

## Beijing CoRe Rice Array-Ready Oligo Set™ (Version 1.0)

---

In a cooperative research partnership with the Beijing Genome Institute, the Beijing CoRe Rice Array set Version 1.0 is offered by Operon. It contains 60727 70-mer oligonucleotide probes representing 55,427 genes from both indica and japonica rice genomes. The set includes an additional 12 negative control oligos. Each probe contains an amino linker at its 5' end.

### Sequence source and gene selection

The Beijing Genome Institute(BGI) ([http://www.genomics.org.cn/bgi\\_new/english/index.htm](http://www.genomics.org.cn/bgi_new/english/index.htm)) annotated the gene sequences of *Oryza sativa* indica and japonica genomes. In addition, BGI designed the Rice Genome CoRe Version 1.0 based on the general design criteria of Operon array ready oligo set. All oligos were designed from cDNAs, expressed sequence tag (EST) sequences, predicted genes of BGI rice genome build and other public resources. The gene sequences data set is available upon customer's request.

### Probe design and selection rules

The 70-mer 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  $80 \pm 5$  °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 sequences.

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 22579 designed oligos (37.2%), which don't meet the rules as mentioned above.

## SUMMARY

Selection rules	Threshold	Probe number
Probe length (bases)	70	38148
Melting temperature (°C)	80 ± 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		22579
Total		60727

The following illustrations show the distribution of all 60727 probes for melting temperature, GC content, distance from 3' end, hairpin stem length, and cross-hybridization identity.

Figure 1. Melting temperature

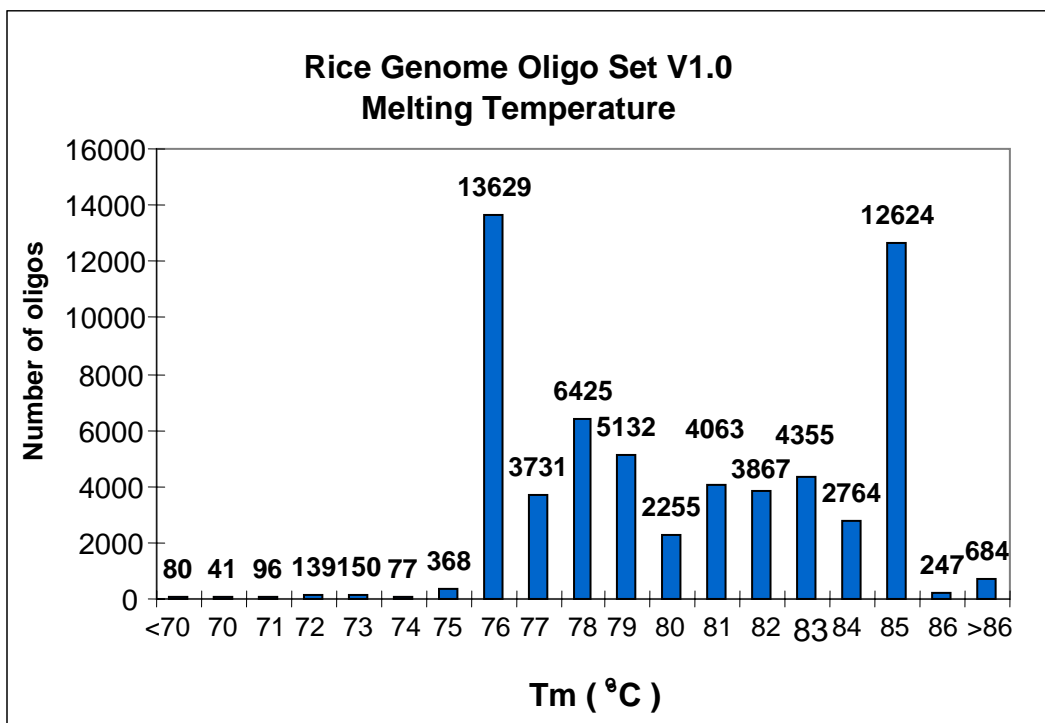


Figure 2. GC Content

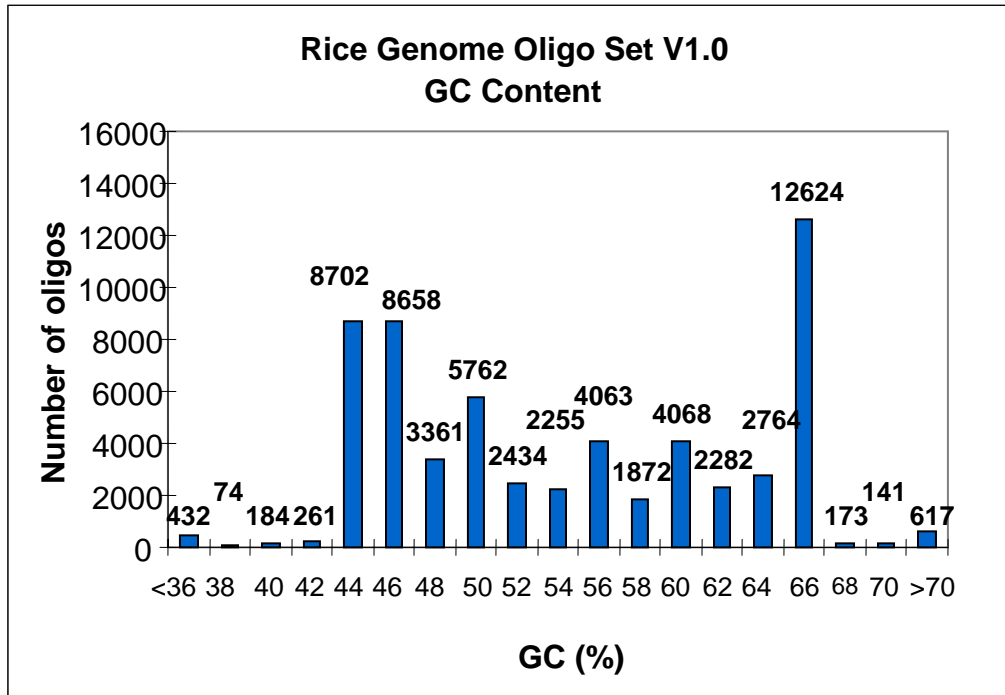


Figure 3. Distance from 3'-end

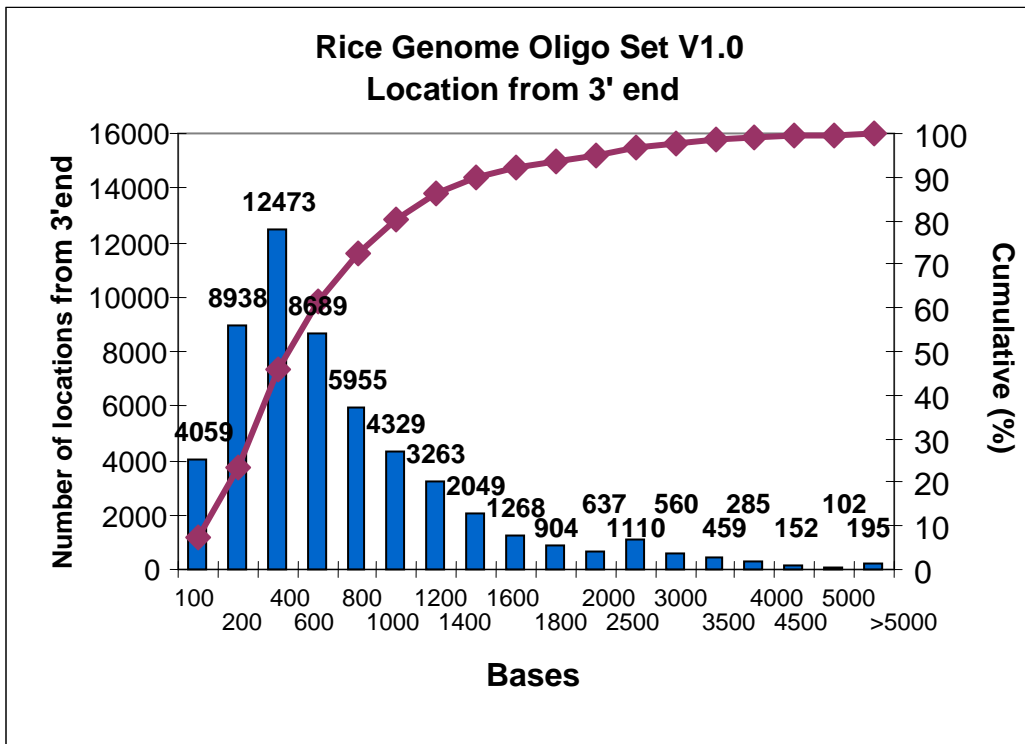


Figure 4. Hairpin stem length

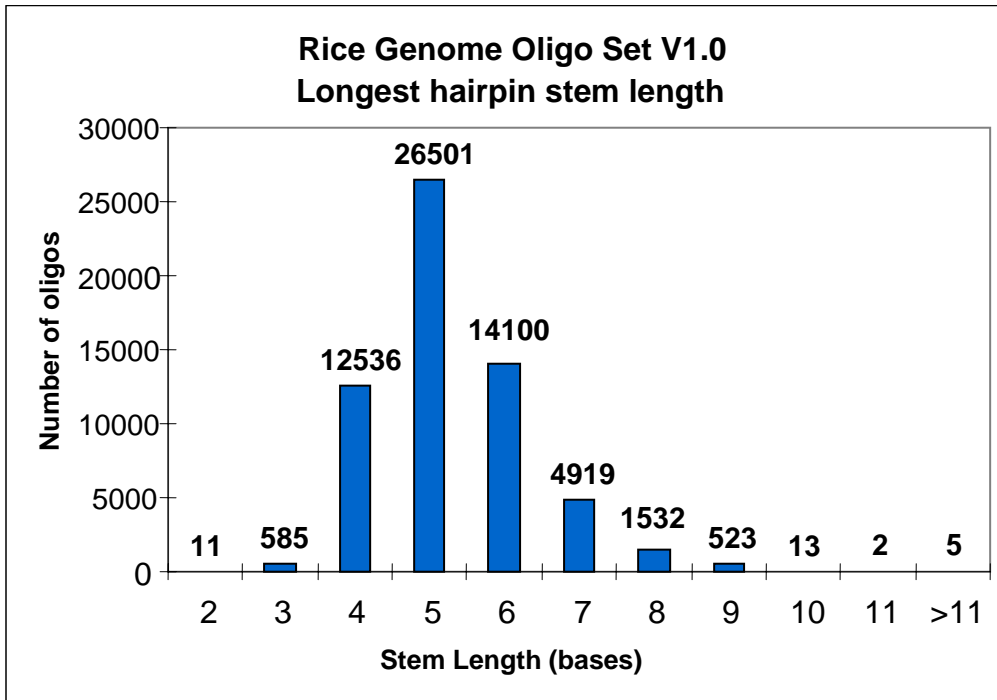


Figure 5. Cross-hybridization score

