

Maize Genome Array-Ready Oligo Set™ (Version 1.0)

The Operon Maize AROS™ Version 1.0 contains 57,452 longer oligonucleotide probes representing 57,452 genes from maize genome. Each probe contains an amino linker at its 5' end.

Sequence source and gene selection

Gene sequences used for probe design are obtained from TIGR Maize Gene Index Release 14 (http://www.tigr.org/tigr-scripts/tgi/T_index.cgi?species=maize) and Maize Oligonucleotide Array Project (<http://www.maizearray.org/index.shtml>).

Probe design and selection rules

The longer probes are selected with an optimal set of parameters as described below.

1. The melting temperatures (T_m) of the probes are restricted within the range of 78 ± 5 °C. T_m is calculated using the following formula: $T_m = 81.5 + 16.6 * \log[Na^+] + 41 * (\#G + \#C)/length - 500/length$ where $[Na^+] = 0.1$ M and $length = \#A + \#C + \#G + \#T$
2. The contiguous single nucleotide repeat or poly (N) tract within a probe is limited to 8 bases or shorter.
3. The hairpin stem length of a probe is controlled at 8 bases or shorter.
4. The cross hybridization score for a probe against other non-representing (non-self) genes in the genome is set 70% or less of BLAST percent identity score.
5. The contiguous base match to other non-self genes is constrained at 20 bases or less.
6. The selection distances of the oligos are within 1,000 bases from the 3' end of the gene sequence.

The probes with the highest specificity (or the least cross-hybridization scores) are selected from a pool of candidates satisfying all the rules as described above.

The exceptions (relaxation of one or more selection rules) are made for the probe candidates of 17453 genes (30.3%), which don't meet the rules as mentioned above.

SUMMARY

Selection rules	Threshold	Probe number
Probe length (bases)	70	39999
Melting temperature (°C)	78 ± 5	
Poly (N) tract length (bases)	< 9	
Hairpin stem length (bases)	< 9	
Distal distance from 3' end	<1000	
Cross-hybridization score (identity %)	<= 70	
Contiguous base match to non-self genes (bases)	<= 20	
Exceptions		17453
Total		57452

The following illustrations show the distribution of all 57452 probes for oligo length, melting temperature, GC content, distance from 3' end, hairpin stem length, and cross-hybridization identity.

Figure 1. Oligo length

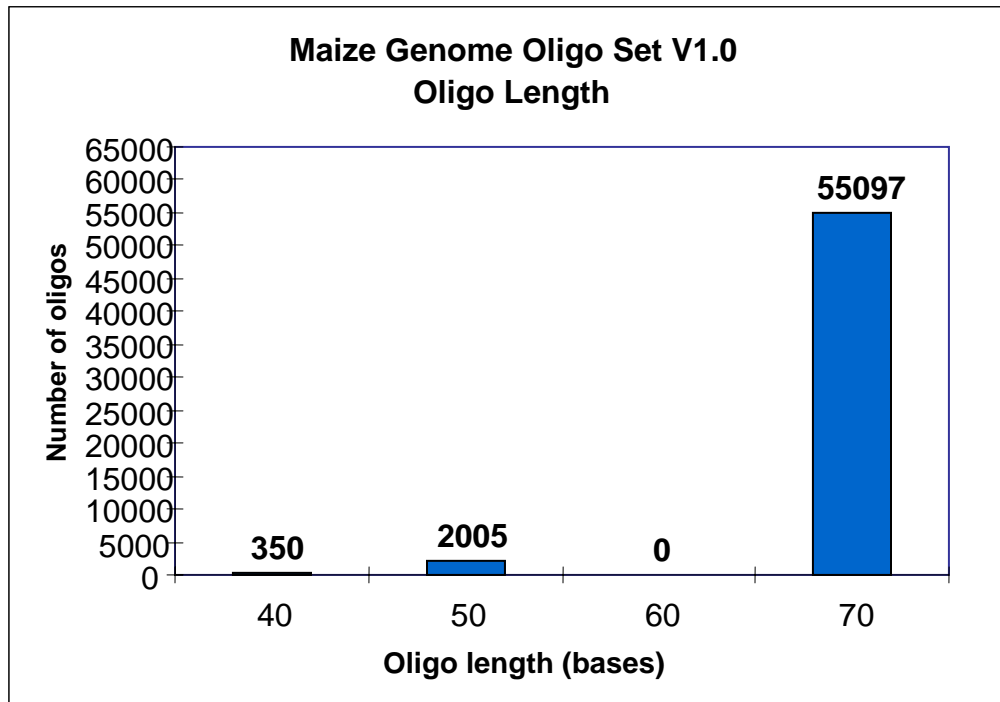


Figure 2. Melting temperature

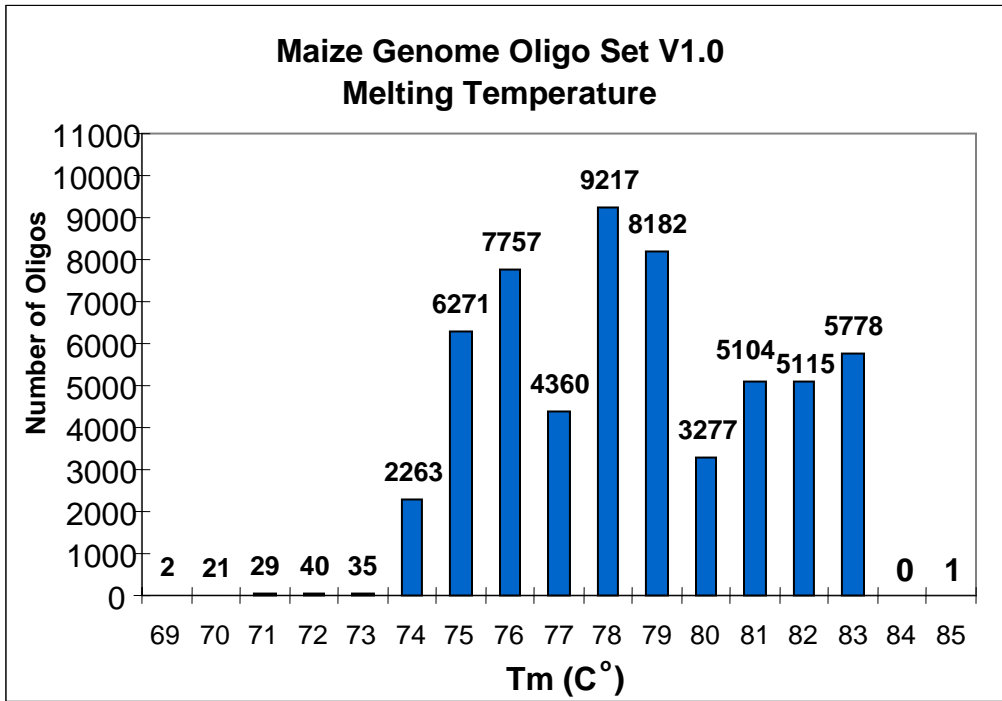


Figure 3. GC Content

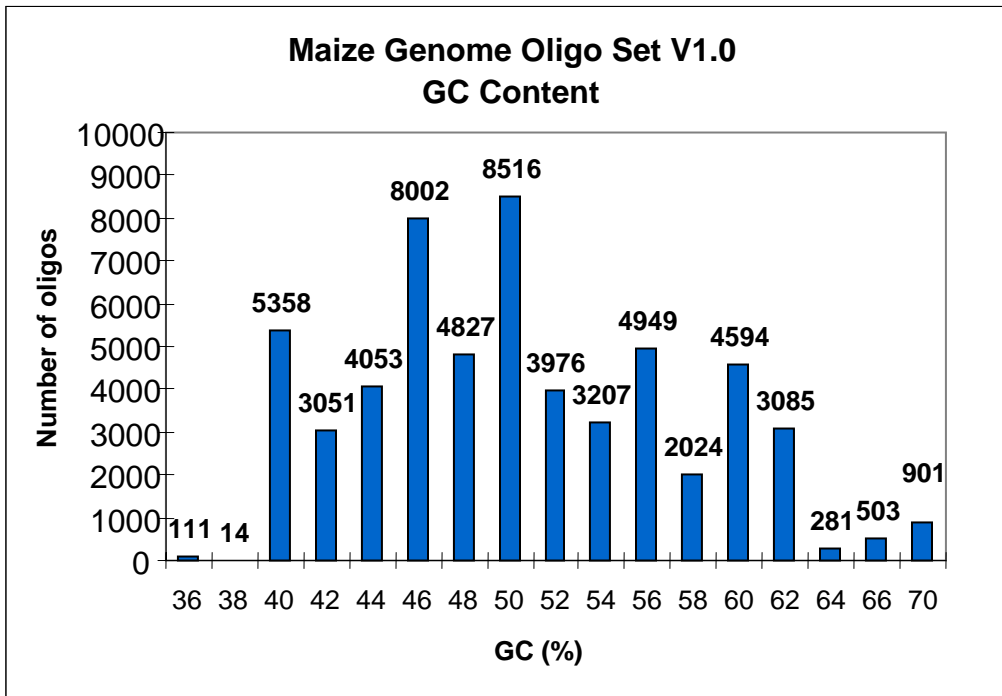


Figure 4. Distance from 3'-end

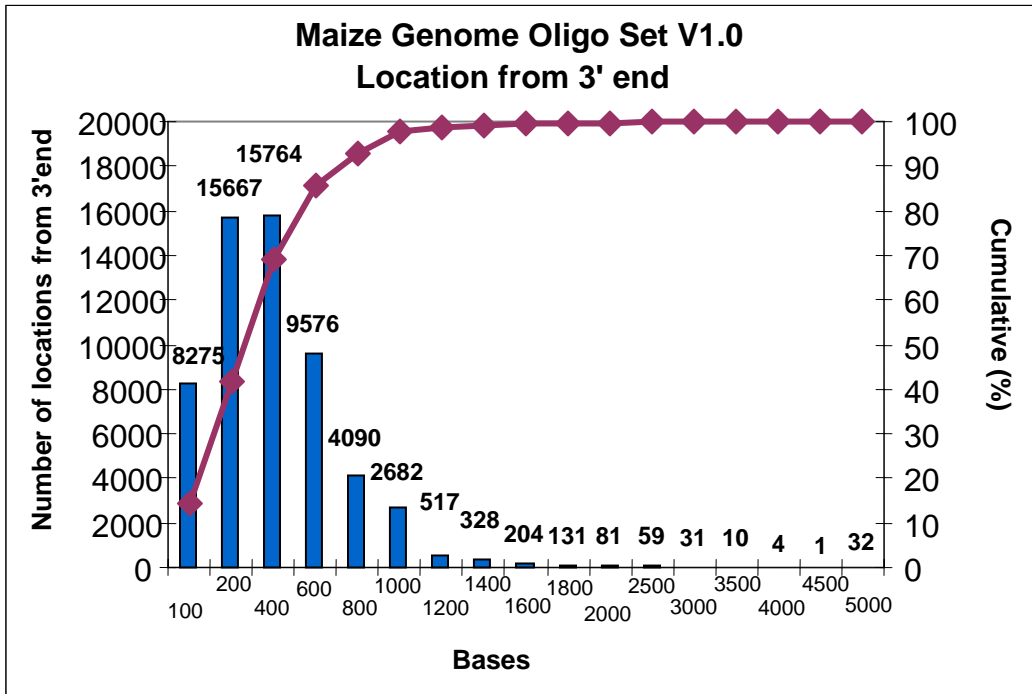


Figure 5. Hairpin stem length

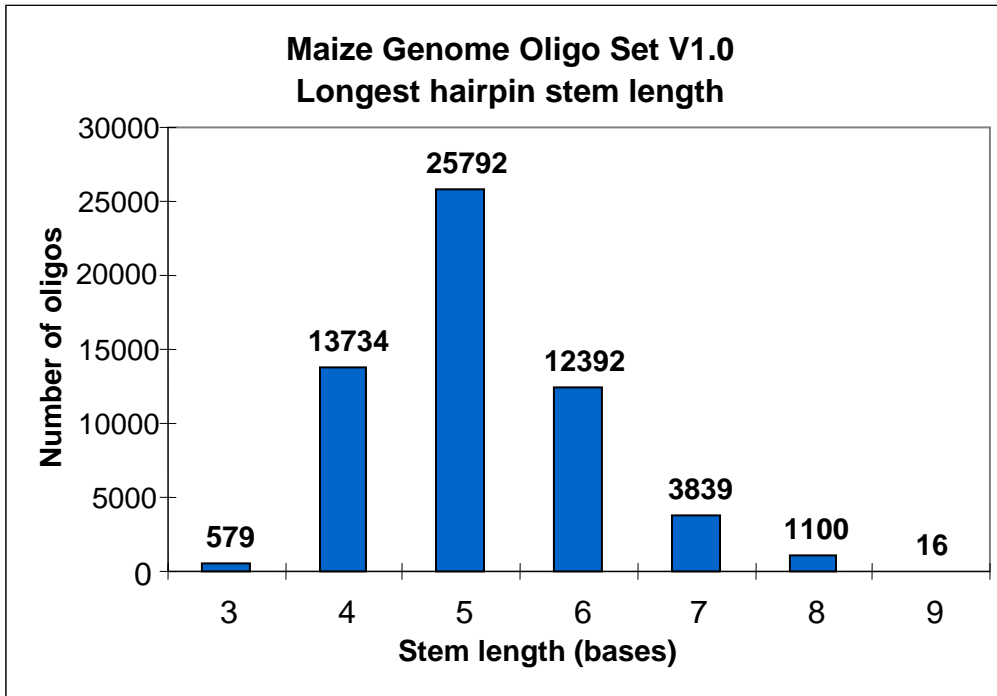


Figure 6. Cross-hybridization score

