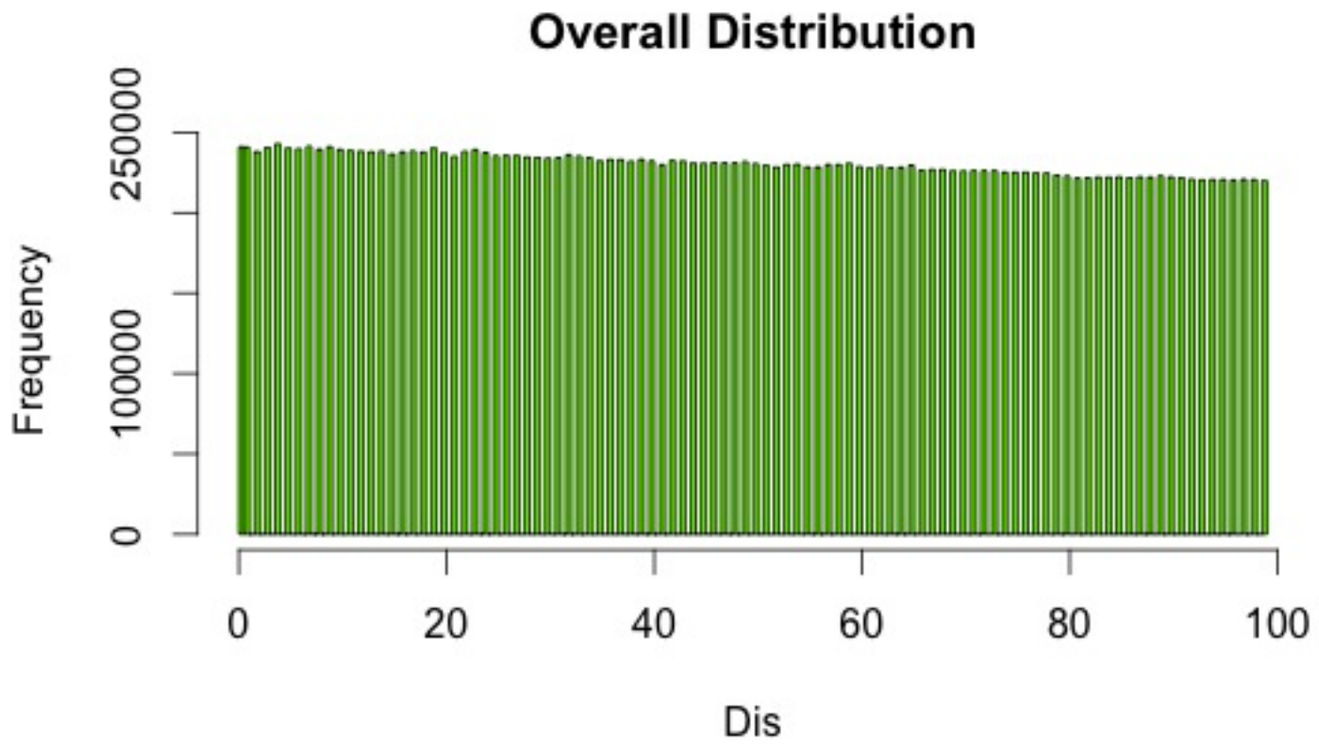
Method

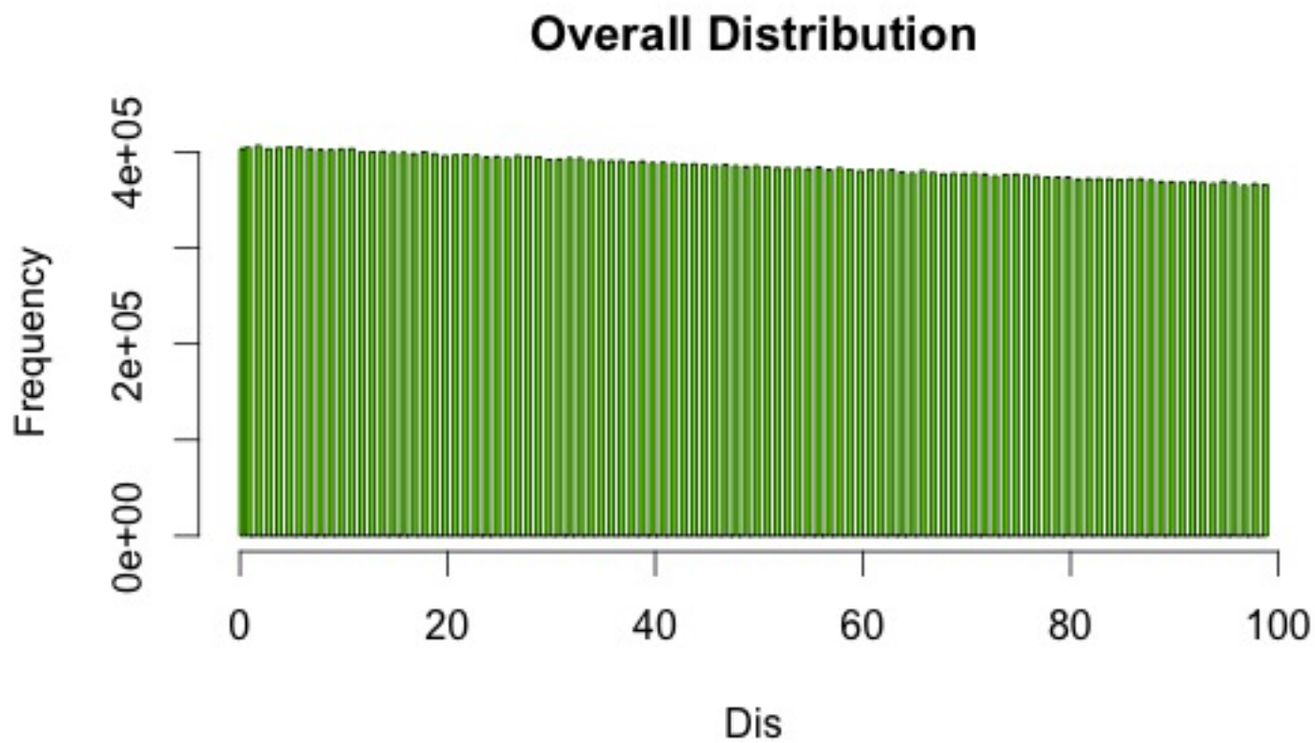
- TargetScan
- Transcript with longest UTR
- In mouse, 3'UTR is not well annotated. Those genes use orthologs of Human.
- Calculate distances between miRNA binding sites.

Overall Distribution

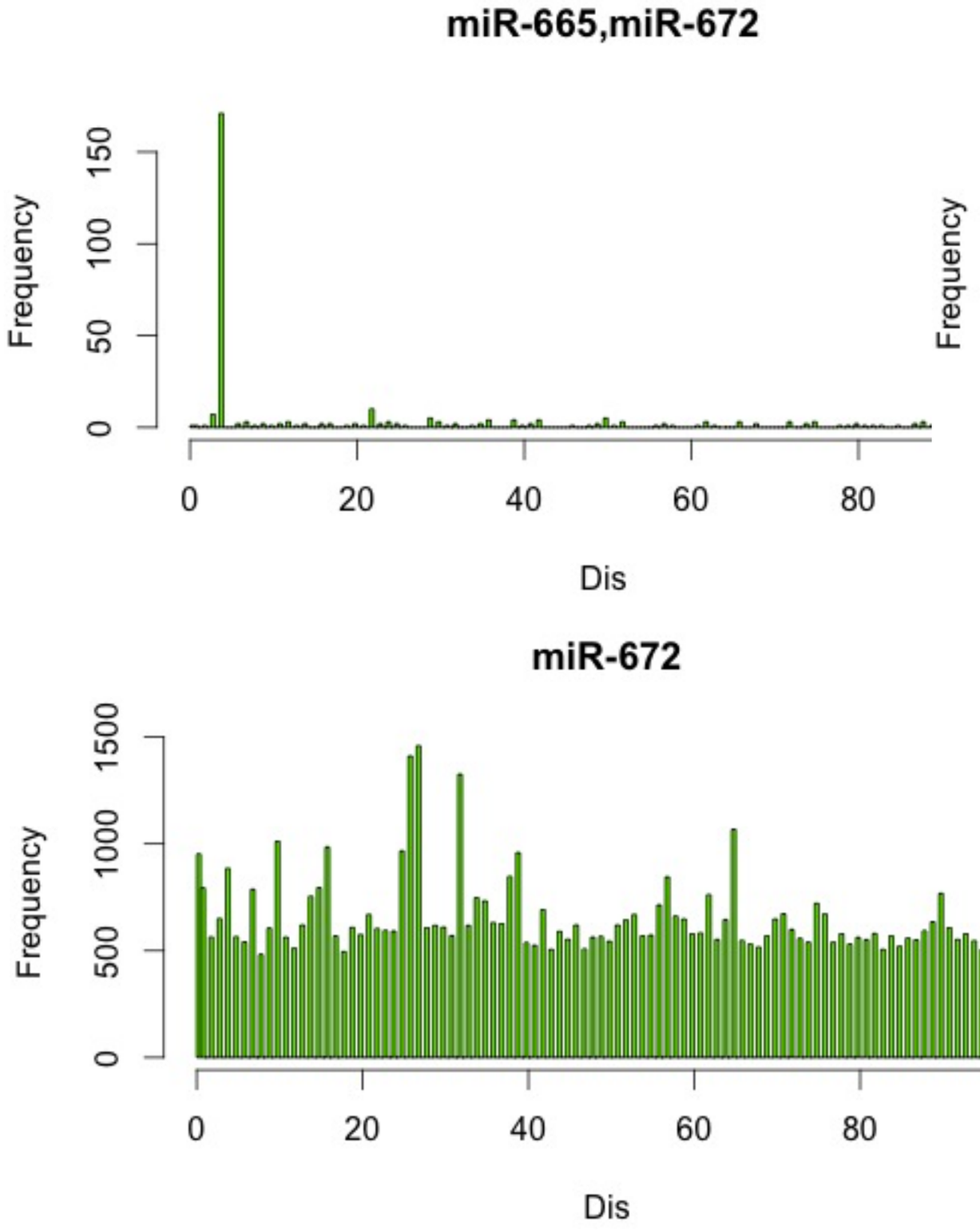


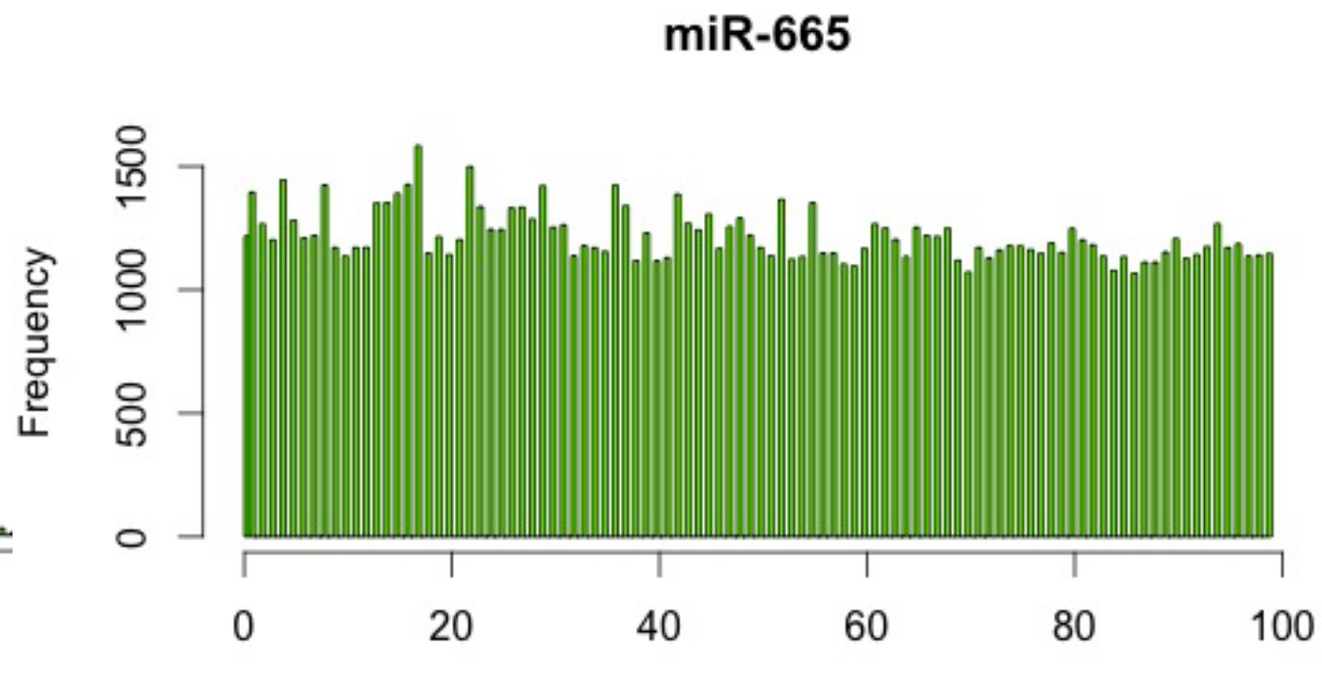
Human

Mouse

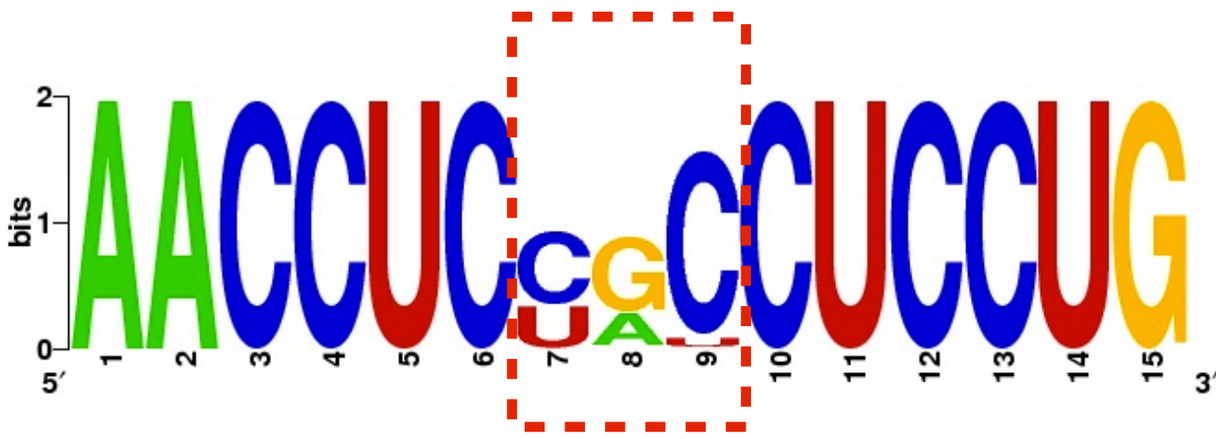


Example

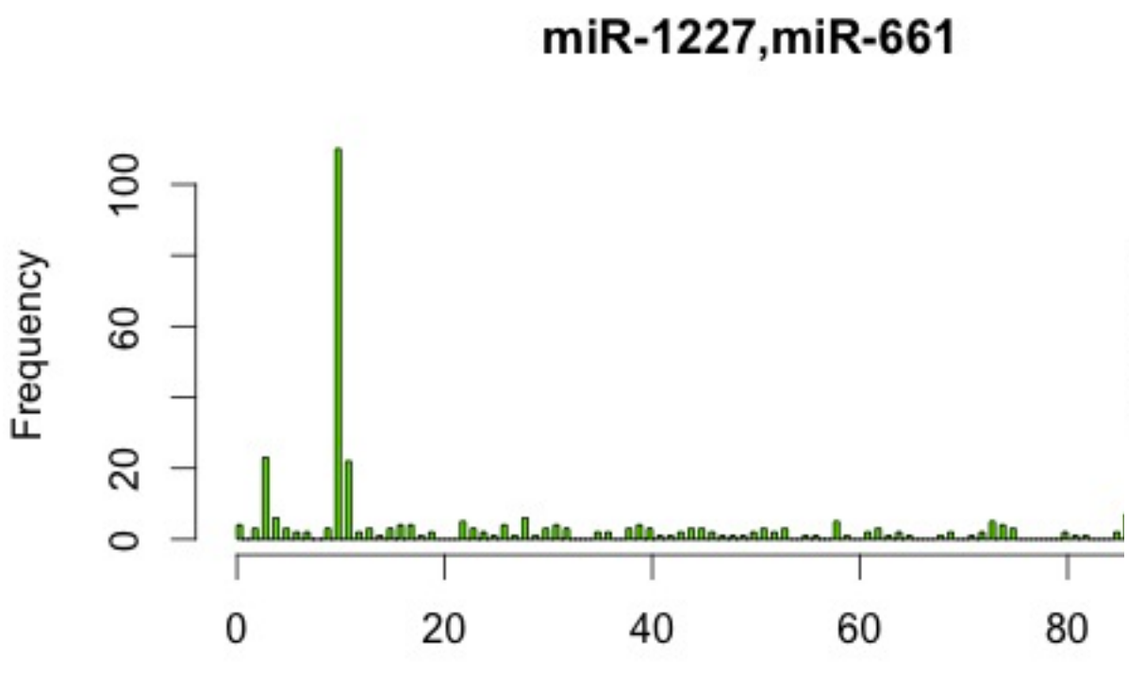

miR-665,miR-672
Frequency
0
50
100
150
0
20
40
60
80
Dis

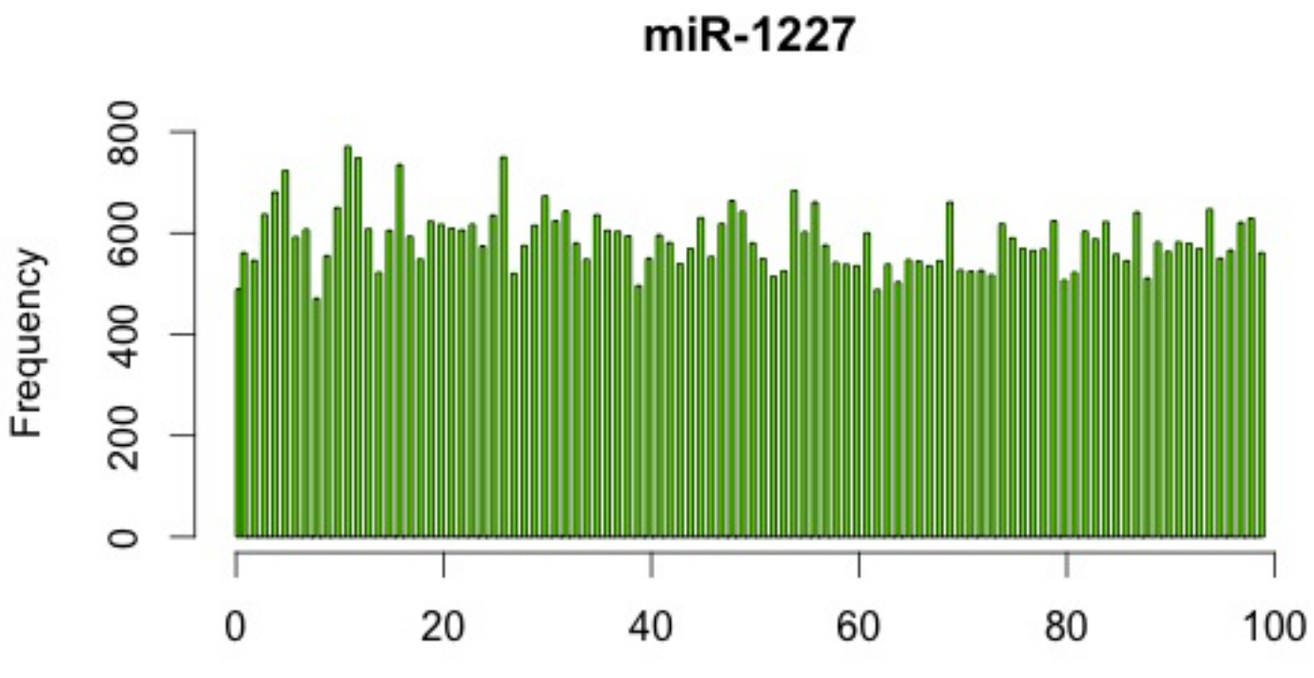

miR-665
Frequency
0
500
1000
1500
0
20
40
60
80
100
Dis

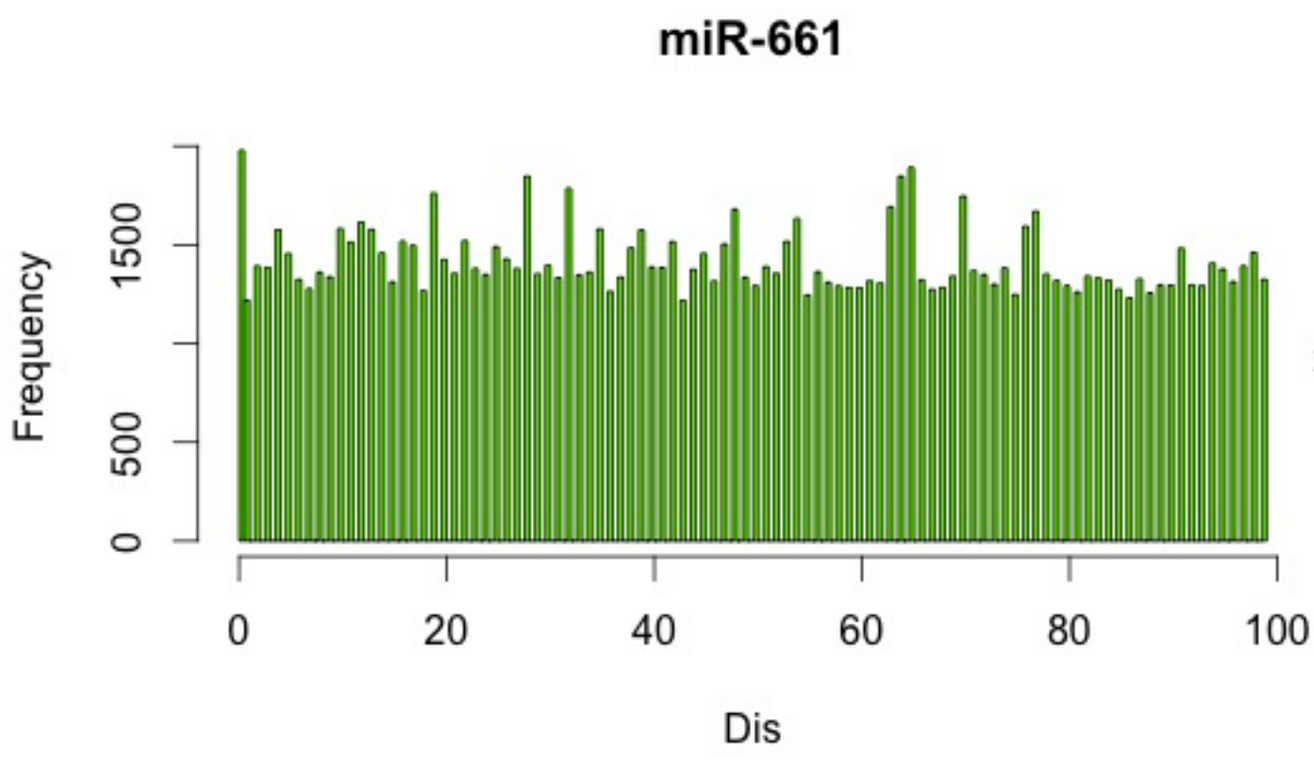
miR-672
Frequency
0
500
1000
1500
0
20
40
60
80
100
Dis


bits
0
1
2
5′
3′

Example


miR-1227,miR-661
Frequency
0
20
60
100
0
20
40
60
80
Dis


miR-1227
Frequency
0
200
400
600
800
0
20
40
60
80
100
Dis


miR-661
Frequency
0
500
1500
0
20
40
60
80
100
Dis

bits
2
1
0
5´
UGGAGUGCA
1
2
3
4
5
6
7
8
9

miR-665

miR-665,miR-658	0
miR-665,miR-672	3
miR-665,miR-137.c	4
miR-665,miR-682	7
miR-665,miR-940	14
miR-665,miR-709/1827	15
miR-665,miR-202	16
miR-665,miR-485/485-5p	21
miR-665,miR-450b-3p	26
miR-665,miR-508-5p	35
miR-665,miR-766	36
miR-665,miR-661	41
miR-665,miR-323-5p	54

- microRNA redundancy
- pairs of microRNA actually interact to co-influence the degradation of mRNA.

- compare between species
- experimental validation
- mechanisms

MicroRNA Interaction network in human: *implications of clustered microRNA in biological pathways and genetic diseases*

Sushmita Mookherjee[1], Mithun Sinha[2], Saikat Mukhopadhyay[3], Nitai P. Bhattacharyya[2,3,*] and P. K. Mohanty[4,†]
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(Dated: January 27, 2009)

C. Co-targeted genes in miRNA clusters may involve in specific pathways