

RNA Standard Characteristics

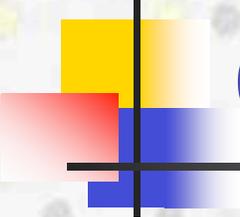
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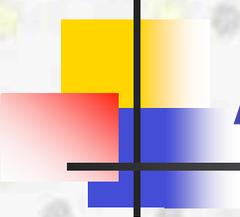
Roche Molecular Systems

ERCC Workshop, Dec. 2, 2003



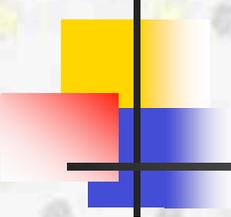
General Characteristics

- Standards compatible with
 - Major microarray platforms
 - Major quantitative PCR platforms
- Composition & availability
 - ~100 different clones
 - Available forms
 - Prequantitated individual RNA's
 - Prequantitated pools



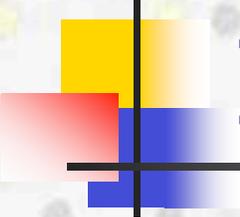
Anticipated uses

- QC of sample collection step
 - Spike-in before or during RNA isolation
- QC of sample labeling step (arrays)
 - Spike-in after RNA isolation, before labeling
- Platform characterization & comparison
- Platform optimization



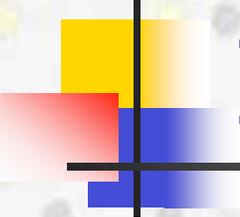
Physical details

- 0.7-2.0 kb in length
- polyA tails (various known lengths)
- Sequence sources
 - *Bacillus subtilis* (Gram-positive prokaryote)
 - *Arabidopsis thaliana* (eukaryotic plant)
 - “Alien” sequences
 - Synthetic (non-natural)
 - Reasonably complex base composition
 - Low BLAST hit frequencies to sequenced genomes



Informatics details

- Publicly available
 - Sequences
 - Production information
 - Vectors & promoters (clone-based)
 - Primers (PCR-based)
 - Compositions
 - Single-clone formulations
 - Pooled clone formulations
 - Probes & primers for quantitative PCR



Initial offering

- 40-50 clones
 - Representatives from all 3 sequence sources
 - Characterized on major platforms
- At least 3 formulations
 - Pairs of formulations suitable for differential quantitation
- Associated infrastructure (protocols, buffers, etc.)