

MEEBOChip v1.0 Feature Set

Gene Core Features

“Constitutive”
Exonic/Genic Probes

Alternatively Spliced/Skipped
Exonic Probes

Non-Coding RNA Probes

BCR/TCR
Genic/Regional Probes

Mitochondrial Probes

Control Core Features

Doped Control Probes

Positive Control Probes

Negative Control Probes

Transgenic/Cassette Probes

Murine Viral Probes

**MEEBOChip
Feature Set
v1.0**

Gene Core Features

**“Constitutive”
Exonic/Genic Probes**

**24481 Candidate Loci
NCBI LocusLink
[June 2004]**

Selected User Supplements

**70mers selection using
MouSDB3 Exonic Annotations:
mRNA & EST-Based
[Rockefeller /Basel/UCSF]**

**70mers selection using
UCSF Exonic Annotations:
Primarily mRNA-Based
[NCBI LocusLink/UCSC GoldenPath/UCSF]**

**70mers selection using
Candidate mRNAs:
Entirely mRNA-Based
[NCBI LocusLink/RefSeq]**

Gene Core Features

**“Constitutive”
Exonic/Genic Probes**

→ One probe that will recognize all known transcripts derived from a single gene (30111 probes)

**Alternatively Spliced/Skipped
Exonic Probes**

→ Probes that will recognize exons that are present in some but not all transcripts derived from a gene (4201)

Non-Coding RNA Probes

→ Probes recognizing non-protein coding transcripts (ribosomal RNAs, miRNAs) (196)

**BCR/TCR
Genic/Regional Probes**

→ Probes recognizing transcripts from genes that undergo somatic rearrangement (372)

Mitochondrial Probes

→ Probes recognizing mouse mitochondrion-derived DNA sequences (13)

34893 total probes

Control Core Features

3072 total probes

Doped Control Probes



Probes recognizing non-mouse sequences that can be spiked into RNA samples

Positive Control Probes



Probes recognizing a small subset of mouse transcripts (used for “landing lights,” normalization, etc.)

Negative Control Probes



Probes designed for use in determining background

Transgenic/Cassette Probes



Probes recognizing elements commonly used for transgenic constructs

Murine Viral Probes



Probes recognizing mouse viral pathogen sequences

Include some tiling controls (to assess effects of distance from 3' end), mismatch controls (to help tune hybridization conditions)

MEEBOChip Array Modules

The feature set is segregated into 3 modules with sub-modules to allow users flexibility in array layout. These comprise:

- I. MEEBOChip Core Collection (MCC):** This is the main backbone of the array and covers ~ 25k genes, including their splice variants.
- II. Positive controls (PC):** these include genes expressed at a range of abundances, and very robust for normalization, PMT adjustment, bright gridding aids serving as "landing lights" strategically placed at the top of each sector, etc.
- III. Doped Controls (DC):** This is the largest collection of 70mers to detect doped/spiked species that are either commercially available now or will soon be readily available.

MEEBOChip Core Collection (MCC) Module

This is the main backbone of the array (**35712 features**) covering over 24685 genes and includes:

1. Rockefeller MouSDB3 constitutive exons/islands (oligo names start with 'scl' followed by a number >0) (**scl: 17886 features**)
2. locuslink2ucsc constitutive exons/islands (oligo names start with 'scl0' followed by a number >0) (**scl0: 7072 features**)
3. mRNA derived 70mers which may span intron/exon boundaries (oligo names start with 'scl00' followed by a number >0) (**scl00: 4982 features in MCC; scl00: 171 features in PC module**)
4. an unprecedented cohort of alternative spliced/skipped exons collected through extensive curation of 5 published datasets by Max Diehn, Ash Alizadeh, Jean Yang, and Catherine Foo (oligo names start with 'scl000' followed by a number >0) (**scl000: 4201 features**)
5. syntenic orthologs of human loci exhibiting cis-antisense transcription based on Yelin et al Nat Biotech 2003. (oligo names start with 'scl0000' followed by a number >0) (**scl0000: 92 features/scl0000r: 92 features**)
6. microRNA Tagged Templates (**miRNA-TT: 184 features**)
7. Vectors/Transgenes/Cassettes (eg, GFP, YFP, beta-Gal, etc) (**VectorTransgenes: 37 features**)
8. mitochondrial genes (**mtDNA: 13 features**)
9. BCR and TCR genes (**BCR_TCR: 372 features**)
10. select murine viruses from the ViroChip (**Virus: 358 features**)
11. rRNA genes (**rRNA: 12 features**)
12. Integrated interspersed negative controls (**Empty Wells: 318 features, Random Sequences: 93 features**)

Positive Control (PC) Module

These features (1152) include genes expressed at a range of abundances, and very robust for normalization, PMT adjustment, bright gridding aids serving as "landing lights" strategically placed at the top of each sector, etc. These include:

1. Tiled mouse genes (n=11, an improved set with a range of sizes and expression levels within "Universal Reference" RNAs from Stratagene) (Tiling: 248, Tiling (terminal)/PMT Adjustment: 33)
2. Normalization mouse genes (n=10 genes, 20 copies of each, based on Vandesompele J et al. 2002 Genome Biol. 3(7):R34) (Normalization: 153, Normalization/PMT Adjustment: 47)
3. Distributed and anchored mismatch controls for 5 mouse genes selected in #2 above (Mismatch Controls; WildType: 15, Mismatch Controls; Distributed: 120, Mismatch Controls; Anchored: 135)
4. Ubiquitin C as a corner placed PMT aid, assuming that sector widths are 28 or 29 spots (Gridding Aid/Corner Marker: 192)
5. Others (Antisense Negative Controls: 38, scl00: 171)

Doped Control (DC) Module

This is the largest collection of 70mers (**1920 features**) to detect doped/spiked species that are either commercially available now or will soon be readily available.

These include:

- MJDC from Stanford (192 species)
 - **MJDC: 931**
 - **MJDC antisense: 192**
- Affymetrix spikes (4 species)
 - **Affymetrix doping sense: 36**
 - **Affymetrix doping antisense: 9**
- Stratagene spikes (10 species)
 - **Stratagene Arabidopsis doping sense: 40**
 - **Stratagene Arabidopsis doping antisense: 10**
- Ambion spikes (8 species)
 - **Ambion doping sense: 40**
 - **Ambion doping antisense: 8**
 - **Ambion doping (picked by Ambion) sense: 40**
 - **Ambion doping (picked by Ambion) antisense: 8**
 - **Ambion DC replication: 272**
- B. subtilis spikes (5 species)
 - **B. subtilis doping sense: 25**
 - **B. subtilis doping antisense: 5**
- Anchored and distributed mismatched versions of 5 genes (4 MJDC, 1 Ambion) with replication
 - **Mismatch Controls; WildType: 15**
 - **Mismatch Controls; Anchored: 135**
 - **Mismatch Controls; Distributed: 120**
- tiled MJDC (4 genes) and Ambion (1 gene) and Affymetrix (4 genes)
 - **DC Tiling: 30**
- antisense versions of all spikes
- others
 - **Random Sequence: 4**