

pri-mir-655

chr14: 101049542-101049666 (+)

	Features	Optimality
Stem length (bp)	34	Suboptimal
Lower stem length (bp)	11	Suboptimal
Mismatched pairs in the stem	4	
Bulged bases in the stem	0	Optimal
Apical loop size (nt)	12	Suboptimal
3' basal segment length (nt)	6	Optimal
Mismatch at -6	Not possessed	
bGWG at -10/-11	Not possessed	

	w/o SRSF3	w/ SRSF3
Cleavage efficiency	0.0 (476 / 476)	1.65 (239 / 476)
Cleavage homogeneity	0.1 (428 / 476)	0.45 (408 / 476)

Rank among tested pri-miRs

Top

Bottom

The diagram illustrates the secondary structure of pri-mir-655, a pre-microRNA hairpin. The structure is composed of several key regions:

- Stem (US: 23 bp):** The upper stem region, labeled "US: 23 bp", is the longest continuous double-stranded segment.
- Lower Stem (LS: 11 bp):** The lower stem region, labeled "LS: 11 bp", is a shorter double-stranded segment.
- Apical Loop (Loop: 12 nt):** A terminal loop structure at the 5' end, labeled "Loop: 12 nt".
- Basal Segments:** The 5' basal segment (BS) is 2 nt long, and the 3' basal segment (BS) is 6 nt long.
- Stem Features:** The stem contains 4 mismatched pairs and 0 bulged bases.
- Sequence:** The nucleotide sequence is shown in a color-coded format: red for Adenine (A), orange for Uracil (U), green for Guanine (G), and blue for Cytosine (C). The sequence is oriented 5' to 3'.