pyrophosphate synthase

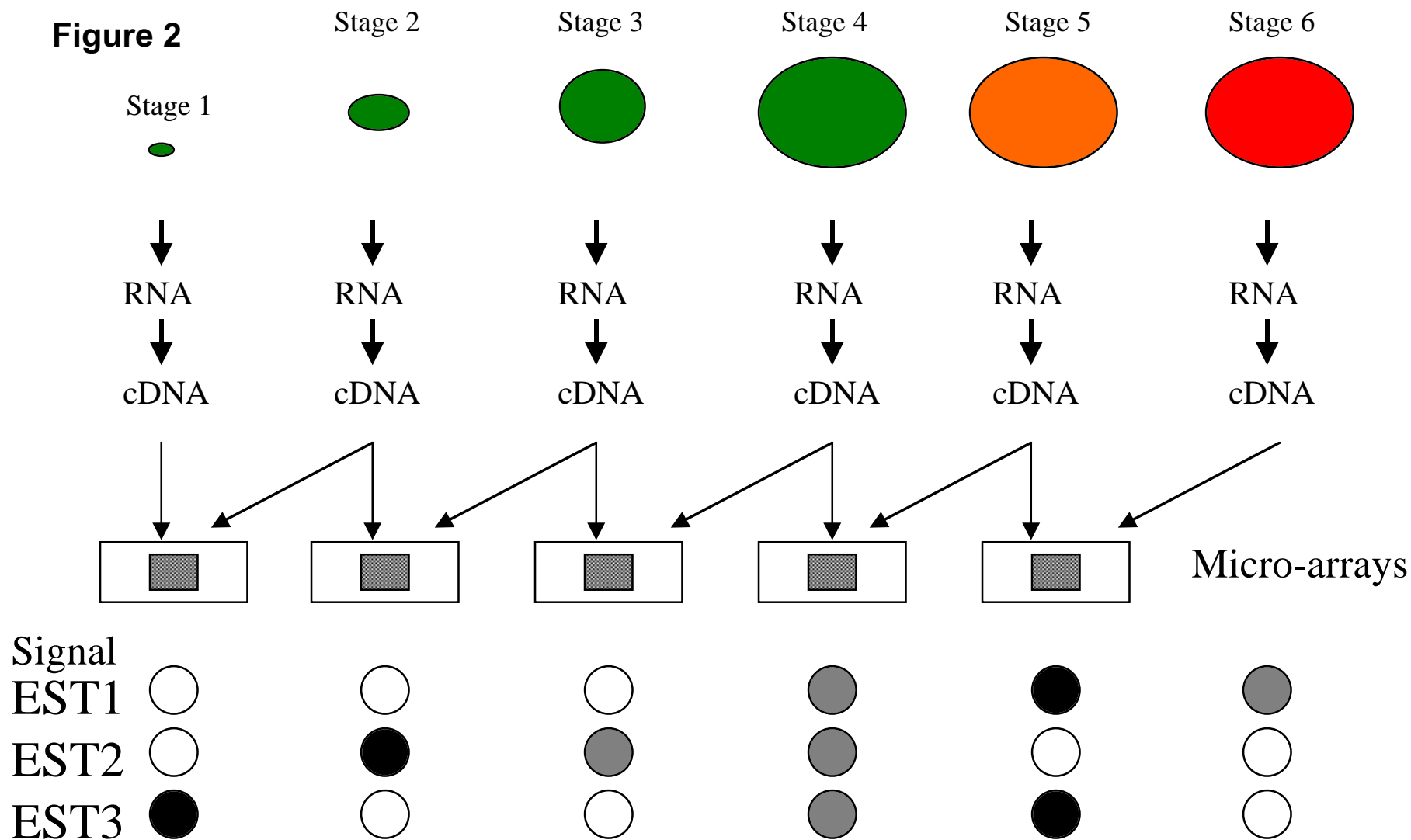
cinnamyl alcohol dehydrogenase isolog

alcohol dehydrogenase (ADH)

**Carotenoid
metabolism**

ADH

Tomato fruit cDNA microarrays. 288 non-redundant tomato ESTs were arrayed on glass slides with a Genetic Microsystems arrayer. All DNAs were arrayed in triplicate (thus 864 spots) and hybridized to fluorescently labeled (Cy3) ripe fruit cDNA from either a “poor” or “good” tasting inbred line developed in the J. Scott breeding program (U of Florida). Microarrays were simultaneously probed with Cy5 labeled ripe fruit cDNA from a control line for comparison to the test lines. Arrays were scanned in a ScanArray 5000 laser scanner and resulting images were superimposed and analyzed with QuantArray software to produce the false color images above. A red signal indicates elevated expression in the “good” or “poor” fruit relative to the control, while green indicates elevated expression in the control. Yellow indicates similar expression in both the control and test probes. **A)** Quadrant of an array hybridized to the “poor” and control fruit probes. Genes up-regulated in the test variety (red) are indicated by arrows, as are two carotenoid biosynthesis genes (5,6) which do not show altered expression but are spotted in this quadrant of the microarray. **B)** Signals of genes of potential interest under this project from the array quadrant in (A) above, in addition to several from the other quadrants of the array (not in A) are shown. It is interesting to note for example that while similar (yellow) ADH levels are found in the “poor” tasting Vs control experiment, reduced (green) ADH in the “good” tasting Vs. control line is indicated. In addition, the “good” line contains higher levels of carotenoids than the control (J. Scott pers. comm.) and demonstrates elevation (red) of several carotenoid biosynthesis genes suggesting a general induction of the carotenoid biosynthesis pathway in this line.



Comparison to more similar tissues is more likely to yield useful results than comparison to a single reference tissue. All samples will be cross-comparable via the resulting linked chain of expression data. A total of 43 stages will be compared for normal fruit in addition to identically aged mutant and heat/cold/C₂H₄ treated tissues.

Figure 3

SUMMARY OF "DEEP" LIBRARY SCREENING

NUMBER PROBE	LIBRARY				
	cLEL (flower)	cLED (carpel)	cLEC (callus)	cLEG (breaker)	TOTAL
NOR	45	506	76	92	719
10A	24	495	154	224	897
RIN	43	388	46	91	568
MC	107	87	70	144	408
COP9	4	68	32	92	196
TCOP11	1	17	5	4	27
TCOP1	2	8	10	4	24
NR	5	6	2	23	36
EIN3	9	6	20	5	40
TCTR1	4	17	6	2	29
DDTFR 8	3	0	0	4	7
TOTAL	247	1598	421	685	2951

Probes:

NOR - tomato *non-ripening (nor)* cDNA

10A - tomato AP2-like EREBP

RIN - tomato *ripening-inhibitor (rin)* cDNA

MC - tomato *macrocalyx (mc)* cDNA

COP9 - *Arabidopsis COP9* cDNA

TCOP11 - tomato *COP11* cDNA

TCOP1 - tomato *COP1* cDNA

NR - tomato ERS-like ethylene receptor cDNA

EIN3 - *Arabidopsis EIN3* cDNA

TCR1 - tomato *CTR1* cDNA

DDTFR8 - tomato steroid receptor-like cDNA

All hybridizations were done at low stringency
(2X SSC, 37C, 0% formamide)

A subset of 1900 clones has been re-arrayed

Figure 4

Library	Tissue	Number of Clones		Filter Grids Available
		Sent to TIGR	Have Available	
cLEC	callus	15,360	55,296	Yes
cLED	< 5 dpa fruit	15,360	98,304	Yes
cLEE	quiescent seed	15,360	15,360	Yes
cLEF	mature green fruit	*15,360	17,664	No
		^7680	7,680	No
cLEG	breaker fruit	**15360	55,236	Yes
cLEI	germinating seeds	15,360	18,048	No
cLEM	6 - 30 dpa fruit	under construction		No
cLEN	red ripe fruit	15,360	17,664	Yes

* Some clones found to have double inserts; not suitable for sequencing.

**Hybridization subtracted for prevelant sequences.

^ Replacement for above.

Figure 5

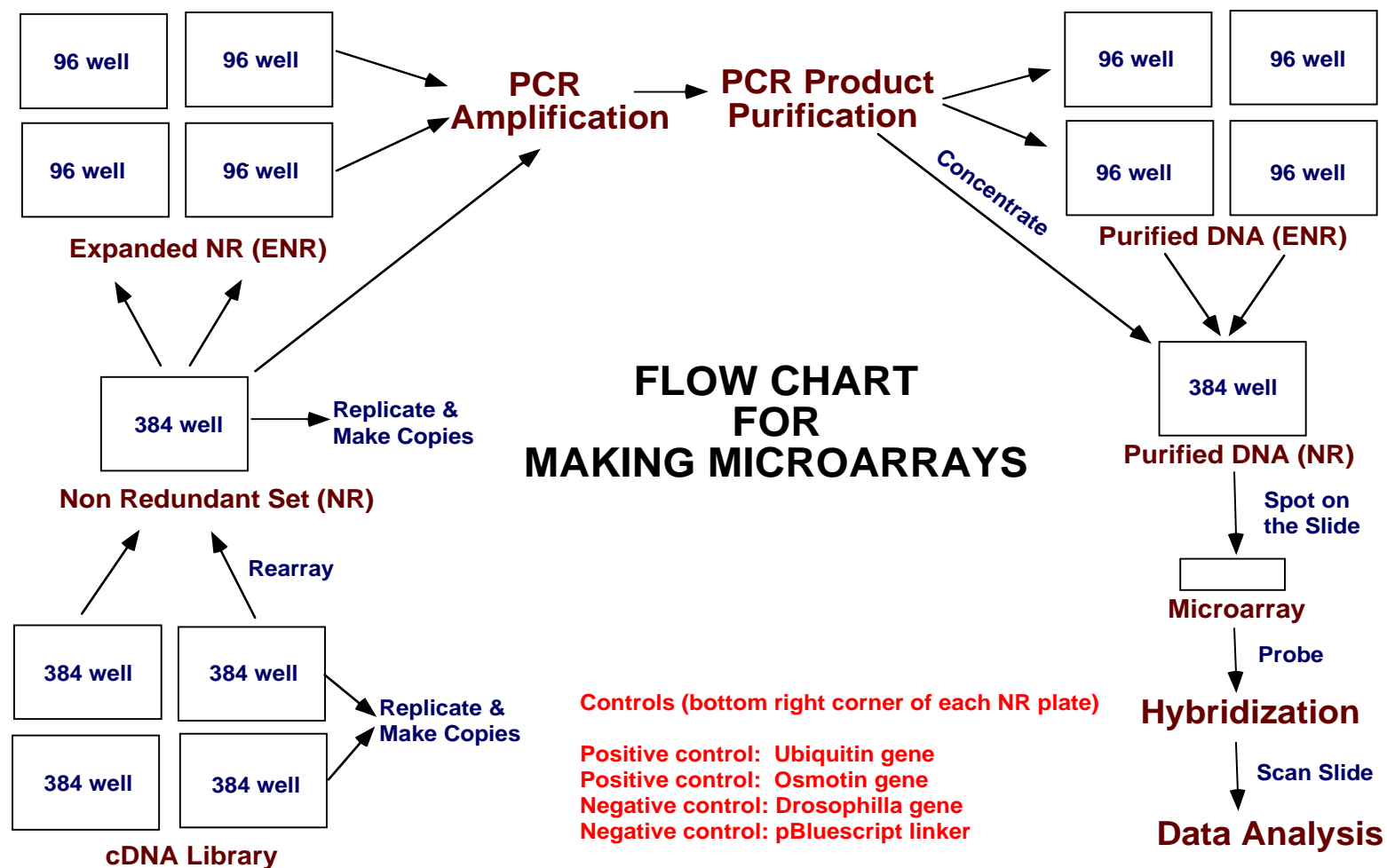


Figure 6

Control spots on amine slide, probed with Cy 3

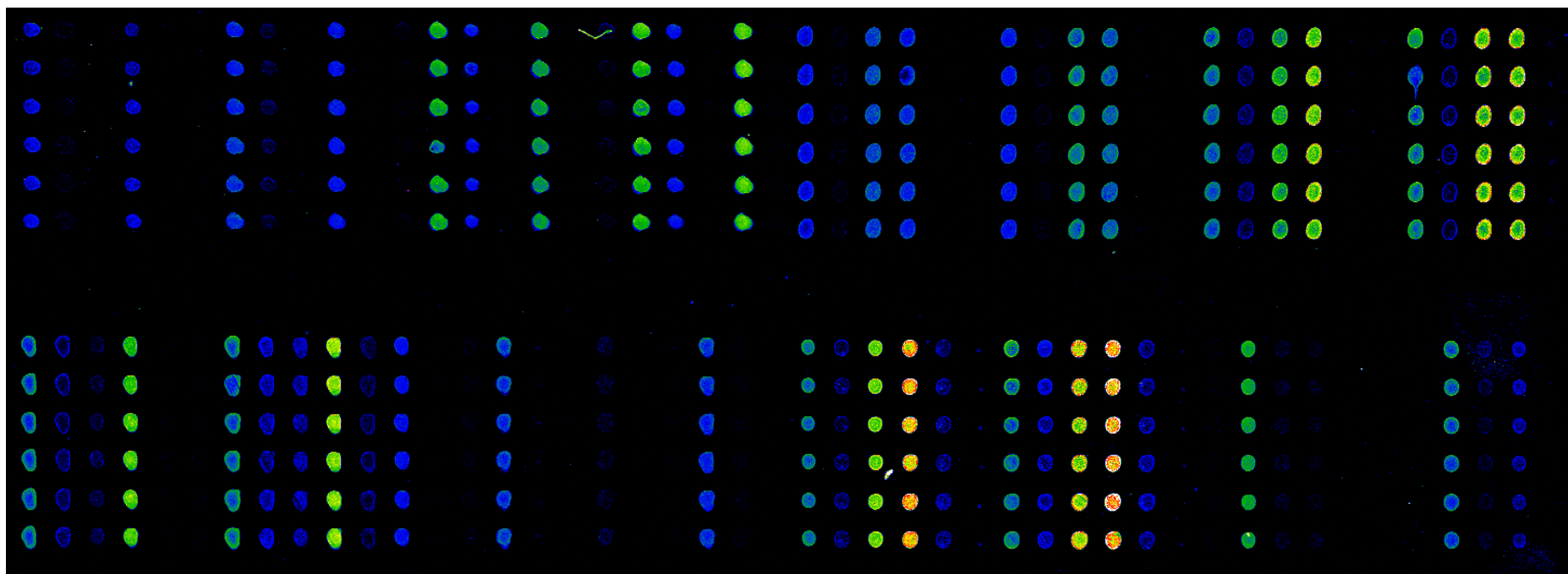


Figure 7

Tomato cDNAs probed with CY3 3DNA Dendrimer Kit

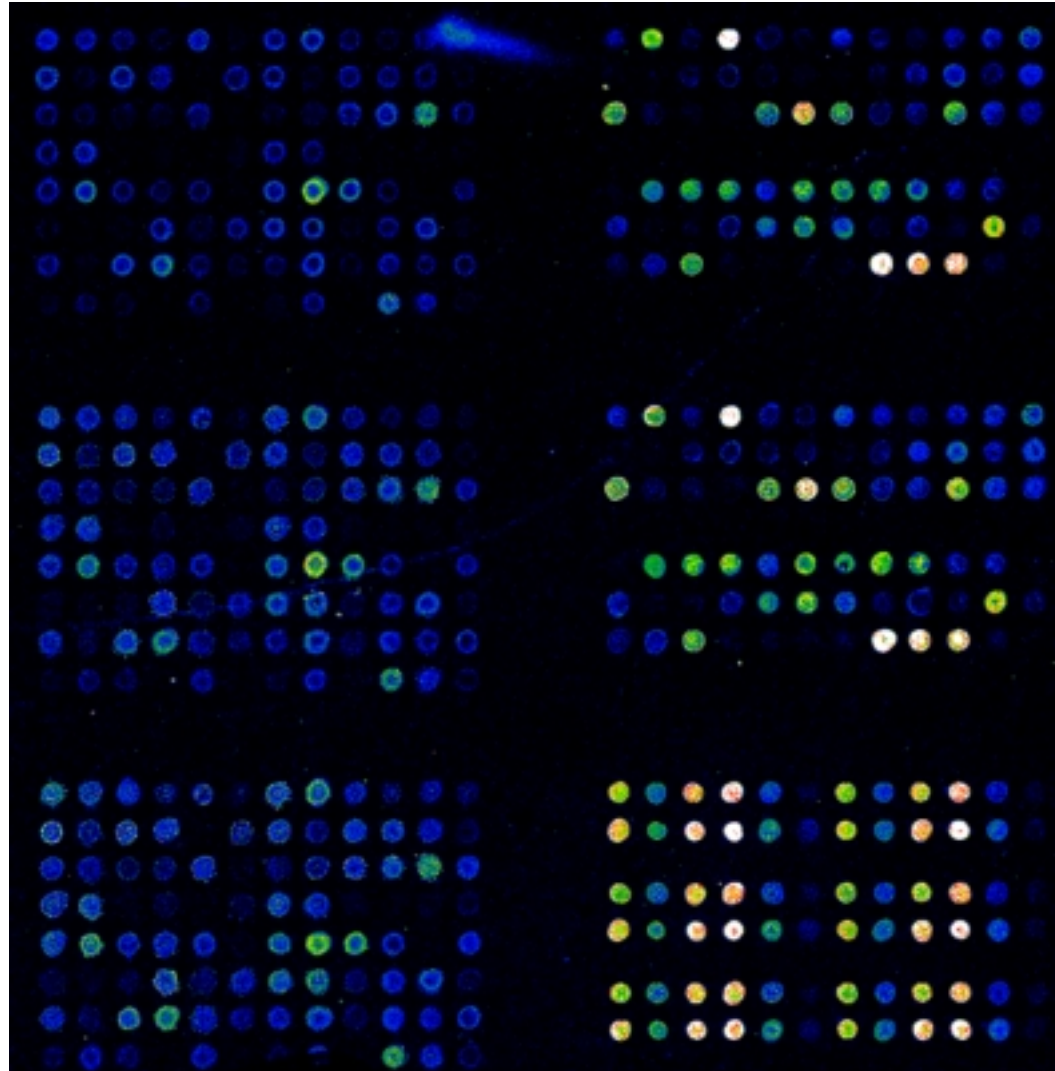
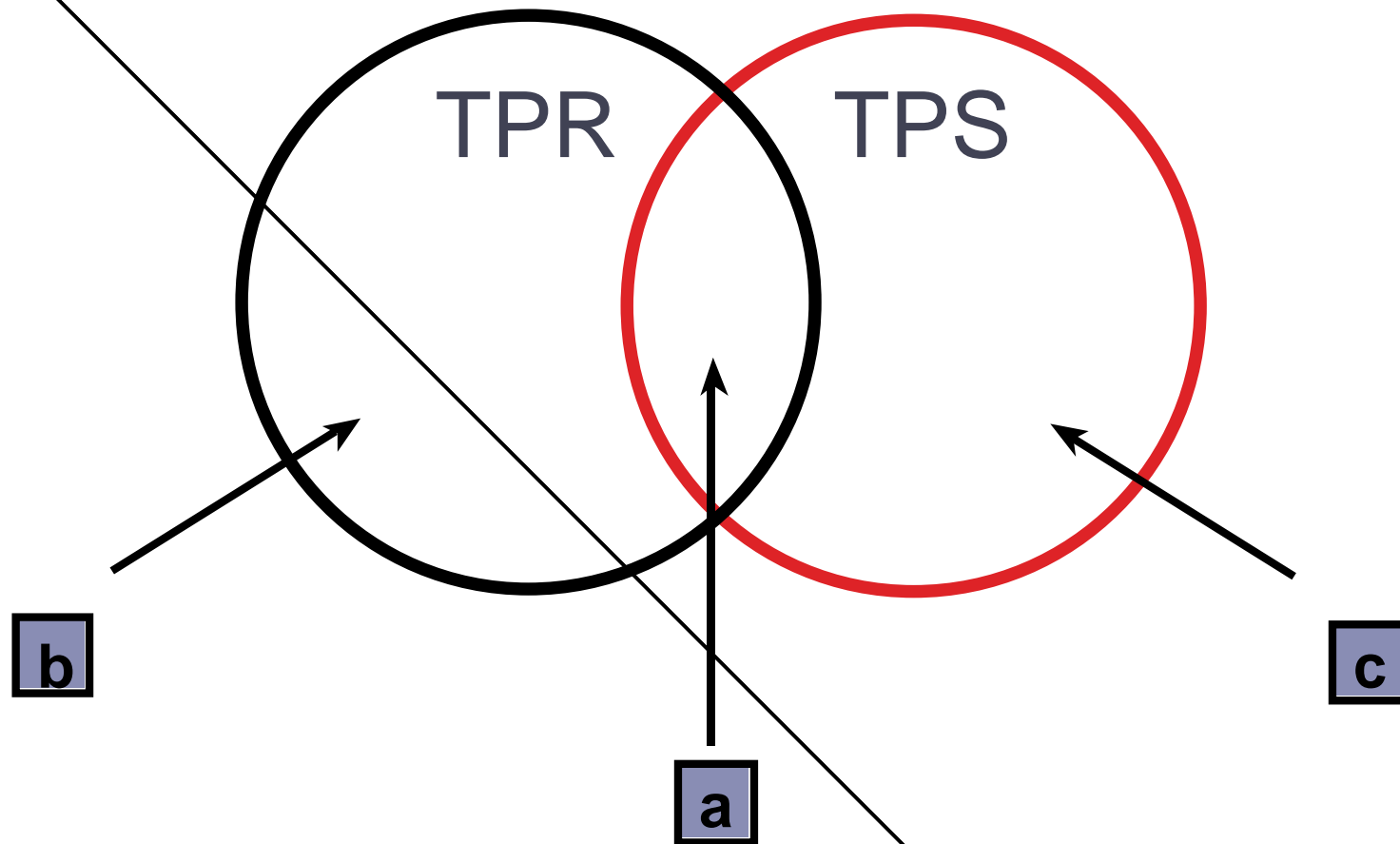


Figure 8

Genes involved in unique and shared pathways



TPR = Pst. resistant
TPS = Pst. susceptible

Figure 9

The flow of tomato ESTs to putative tomato-arabidopsis orthologs.

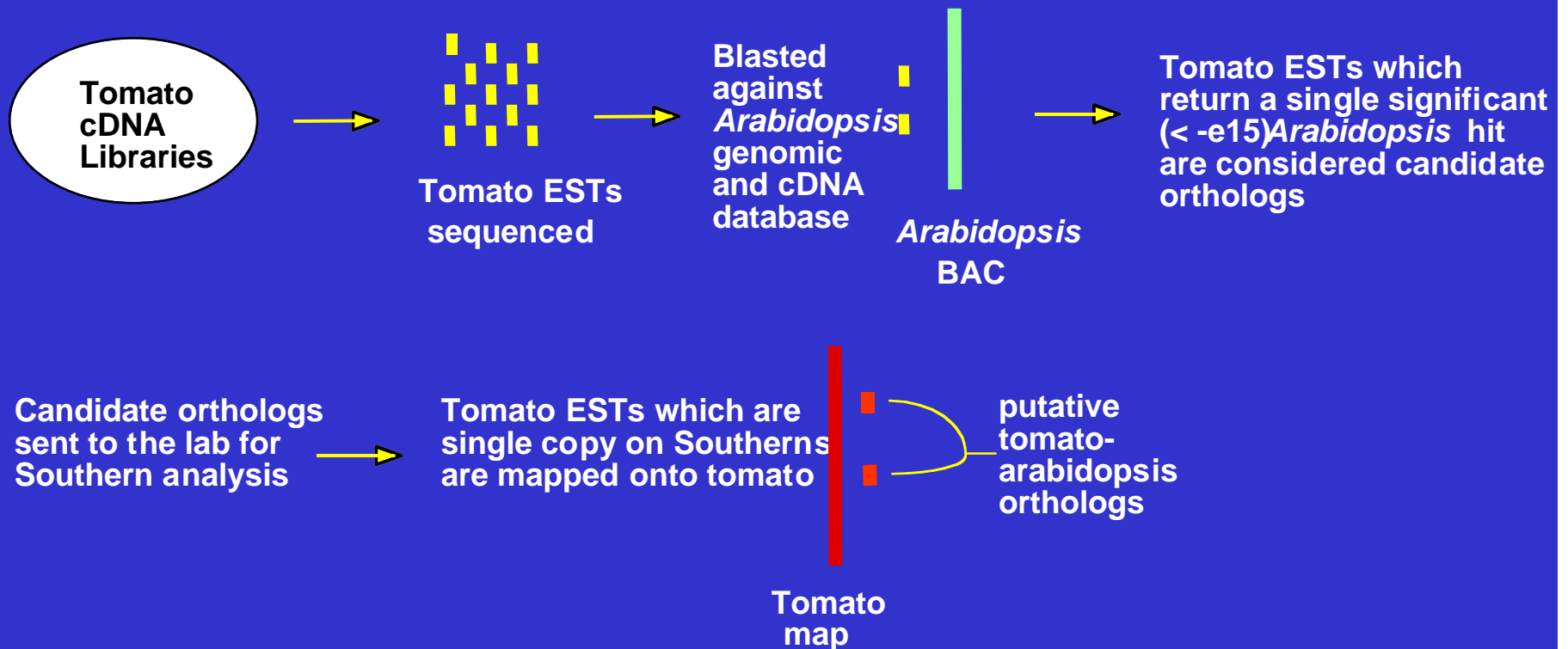


Figure 10

Arabidopsis tiling path

At.ch.bin	Accession	Clone name	GI	Date Added
1.00100	AC007323	T25K16	5729683	28-Oct-99
1.00200	U89959	T7I23	1877523	28-Oct-99
1.00250		F22M8		15-Nov-99
1.00300	AC009525	F22D16	5882752	28-Oct-99
1.00400	AC006550	F10O3	4580745	28-Oct-99
1.00500	AC005278	F15K9	3789706	28-Oct-99
1.00600	AC002560	F21B7	2618677	28-Oct-99
1.00700	AC003027	F21M11	4079614	28-Oct-99
1.00800	AC002411	F20D22	2570223	28-Oct-99
1.00900	AC000104	F19P19	2341023	28-Oct-99
1.01000	AC002376	T1G11	2494110	28-Oct-99
1.01100	AC004809	F13M7	3399678	28-Oct-99
1.01200	AC005322	T7A14	4027862	28-Oct-99
1.01300	AC000098	yUP8H12	2358139	28-Oct-99
1.01400	AC005106	T25N20	3366536	28-Oct-99
1.01500	AC007153	F3F20	4580365	28-Oct-99
1.01600	AC009999	T20M3	5868931	28-Oct-99
1.01700	AC011001	F4H5	6056181	28-Oct-99

Figure 11

Arabidopsis BAC Tiling Path

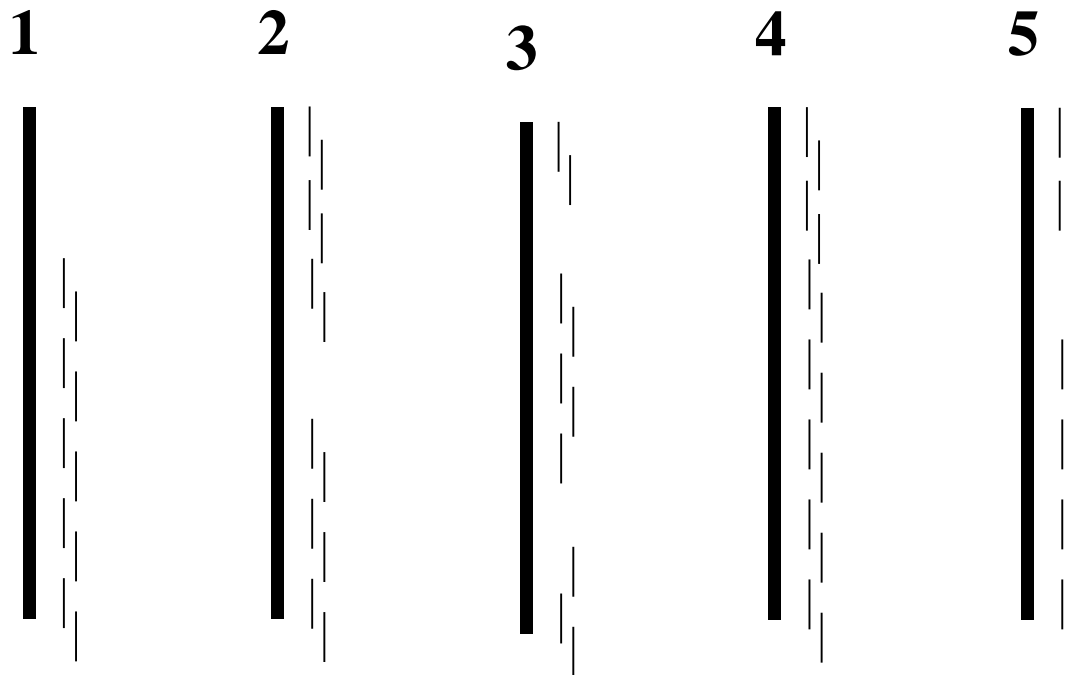


Figure 12

Tomato EST Putative Ortholog List

QUERY	Cornell Clone	Single Match	E-value	exponent	Next E Value	exponent	delta:e-value	Contig/Single
TMEAC59TH	cLET01J21	AL078620	4.00E-21	-20	2.00E-11	-11	-10	
TMEAE58TH	cLET02I19	AC008262	1.00E-21	-21	1.00E-11	-11	-10	
TMEAC95TH	cLET01P21	AL035394	4.00E-16	-15	6.00E-06	-5	-10	
TMEADA06TH	cLET01B12	AB026636	5.00E-20	-19	2.00E-08	-8	-12	8537
TMEAC88TH	cLET01P07	AL109796	5.00E-16	-15	5.00E-04	-3	-12	
TMEAG05TH	cLET02B09	AL050351	6.00E-25	-24	6.00E-13	-12	-12	
TMEAD58TH	cLET01J20	Z97337	3.00E-27	-27	1.00E-14	-14	-13	7475
TMEAG03TH	cLET02B05	AL049523	1.00E-24	-24	1.00E-11	-11	-13	7563
TMEDA40TH	cLET20H07	AL031032	7.00E-15	-14	1.60E-01	-1	-13	
TMEDA64TH	cLET20L07	AC006955	6.00E-15	-14	3.10E-01	-1	-14	

Figure 13

**Synteny exists and can be detected as determined by
mapping end of tomato chromosome 2**

