rank	motif	–log10 p–value	best match
1	2.0 1.5 1.0 0.5 0.0	255	let–7/miR–98
2	2.0 1.5 1.0 0.5 0.0	137	miR-194
3	2.0 1.5 1.0 0.5 0.0	111	miR-29
4	2.0 1.5 1.0 0.5 0.0	96	miR-200
5	2.0 1.5 1.0 0.5 0.0	45	miR-30
6	2.0 1.5 1.0 0.5 0.0 GCAGCUAGE	45	miR–22
7	2.0 1.5 1.0 0.5 0.0	41	miR–24
8	2.0 1.5 1.0 0.5 0.0 CGCACAAC	33	miR-210