OligoPicker – an Open Source Program to Design Probes for Oligo Array

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Microarray Type

cDNA Array	Oligonucleotide Array
Stanford University, Incyte, RIKEN, etc.	Affymetrix, Operon, MGH, etc.

Issues With Existing Oligo Probe Selection Programs

- Most programs use Blast score to avoid cross-hybridization
- Performance is slow
- No test on the algorithms

Oligo Probe Design Criteria

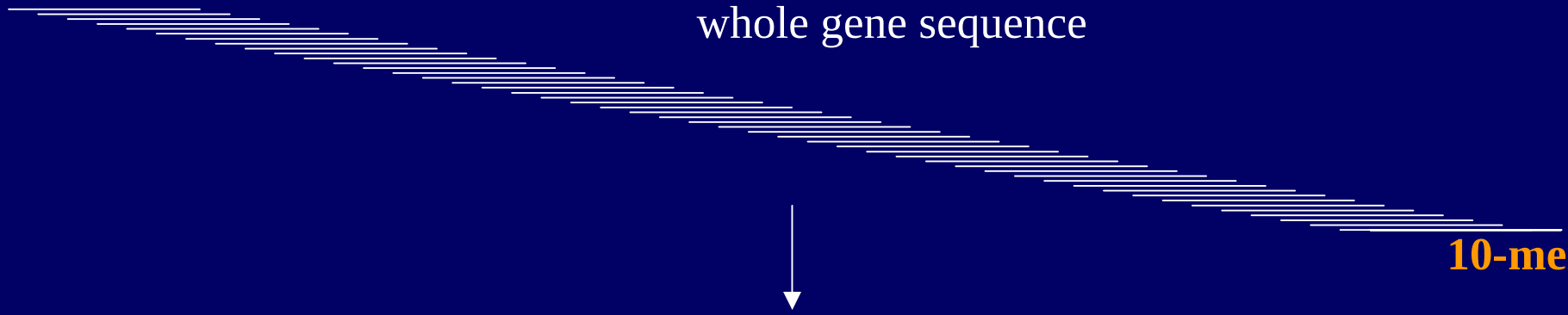
- Oligo Tm is in 10°C range (±5°C to the median Tm) .
- Oligo does not have low-complexity region.
- Either 5’ or 3’ end preference according to user’s instruction.
- Oligo does not self-anneal to the cognate cDNA
  (at most 9 perfect matches to the cDNA complement).
- Comparing to all other sequences:
  - Every 15-mer in the oligo is unique.
  - Oligo blast score < 30

Identify Repetitive 15-mers in Probe Candidates (I)

Store all existing 10-mers among all sequences in the data set

GTCATTGATGAAGCGCATTGTGTGGTCAGTGGGGTC.....ATGATTTTCGTCAAGATTACAAAACCTTATGACTCGGGGATA

whole gene sequence

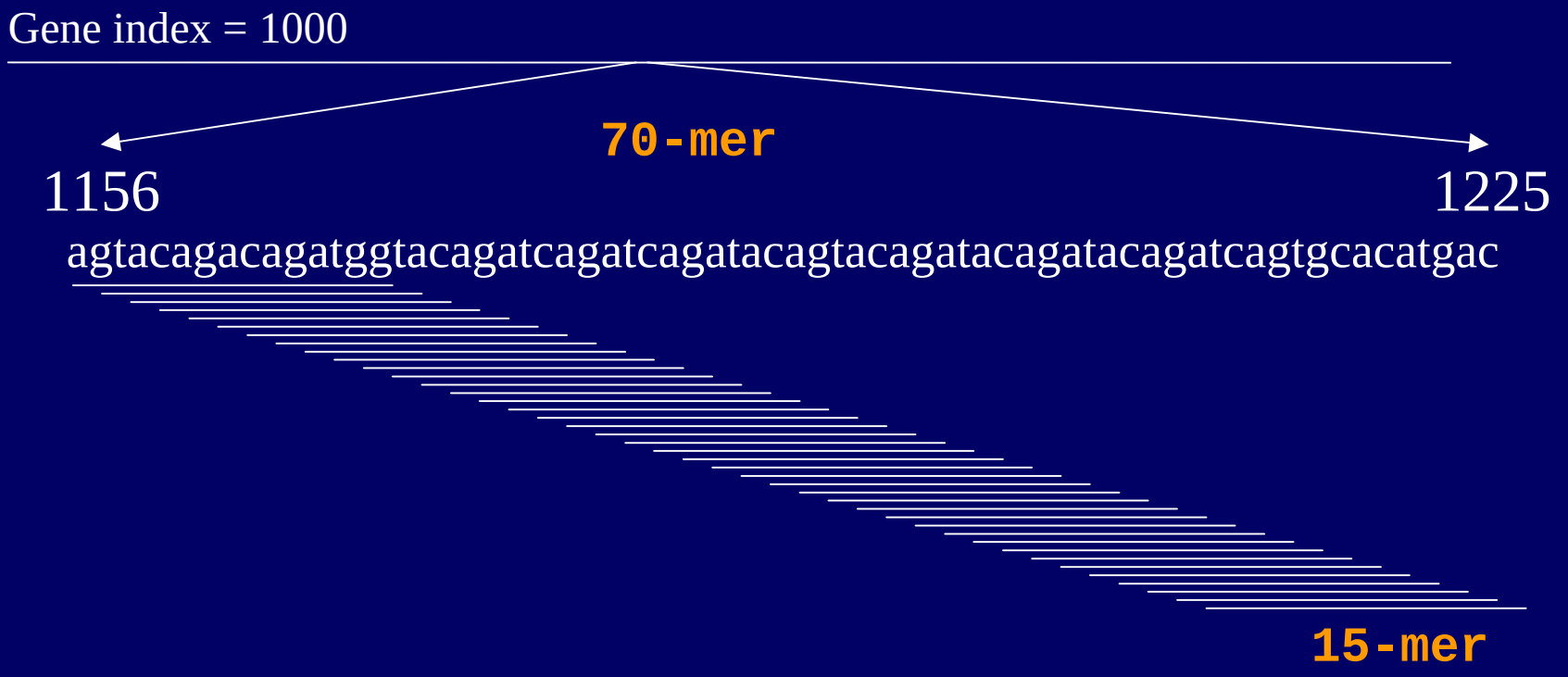


10-mer

gtaccagtgc (index1, position1), (index2, position2), (index3, position3)

…..

Identify Repetitive 15-mers in Probe Candidates (II)




```
tgtacagacagatgg (15-mer)
tgtacagaca         1000, 1156, 4599, 890, 8999, 1900
     agacagatgg    67, 899, 1000, 1161, 4599, 895
```

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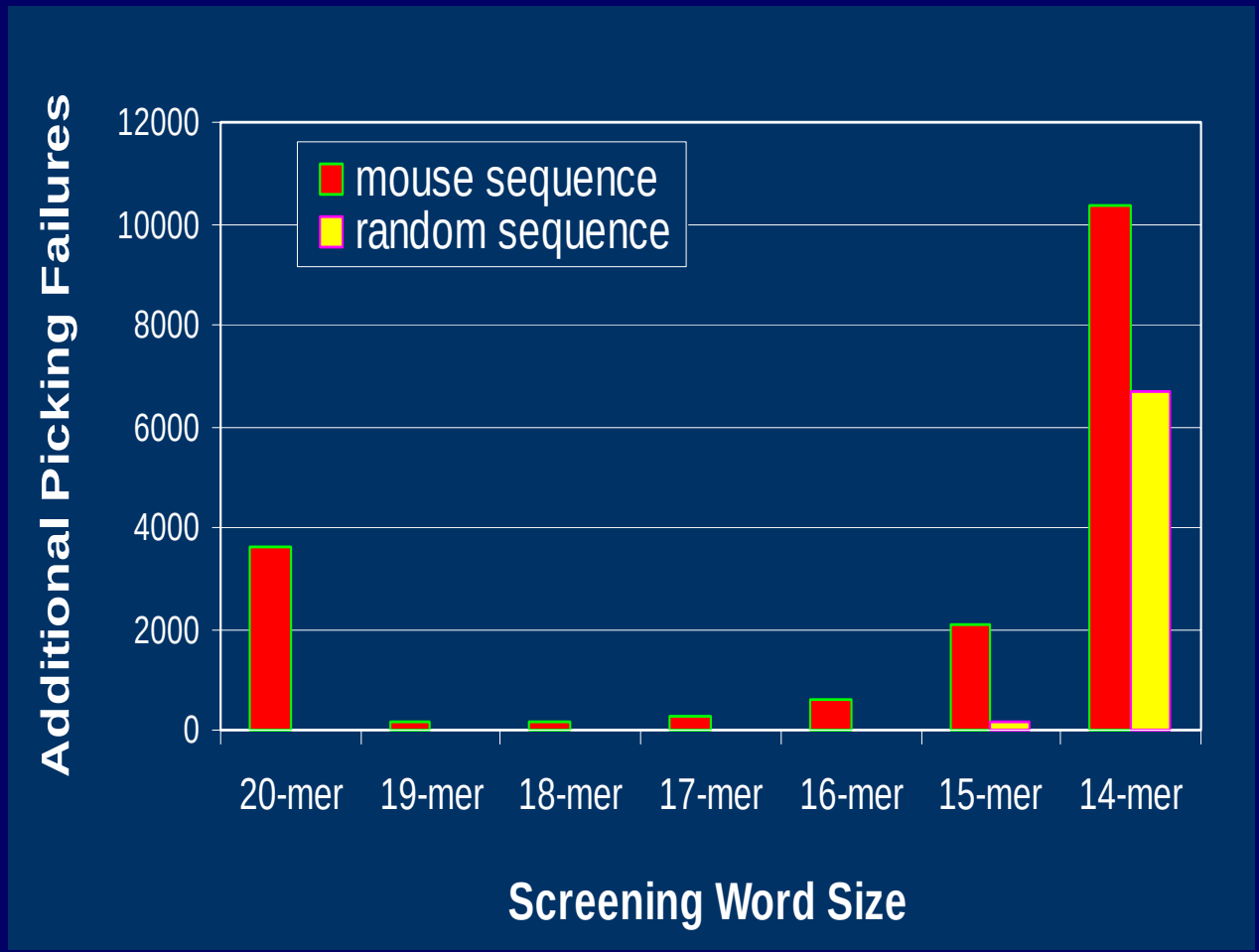
Impact of Contiguous Matches on Probe Selection



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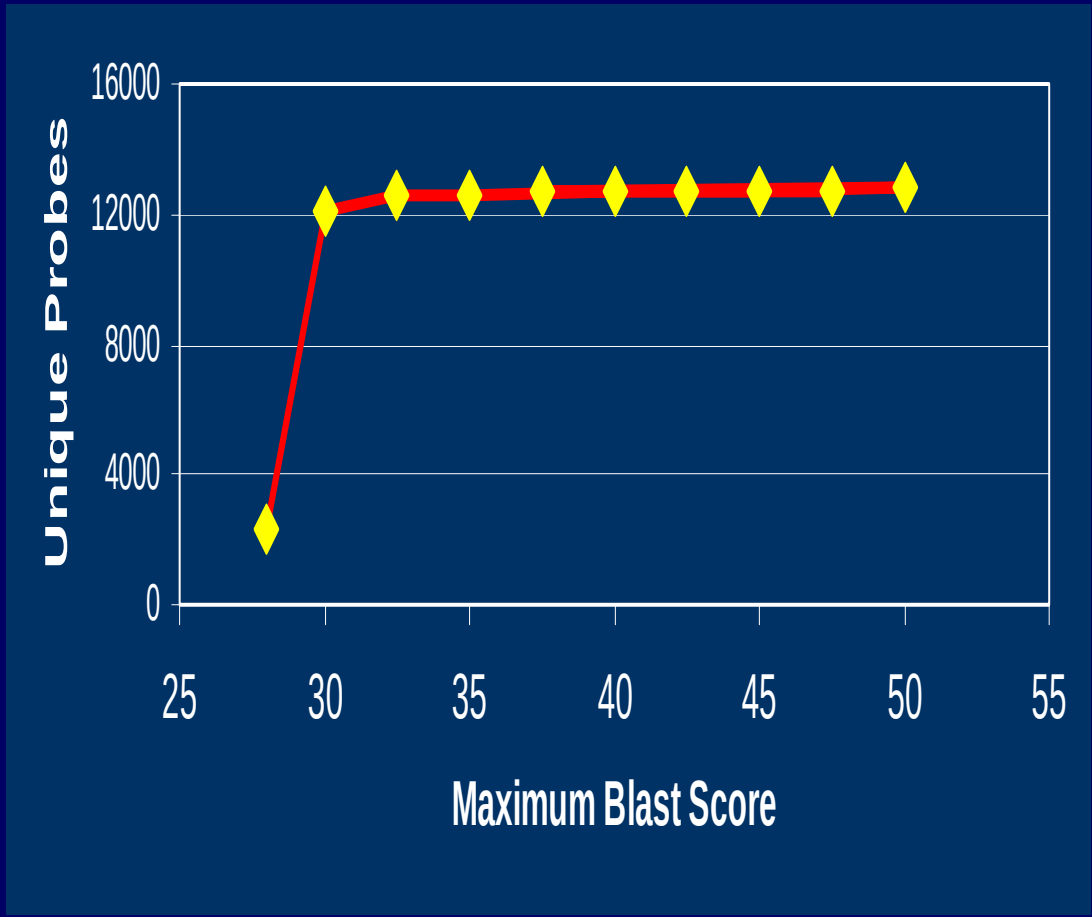
Impact of Blast Score Filter



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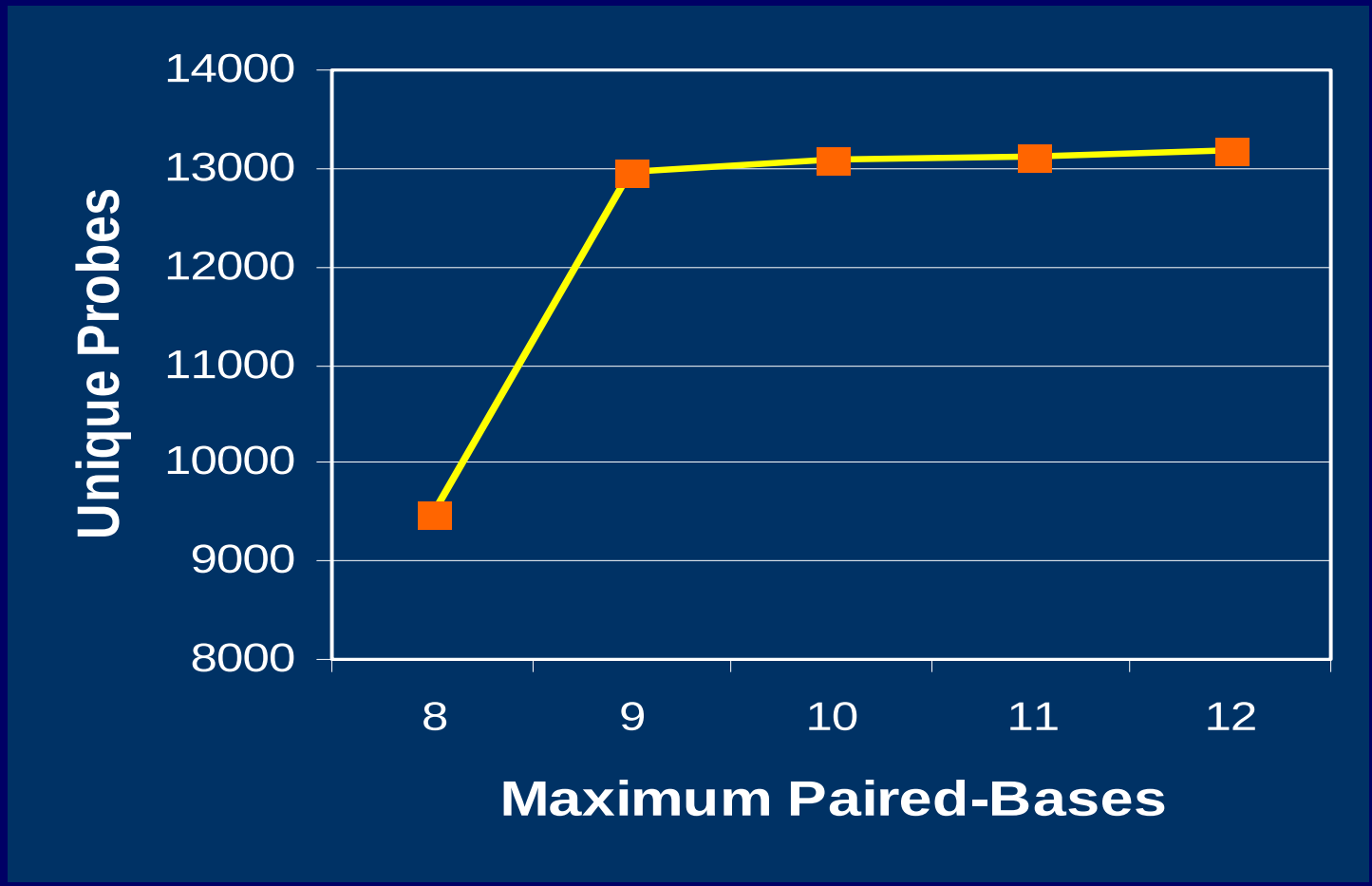
Impact of Self-annealing Filter



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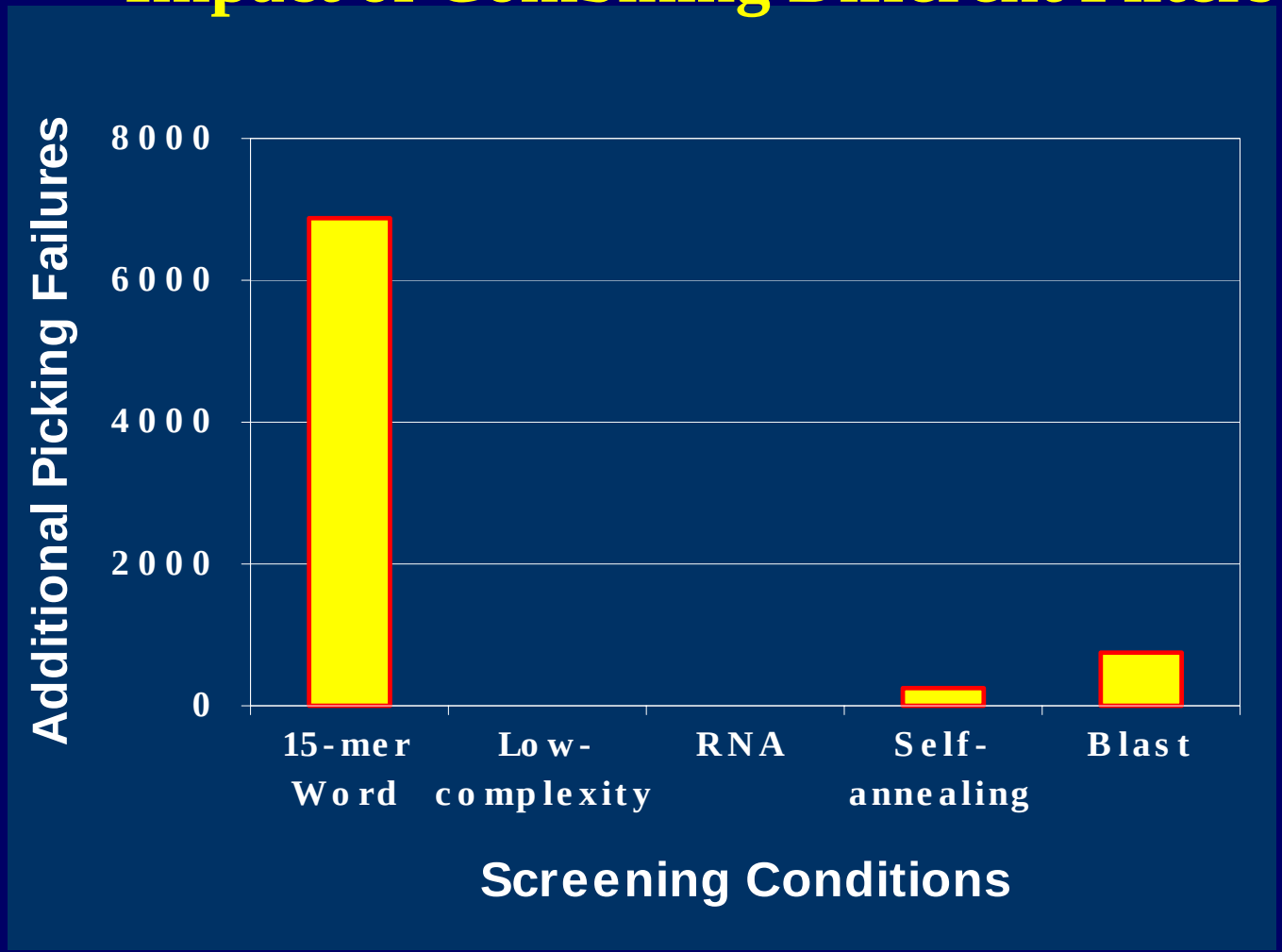
Impact of Combining Different Filters



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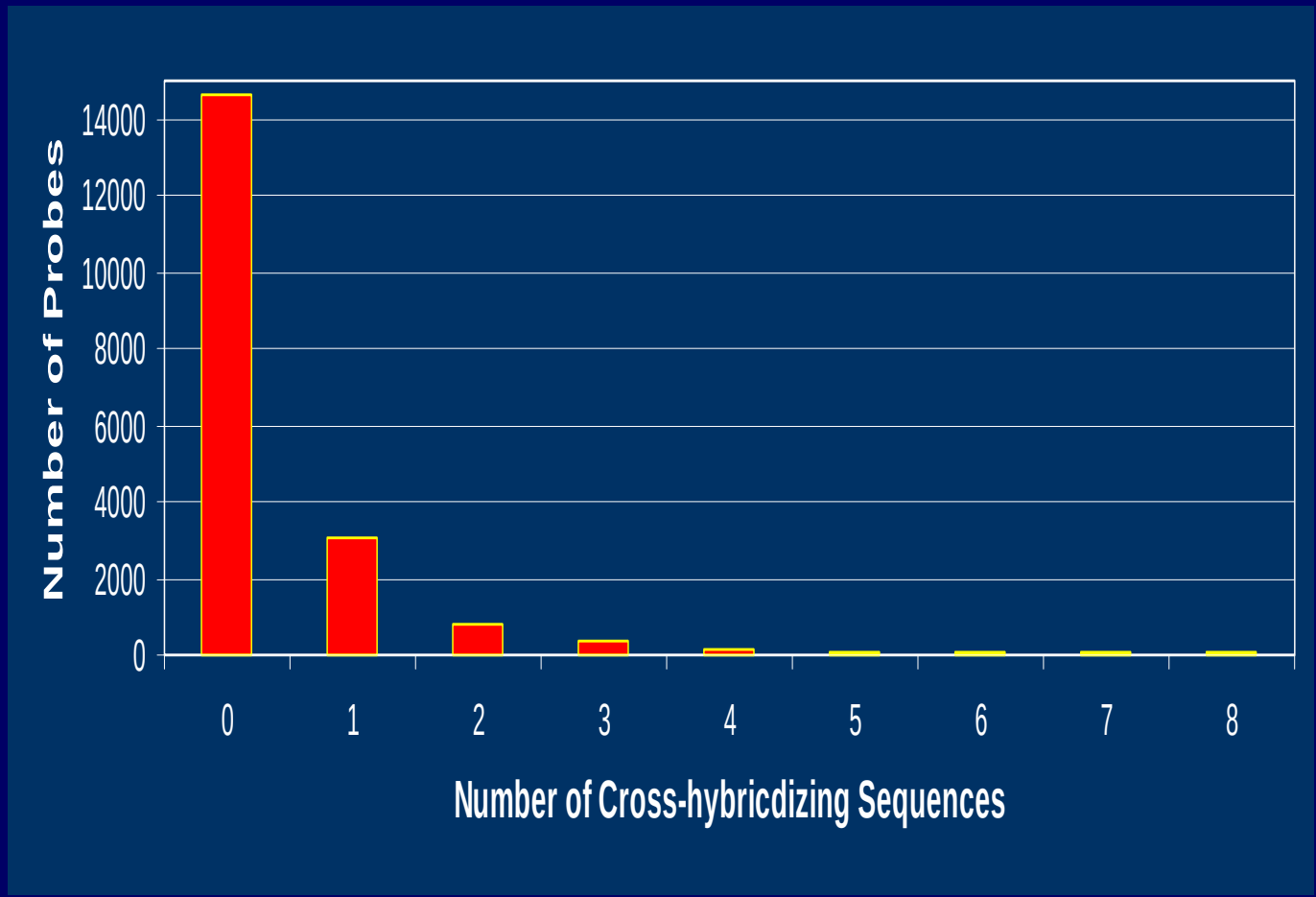
Distribution of Cross-hybridizing Probes



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