

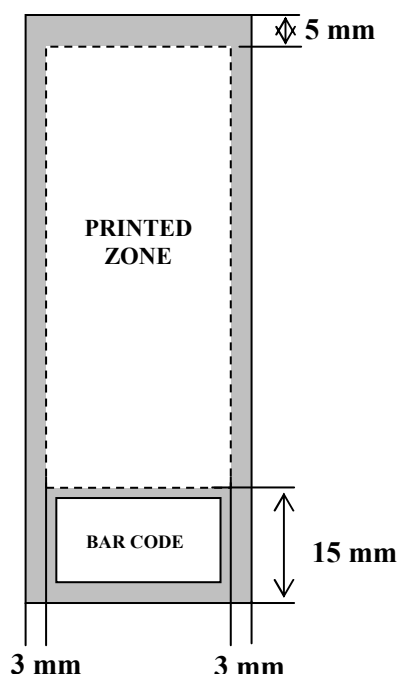
<b>UMR 990- GBF</b> <b>INRA/INP-ENSAT</b> <b>Site INRA</b> <b>Auzeville</b> <b>31326 Castanet</b> <b>Tolosan</b>	<b>REGISTRATION</b>	Réf. : E-MET-001 Version :1 date : 07-06-22 Page : 1 sur 4
	<b>EU_TOM1_12K</b>  <b>TOMATO <math>\mu</math>ARRAY DESCRIPTION</b>	

***Information on the general use of 12K oligonucleotide  
Tomato Microarrays “ EU\_TOM1\_12K ”***

**Design and properties of the 12K tomato oligo microarrays EU\_TOM1\_12K**

Each microarray contains 12,672 spots in 48 grids of 17 rows and 16 columns. The 48 grids were arrayed in a 4x12 pattern of 4 metacolumns and 12 metarows. In each grid, 8 positions are not arrayed leading to 384 positions that do not contain spots across the arrays.

Position of the spotted area is (slide format 25 x 75.6 x 1 mm):



The spots contain 11,890 different 70mer oligonucleotides including positives and negatives control oligos (among with 3 Aliens oligos and one randomly generated negative control). Since controls (see below) are spotted multiple times this gives a total of 12,160 spots containing 70mer oligonucleotides. A total of 512 wells containing no 70mers but only spotting buffer are distributed across the 12 K tomato arrays. These controls are designated “buffer”.

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Usually, spots have a comparable size (around 140  $\mu$ m diameter). In some cases, spots appear to be smaller or larger. This is due to different viscosities of the spotting solutions (oligo concentration, etc.) and/or to different spotting pin properties.

Each spot was dotted once with ~20  $\mu$ M 70mer oligonucleotides in phosphate type buffer containing SDS.

### ***Solanum Lycopersicum* genes represented by EU\_TOM1\_12K microarrays**

Oligonucleotides were designed and synthesized by Operon Biotechnologies

There are 11,860 genes from the tomato represented on the microarray. The majority of the probes were designed from gene sequences gathered from the Lycopersicon Combined Build #3 - - Unigene database at Cornell University.

The remaining number of oligos are designed from sequences in GenBank.

All oligos are modified with a 5' amino group to facilitate oligo attachment.

To describe the contents of the array, we make available a Gal file (EU\_TOM1\_12K.gal). This file contains position and content of the spots in the format required for the image analysis software Genepix Pro 3.x (Molecular Device).

Using the ID-file you can link expression profiles obtained for each spot with the annotation of the corresponding gene.

### **Controls on EU\_TOM1\_12K microarrays**

3 Aliens controls that can serve for estimating the amount of non-specific hybridization on the slides in both the Cy3 and the Cy5 channel. Also the negative controls can be used for this purpose.

opLeV01C0000028	Alien1	Stratagene SpotControl Alien oligo	CCAGCAGTAACTAGAGCACGTCTTCGACCAAACTGGATATTGCAGCCTCGTCGTAGCCTCGCACCTTCA
opLeV01C0000029	Alien2	Stratagene SpotControl Alien oligo	CATATCAAGTGTATGAGGGCAATTCGACCCATACTCAGATTTCCGCCGCTTGGGTGGTATGACCGTA
opLeV01C0000030	Alien3	Stratagene SpotControl Alien oligo	GCGCCTCGTTCGGTGTGGTCGCGTCTTGTATATCATGGACTACAAGTCTGTGCGGTCTGGGTGCGTGT

### **Others controls**

#### *Positive controls*

Oligo ID	Gene ID	description	Oligo sequence
opLeV01C0000001	sgn U214005	ethylene-response protein 1-aminocyclopropane-1-carboxylate synthase	TGTCCATATTATAAAGGCTTCTACAAGACATCCTCTGTTTACCTTGCCTTACTCGTATGTTGCTTTGTAC
opLeV01C0000002	sgn U220379	ripening protein E8	AGGGGTTTATTGTTGGATGGATTTCGGGTCAATGTTGAAAGAAGCAACTAGATGCTGAGATGTCACCTT
opLeV01C0000003	sgn U212804	phytoene synthase	CAATTATTTGACTTACGAAATCACTCTTCACTATTGTCATTACAGGTTTCGACAGCTACGGTAAACAGGGA
opLeV01C0000004	sgn U212843	polygalacturonase	CCGGCAGCCTTAGATAGGTGGGAAAATAGGCTAGAAGATGTTTTCAATGGGCGGCCATTTGACATGCTCG
opLeV01C0000005	sgn U213213		GTCCATTTTAAACAATGCTGAACATGTTACACCACACTGCACTTCACTAGAAAATTTGAGAGGATGAAGCTC

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opLeV01C0000006	sgn U212614	MADS-box transcription factor MADS-RIN	GGTGTTACCTTTCAAACATCATGGCATTGTGGTGAGCAAAGTGTACAATATAGACATGAACAGCCTTCTC
opLeV01C0000007	sgn U215711	expansin 1 protein LeExp1	TGCCATATGTTTCTCAAACCTGTGCTCAGTACCGCGCTGGCATTGTTCTCTGTAACCTATCGCAGGATCCCATG
opLeV01C0000008	sgn U221920	lycopene beta cyclase	GCTGCGGCTCCTGTTGTTGCCAATGCCATAATCAATACCTCGGTTCTGAAAGAAAGTCATTGCGGTAATG
opLeV01C0000014	sgn U223021	hypothetical chloroplast protein RF19	GCCCTTAGGAATCAGTCTACAACAGGAGGATTGAATACCCCTTCCACCGTGGTTGCTGCTGGAATGGCGA
opLeV01C0000015	sgn U216071	embryo abundance protein (EMB20)	ACGTCATTGTTCCCTTCCCATCCAAAAGCTTAAACGTAACACACTTTTCGTAGACGTATTATCAGTCAA
opLeV01C0000016	sgn U213363	auxin-inducible protease inhibitor	TGTGATGGAGAATCTGAATGGGTAAAGCGAGAAGGATAATAATCTCGAGAAGGATTGCACAAAAGAATGTG
opLeV01C0000017	sgn U212891	ubiquitin-conjugating enzyme	GGGGCGGGCCCCCTTCCCTTAAAGGGGGGGTTTTAAATTTTCGGGGG
opLeV01C0000018	sgn U223909	unknown protein [Arabidopsis thaliana]	TAGCACTGTGGATGATGCCATTGCTCACTTGGCTATTTAGATAGTTTCCACCGGATAGGCATCCCGAG
opLeV01C0000019	sgn U215360	putative similar to protein phosphatase	ATGGGCTTTGGAATGTCTCTCTAACGAGGAGGCGGTGACCATTGTGAGGACATAAAAGATGCTGAGGC
opLeV01C0000020	sgn U213502	eukaryotic translation initiation factor	GCTGATCTCCTTTGAGGTGGTTTTGGCTCTGTGAGGGGAATTGTTCTTCCCTACAAGTAGTAGTCTAA
opLeV01C0000021	sgn U215980	putative RNA helicase	CGGTTATGGTGACCAATGGTGAGTCTTTTGTACAGAAATCTCATGTTGAAGTTGTGCGATGCCTGTGAT

### Negative controls

Oligo ID	Gene ID	description	Oligo sequence
opLeV01C0000009	AF126021	Homo sapiens	CCTAGCATGTACCAGCGCCTAGGGCTGGACTACGAGGAACGAGTGTGCCGTCCATTGTCAACGAGGTGC
opLeV01C0000010	BC011786	Homo sapiens	GCCTGCCGCTCCGGTCCACCTTGCGGCCCGTGTGTTGACTCAACTCAGCTCCTTAAACGTAATATTTCCG
opLeV01C0000011	NM_004048	Homo sapiens beta-2-microglobulin	CTCACTGAATTCACCCCACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAG
opLeV01C0000012	U11861	Human G10 homolog	TGCCTGCGGTGCATTGACACACGGGACCAACTTCGGGACGAACTGCATCTGCCGCGTCCCAAAAGCA
opLeV01C0000013	NM_000518	Homo sapiens hemoglobin	TGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGTGCTCGGTGCCTTTAGTGATGGCCTGGCT
opLeV01C0000022	X52327	pBluescript II KS(+) vector DNA	CGTTGATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC
opLeV01C0000023	S69414	uidA=beta-glucuronidase Escherichia coli	GATGTGGAGTATTGCCAACGAACCGGATACCCGTCGCAAGGTGCACGGGAATATTTGCGGCCACTGGCG
opLeV01C0000024	X84848	P. pyralis luc gene	TGTGGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAGGACCTATG
opLeV01C0000025	V01499	E. coli gene aph(4)	TGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGATTGGTCTTGACCAACTCTATCAGAGCTTGGTT
opLeV01C0000026	X57709	E.coli Transposon Tn5 DNA	TGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT
opLeV01C0000027	rand6	Randomly generated negative control oligo	CAACGTTCCGCGTTCGCTAGTGATCCGATGAACACCTTAACTGATACCTTGTGGGATACAAAAATCGT

## Quality control of EU\_TOM1\_12K microarrays

Microarrays were visually inspected for irregular grid patterns.

One slide per printing series was tested by hybridization to Alexa Fluor 555-labeled random nonamers to verify the printing (spot morphology).

Usually, more than 99.5% of all oligonucleotide-containing spots were efficiently transferred to each EU\_TOM1\_12K array.

## Packaging and Handling

Spotted oligonucleotides arrays were immobilized by humid treatment afterward they were stored in plastic box in a dessicator at 18-20 °C, protected from light.

Arrays are packaged in plastic boxes labeled with internal numbers from the print run. These numbers are not identical to the bar code numbers on the slides that can be used by users for identifying slides during hybridizations.

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Please keep track in your experiments, which microarrays you are using. Preferentially use only slides from the same series (and, if possible, with the nearest possible numbers for experiments you intend to compare).

What you see after unpackaging is the dried spotting solution, this disappears during slide processing.

Take care of the slides: wear gloves (without powder), do not scratch them and keep slides in the plastic box in a dessicator at 18-20°C. After taking out in dividual slides, immediately re-place in the dessicator. Individual Nexterion Slide E microarrays are labeled with a barcode at the bottom. In this case, the DNA faces up if the number can be read.

Only touch the slides at the area covering the bar code Number or at the top edges of the slide since the spotted area cover almost all the surface area.

The arrays can be hybridized under a 20X60mm coverslip or in automatic hybridization stations (Lucidea – Amersham or Ventana Discovery- Ventana Medical Systems, Inc).

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