

Magnaporthe Array-Ready Oligo Set™ (Version 1.0)

The Operon Magnaporthe AROS™ Version 1.0 contains 11676 longmer oligonucleotide probes representing 11676 open reading frames (ORFs) from *Magnaporthe grisea*. Each probe contains an amino linker at its 5' end.

Sequence source and ORF selection

Predicted ORFs were downloaded from the Whitehead Institute/MIT Center for Genome Research (http://www-genome.wi.mit.edu/cgi-bin/annotation/magnaporthe/download_license.cgi).

Probe design and selection rules

The longmer 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) ORFs in the genome is set 70% or less of BLAST percent identity score.
5. The contiguous base match to other non-self ORFs is constrained at 20 bases or less.

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 60 ORFs (0.5%), which don't meet the rules as mentioned above.

SUMMARY

Selection rules	Threshold	Probe number
Probe length (bases)	70	11616
Melting temperature (°C)	78 ± 5	
Poly (N) tract length (bases)	< 9	
Hairpin stem length (bases)	< 9	
Cross-hybridization score (identity %)	<= 70	
Contiguous base match to non-self ORFs (bases)	<= 20	
Exceptions		60
Total		11676

The following illustrations show the distribution of all 11676 probes for oligo length, melting temperature, GC content, distance from 3' end, hairpin stem length, and cross-hybridization identity.

Figure 1. Oligo length

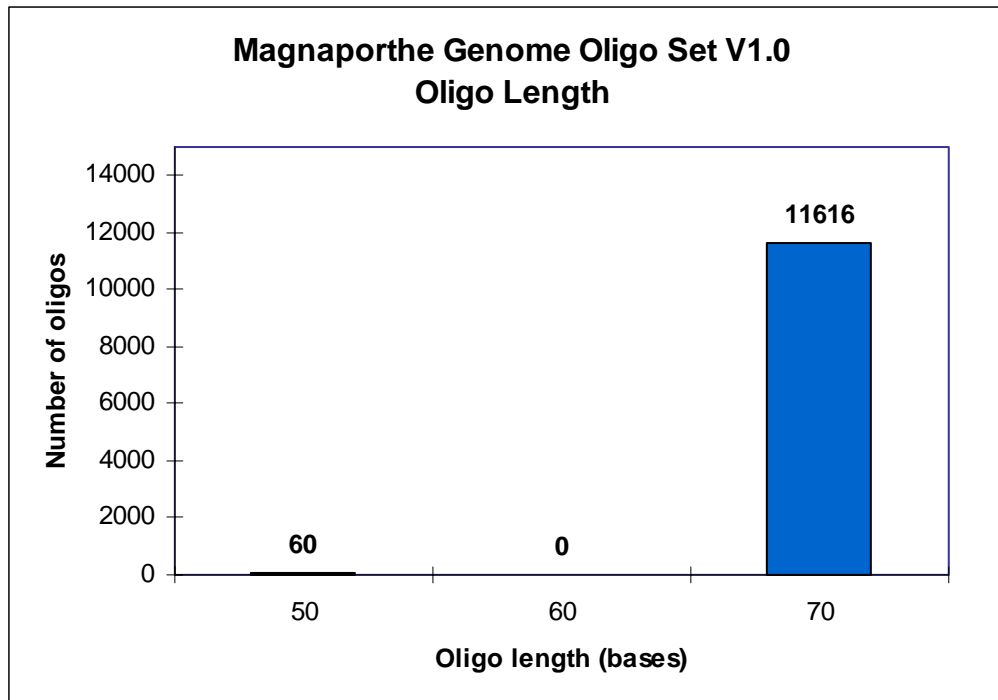


Figure 2. Melting temperature

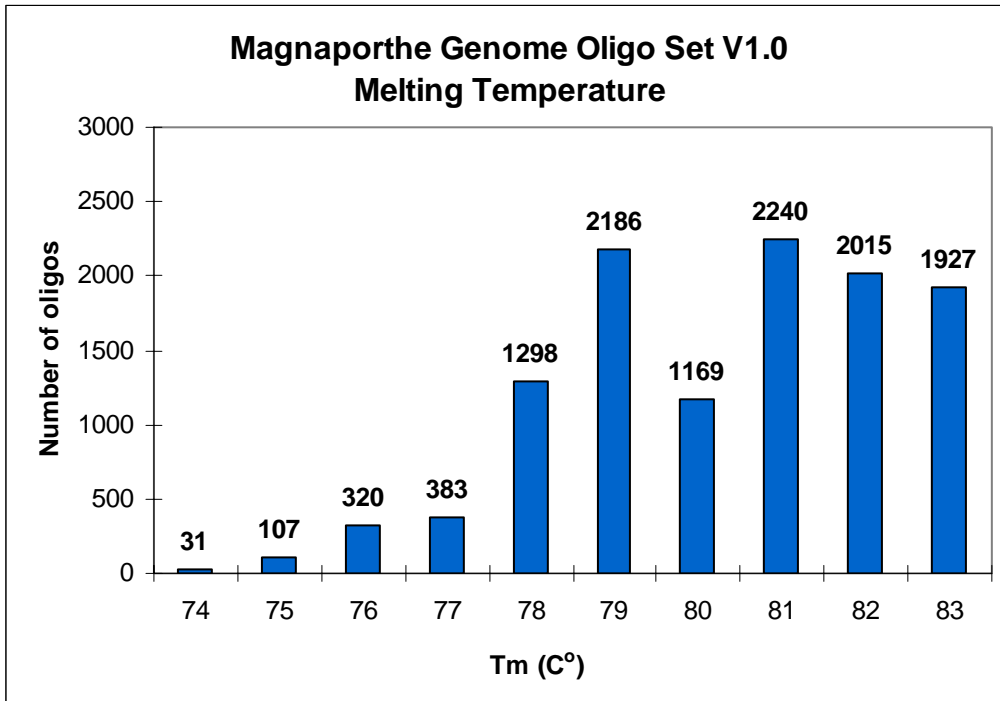


Figure 3. GC Content

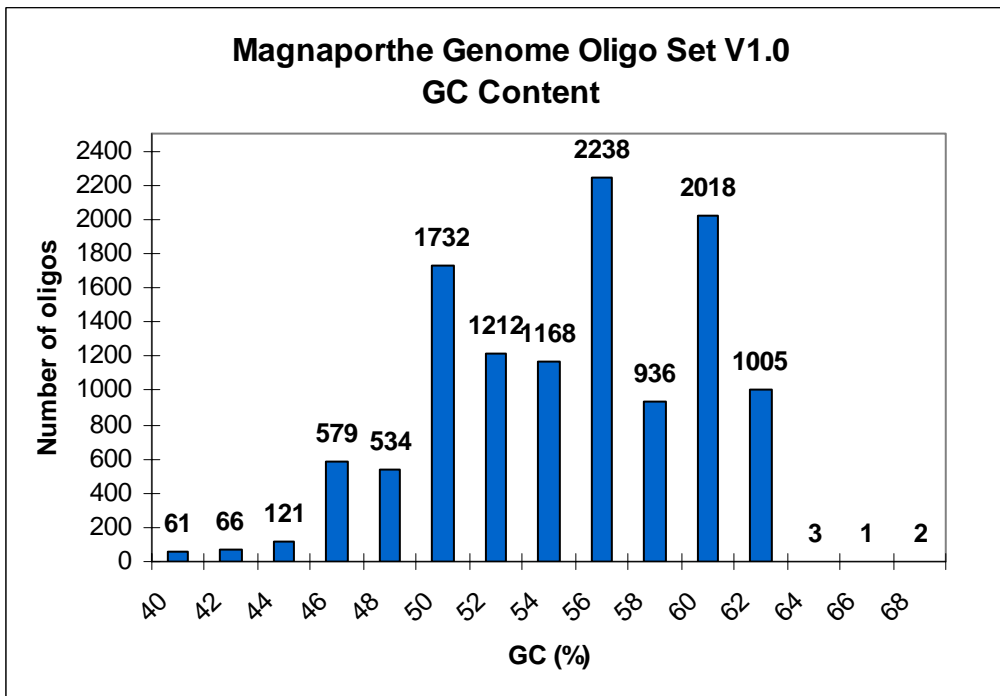


Figure 4. Distance from 3'-end

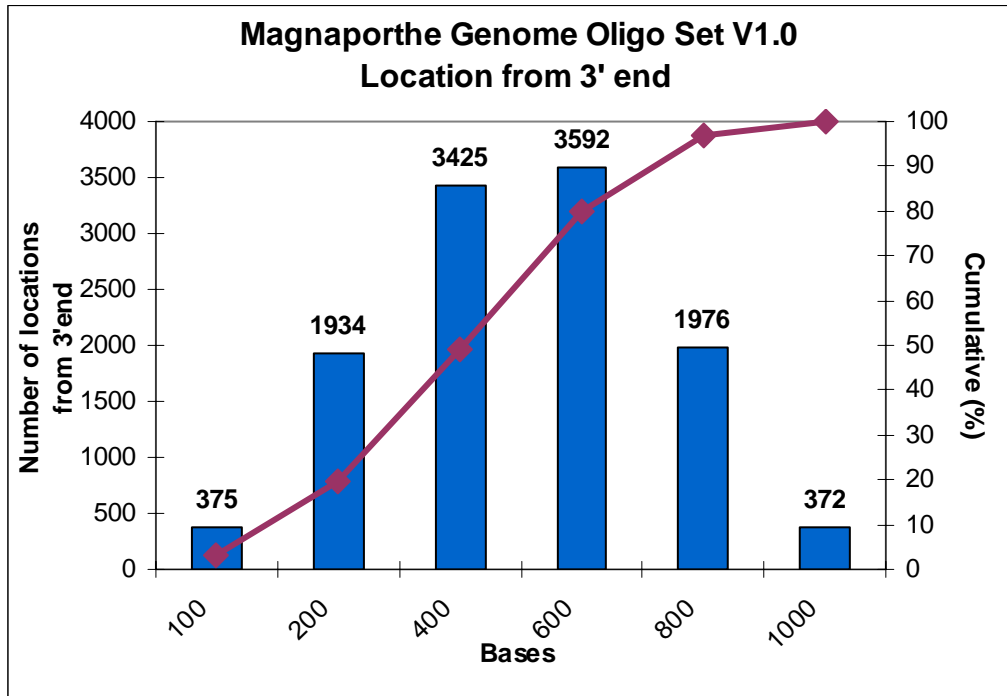


Figure 5. Hairpin stem length

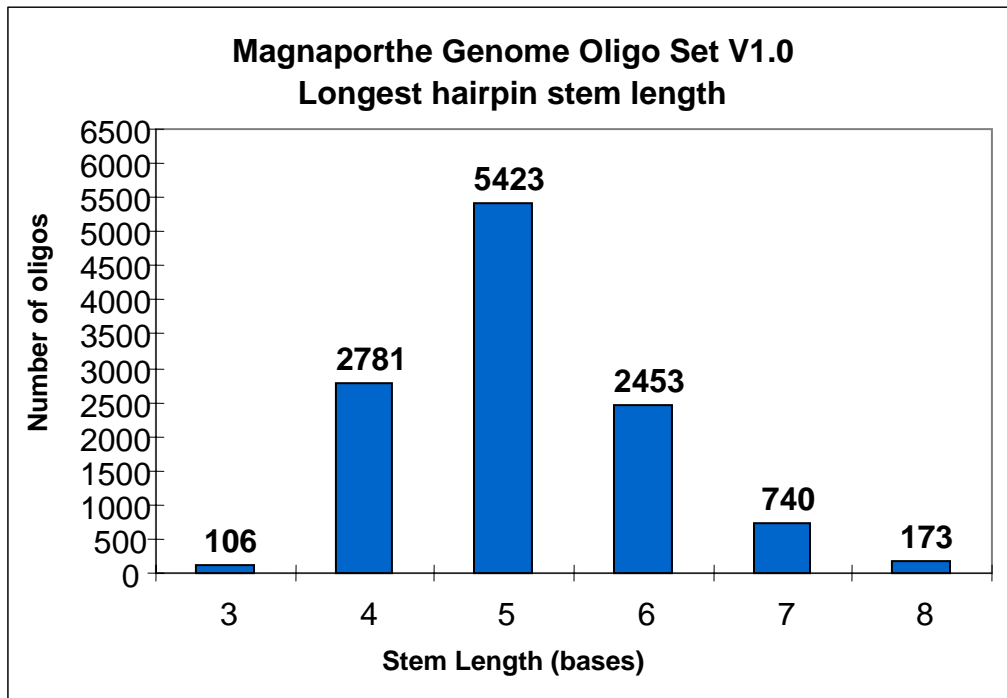


Figure 6. Cross-hybridization score

