

Mature miRNA Sequences

miRBase

48,885 records

30,721 unique



Overlapping positional scan



2-mer windows 3-mer windows

Position-resolved k-mer analysis

All sequences

Observed frequency by start



Taxonomic landscape

10 mutually exclusive groups



Non-randomness tested with two independent nulls

1 Within-sequence shuffle
length + base counts fixed

2 Position $\times$ length shuffle
column counts fixed by length

10,000 / null

abundance

position

entropy

Observed profiles

Permutation effects

BH-adjusted inference

The positional analysis reveals

1 **CG + UA**

are broadly depleted across positions



2 **UA at start 0**

is a consistent 5' positional exception



3 **In Various taxa**

lineages modulate positional concentration

