

Supplementary Table S4.
Putative miR Promoter Analysis for Transcription Factor (TF) Binding Sites

http://jaspar.genereg.net/cgi-bin/jaspar_db.pl

miR-138-1 -3kb region (1-3,001)

9 putative sites were predicted with these settings (100%) in sequence named **hg18_dna**

<i>Model ID</i>	<i>Model name</i>	<i>Score</i>	<i>Relative score</i>	<i>Start</i>	<i>End</i>	<i>Strand</i>	<i>predicted site sequence</i>
MA0095.1	YY1	8.383	0.999993345000489	154	159	-1	GCCATC
MA0095.1	YY1	8.383	0.999993345000489	291	296	-1	GCCATC
MA0081.1	SPIB	10.470	1.00001471989147	322	328	1	AGAGGAA
MA0081.1	SPIB	10.470	1.00001471989147	945	951	1	AGAGGAA
MA0095.1	YY1	8.383	0.999993345000489	1126	1131	-1	GCCATC
MA0133.1	BRCA1	8.351	1.00001505763814	1311	1317	-1	ACAACAC
MA0037.1	GATA3	8.388	0.999994892993597	1683	1688	1	AGATAG
MA0037.1	GATA3	8.388	0.999994892993597	1877	1882	1	AGATAG
MA0095.1	YY1	8.383	0.999993345000489	1882	1887	-1	GCCATC

miR-138-2 -3kb region (1-3,001)

5 putative sites were predicted with these settings (100%) in sequence named **hg18_dna**

<i>Model ID</i>	<i>Model name</i>	<i>Score</i>	<i>Relative score</i>	<i>Start</i>	<i>End</i>	<i>Strand</i>	<i>predicted site sequence</i>
MA0037.1	GATA3	8.388	0.999994892993597	358	363	1	AGATAG
MA0095.1	YY1	8.383	0.999993345000489	883	888	-1	GCCATC
MA0037.1	GATA3	8.388	0.999994892993597	2380	2385	-1	AGATAG
MA0037.1	GATA3	8.388	0.999994892993597	2546	2551	-1	AGATAG
MA0133.1	BRCA1	8.351	1.00001505763814	2891	2897	1	ACAACAC