

The YBOX Set Version 1.0

Introduction

The YBOX set (Yeast Brown Lab Oligo Extension) v1.0 was designed by the P. Brown lab at Stanford and synthesized by Operon. Designed to extend and improve the performance of the Operon Yeast Genome Array-Ready Oligo Set (AROS) v1.1 (<http://www.operon.com/>), the YBOX set contains 3072 70mer oligo probes that were designed with a target GC-content identical to the AROS set to ensure compatibility while also minimizing cross-hybridization and secondary structure. YBOX enhances the capabilities of the AROS v1.1 set by enabling analysis of the expression patterns of multiple features of the yeast genome in addition to ORFs, and includes an extensive set of positive and negative control sequences to allow for quantitative assessment of array hybridization quality and data normalization. Sequence design for the YBOX set was based on the genomic annotation from the Saccharomyces Genome Database (<http://www.yeastgenome.org>) as of July, 2005, and utilized the ArrayOligoSelector program (<http://arrayoligosel.sourceforge.net/>) with a preferred cross-hybridization threshold of -35 kcal/mol. Included in the YBOX set are probes for the following extended features:

- All non-coding RNAs (tRNAs, snoRNAs, rRNAs, etc) (162)
- Recently characterized ORFs not present in AROS v1.1 (133)
- Improved probes for ORFs with low sequence uniqueness (266)
- All yeast introns >40bp plus splice-junction probes to distinguish spliced and unspliced transcripts (390)
- Gene-tiling probes spanning full-length transcripts to detect location-specific biases in labeling techniques (317)
- Tag/Marker elements common in transgenic constructs (22)
- Centromeric, Telomeric, ARS, and Intergenic Elements (369)
- 2-Micron Plasmid Genes (4)
- Regions <100bp downstream of known poly-A sites to facilitate studies of RNA processing (120)

Control Sequences

An extensive set of probes for non-yeast control sequences are included multiple times to enable detailed evaluation of the sensitivity and specificity of array performance and data normalization. Control sequence probes were designed in conjunction with the MEEBO Array (<http://alizadehlab.stanford.edu/>) and clones for producing Doping RNAs by in vitro transcription will be made publicly available via the Stanford Functional Genomics Facility and/or the ATCC.

- 64 Doping control probes for sequences that can be spiked into RNA samples at known concentrations to measure array signal accuracy, precision, and sensitivity (512)
- 380 Mismatch control probes that represent imperfect matches to multiple doping control sequences with varying degrees and arrangements of mutations to detect array signal specificity (760)
- 20 Negative control probes that are reverse complements of doping control sequences (20)

Annotation Resources

Complete annotation files including full descriptions of all probe sequences are available through www.operon.com.

| Catalog # | Description |
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| 810112 | YBOX (Yeast Brown lab Oligo array eXtras, 300 pmol |
| 810197 | YBOX control set, 300 pmol |