

Supplementary Table 1. Putative E2F1 binding site in TMPO-AS1 promoter region

Matrix ID	Name	Score	Relative score	Start	End	Strand	Predicted sequence
MA0024.2	E2F1	3.06245	0.81409542	91	101	-	caagagcgaga
MA0024.3	E2F1	6.87706	0.804139174	120	131	+	gatggcgcgatc
MA0024.2	E2F1	2.98494	0.812929319	120	130	-	atcgcgccatc
MA0024.3	E2F1	6.81554	0.803114898	120	131	-	gatcgcgccatc
MA0024.2	E2F1	5.59617	0.852214466	121	131	+	atggcgcgatc
MA0024.2	E2F1	5.40621	0.849356656	152	162	-	aacccgggagg
MA0024.2	E2F1	6.06232	0.85922765	171	181	-	gaggcaggaga
MA0024.2	E2F1	4.44478	0.834892136	183	193	-	gtggcggcggc
MA0024.2	E2F1	6.89181	0.871707113	288	298	-	caggcgggtgg
MA0024.2	E2F1	6.60793	0.867436133	322	332	+	caggcgtgagc
MA0024.2	E2F1	3.22894	0.816600153	412	422	+	taagcgggtac
MA0024.1	E2F1	7.04914	0.808904868	472	479	-	ttttgcgg
MA0024.1	E2F1	8.83194	0.870250556	532	539	+	tttggcac
MA0024.2	E2F1	5.4983	0.850742026	664	674	+	tagccgggaaa
MA0024.1	E2F1	7.99297	0.841381869	667	674	-	tttcccg
MA0024.2	E2F1	3.99712	0.828157248	853	863	+	aactcggcagg
MA0024.2	E2F1	6.60793	0.867436133	1131	1141	-	caggcgtgagc
MA0024.2	E2F1	13.7528	0.974928868	1165	1175	+	gaggcgggagg
MA0024.2	E2F1	5.06681	0.844250434	1288	1298	+	tactcgggagg
MA0024.2	E2F1	6.06232	0.85922765	1301	1311	+	gaggcaggaga
MA0024.2	E2F1	5.40621	0.849356656	1320	1330	+	aacccgggagg
MA0024.3	E2F1	13.8796	0.92072957	1434	1445	+	ataggcgcctaa
MA0024.3	E2F1	13.8661	0.920505683	1434	1445	-	ttaggcgcctat
MA0024.2	E2F1	3.0082	0.813279254	1435	1445	+	taggcgcctaa
MA0024.1	E2F1	8.83194	0.870250556	1438	1445	-	ttaggcgc
MA0024.1	E2F1	10.1517	0.915662968	1490	1497	-	tttggcgg
MA0024.2	E2F1	7.60658	0.882460632	1580	1590	+	aaggcgggaat
MA0024.2	E2F1	3.59314	0.822079413	1659	1669	-	ctcgcagcaga
MA0024.2	E2F1	10.7798	0.930201137	1684	1694	+	aaagcgggaaa
MA0024.1	E2F1	10.4439	0.925718898	1687	1694	-	tttccgc
MA0024.2	E2F1	3.37837	0.818848324	1694	1704	+	aacgctcgaac
MA0024.1	E2F1	8.83194	0.870250556	1719	1726	+	tttggggc
MA0024.3	E2F1	6.80332	0.802911375	1719	1730	+	tttggggccacc
MA0024.2	E2F1	3.42453	0.819542695	1719	1729	-	gtggcccaaaa
MA0024.2	E2F1	5.48272	0.850507706	1781	1791	+	caggcggctgg
MA0024.2	E2F1	3.97949	0.82789194	1872	1882	+	agaacgcgaac
MA0024.2	E2F1	6.17614	0.860940035	1910	1920	-	ggcgcgggagc
MA0024.2	E2F1	3.74652	0.824387077	1912	1922	-	caggcgcggga
MA0024.2	E2F1	6.80057	0.870334447	1919	1929	-	ggggctgcagg
MA0024.2	E2F1	5.63652	0.852821542	1978	1988	+	gaggcccagg
MA0024.2	E2F1	5.71957	0.854071075	1988	1998	+	ggggcggccgg

Supplementary Figure1. Putative miRNA binding site in TMPO-AS1

Basic information for lncRNA:NONHSAT030138.2

lncRNA ID [NONHSAT030138.2](#)
Alias [TMPO-AS1:1](#), [ENST00000548760](#), [ENST00000548760.2](#), [RP11-181C3.2-001](#), [OTTHUMT00000407972.3](#)
Position [chr12:98512972-98516422\[-\]](#)
Structure 
Sequence 
Gene [NONHSAG012025.2](#)
Gene Alias [TMPO-AS1](#), [ENSG00000257167](#), [RP11-181C3.2](#), [ENSG00000257167.2](#), [OTTHUMG00000170209.3](#), [TMPO-AS1](#)

miRNAs bind to lncRNA:NONHSAT030138.2

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