rank	motif	–log10 p–value	best match
1	2.0 1.5 1.0 0.5 0.0 AAGCAGGG	72	miR-4667-3p
2	2.0 1.5 1.0 0.5 0.0	42	miR-26/1297/4465
3	2.0 1.5 1.0 0.5 0.0	32	miR–21
4	2.0 1.5 1.0 0.5 0.0 SGEASA	26	miR-629
5	2.0 1.5 1.0 0.5 0.0	16	miR-3183/4723/6769
6	2.0 1.5 1.0 0.5 0.0 AgAGG_gG G	14	miR-4640-3p
7 *	2.0 1.5 1.0 0.5 0.0 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3	hsa-miR-4753-3p