

Table S2

Gene description	Symbol	Species	Accession Number	Motif position in 5'-UTR ¹	Motif Length	QGRS Mapper Motif ²	QGRS Mapper score ³	Percent inhibition ⁴	PubMed ID
Zic family member 1	ZIC1	human	NM_003412.3	678	23	<u>GGGGGGGGCGGG</u> <u>GGAGGCCGGGG</u>	58	74%	18515550
ADAM metalloproteinase domain 10	ADAM10	human	NM_001110.3	68	18	<u>GGGACGGGTAGG</u> <u>GGCGGG</u>	42	64%	22065584
Cyclin D3	CCND3	human	NM_001760.4	65	20	<u>GGGCGGCGGGCG</u> <u>GGCTGGGG</u>	39	53%	22858673
Matrix metalloproteinase 16	MMP16	human	NM_005941.4	213	17	<u>GGGAGGGAGGGA</u> <u>GAGGG</u>	40	55%	19397366
Alpha synuclein	SNCA	human	NM_000345.3	2	20	<u>GGAGAAGGAGAA</u> <u>GGAGGAGG</u>	21	30%	
Alpha synuclein	SNCA	human	NM_000345.3	26	11	<u>GGAGGAGGAGG</u>	21	29%	
Alpha synuclein	SNCA	human	NM_000345.3	53	18	<u>GGGGCCCAAGAA</u> <u>GGGGG</u>	12	36%	

¹Motif location from start of 5'-UTR.

²Predicted motif of G-quadruplex forming sequence according to QGRS Mapper algorithm; no overlaps included, see Kikin et al., 2006 for details.

³The QGRS Mapper scoring system evaluates a quadruplex forming G-rich sequences for its likelihood to form a stable G-quadruplex. Higher scoring sequences will make better candidates for G-quadruplex.

⁴Percent inhibition of translation based on G-quadruplex mutagenesis studies using the psiCHECK2 Dual-luciferase reporter assay system.