

## Supplementary material:

**Table 1:** Potential miRNA-Target pairs derived from miRanda above the threshold values. MFE\* is calculated from RNAhybrid Program and Inhibition\*\* is predicted according to the findings of Brodersen *et al.* (2008).

Cotton miRNA	miRNA-Target pair	Target binding position	Score	MFE* (kCal/mol)	% Complem-Inhibition** -entarity	
<i>AC1</i> Gene						
ghr-miR395a,d	Query: 3' uucAAGGGGGUUUGUGAAGUu 5'	795-815	166	-28.1	100.00	Cleavage
	Ref: 5' ocaTTTCCTCAAAACACTTTAa 3'					
ghr-miR395a,d	Query: 3' uucaagGGGGUUUGUGAAGUu 5'	210-230	139	-28.0	100.00	Cleavage
	Ref: 5' caqaaaCCCCAGACATTTCGa 3'					
<i>AC4</i> Gene						
ghr-miR395a,d	Query: 3' uucaagGGGGUUUGUGAAGUu 5'	53-73	139	-28.0	100.00	Cleavage
	Ref: 5' cagaaaCCCCAGACATTTCGa 3'					
<i>AV1</i> Gene						
ghr-miR168	Query: 3' ggGUGCUGGACGUGGUUcgu 5'	688-707	116	-25.2	93.33	Cleavage
	Ref: 5' taCATGGCTTGACTCAtgc 3'					
ghr-miR779	Query: 3' uacucgucgUUGUACUUCUgu 5'	490-510	128	-22.6	90.00	Translation
	Ref: 5' aotaccccAaCCGTGAAGAc 3'					
ghr-miR3476	Query: 3' cguCGGUUGUUUGGUCAAGu 5'	475-495	143	-25.0	88.24	Cleavage
	Ref: 5' tttGATAACGAGCCAGTACg 3'					