

Table S2: 5'UTR variants

Variant	TF Name	TF Family	TF Class	JASPAR ID	TFBS Position (hg19)	TFBS Sequence	Strand	Count: A/ C/ G/ T	%A/ %C/ %G/ %T	Score: ref/alt	Score Change	Score%: ref/alt	Score% Change
MSH6* Chr2:48010297:G>T NM_000179.2:c.-76G>T PhastCons/phyloP: 0.984/2.304	CTCF	More than 3 adjacent zinc finger factors	C2H2 zinc finger factors	MA0139.1	Chr2:48010291-48010309	CCGCCAGCAGGAGCCGCGC	+	40/528/334/11	4.4/57.8/36.6/1.2	28.47/27.76	0.98	40.67/39.66	0.98
	STAT3	STAT factors	STAT domain factors	MA0144.2	Chr2:48010287-48010297	TTTCCC GCCAG	-	7312/3801/8571/1936	33.8/17.6/39.6/9.0	17.01/16.39	0.96	40.49/39.03	0.96
	E2F7	E2F-related factors	Fork head / winged helix factors	MA0758.1	Chr2:48010286-48010299	ATTTC CCAGCAGCA	+	930/1/3/6	98.9/0.1/0.3/0.6	22.95/22.96	1.00	44.14/44.15	1.00
	E2F1	E2F-related factors	Fork head / winged helix factors	MA0024.3	Chr2:48010287-48010298	TTTCCC GCCAGC	+	510/80/58/182	61.4/9.6/7.0/21.9	17.01/17.39	1.02	36.97/37.8	1.02
RFC3 chr13:34392210:A>G NM_002915.3:c.-106A>G PhastCons/phyloP: 1.000/2.707	GABPA	Ets-related factors	Tryptophan cluster factors	MA0062.2	Chr13:34392201-34392211	CCGGTAGTGAC	+	264/262/415/49	26.7/26.5/41.9/4.9	18.14/18.44	1.02	45.35/43.92	0.97
	JUN	Jun-related factors	Basic leucine zipper factors (bZIP)	MA0488.1	Chr13:34392204-34392216	GTAGTGACGTCAC	+	20967/0/0/1	100.0/0.0/0.0/0.0	19.77/17.77	0.90	42.98/37.02	0.86
	CREM	CREB-related factors	Basic leucine zipper factors (bZIP)	MA0609.1	Chr13:34392206-34392215	AGTGACGTCA	+	999/0/0/0	100.0/0.0/0.0/0.0	16.75/14.75	0.88	46.51/38.8	0.83
	JUND	Jun-related factors	Basic leucine zipper factors (bZIP)	MA0491.1	Chr13:34392206-34392216	AGTGACGTCAC	+	38710/0/0/0	100.0/0.0/0.0/0.0	14.17/13.06	0.92	37.29/32.66	0.88
	ATF1	CREB-related factors	Basic leucine zipper factors (bZIP)	MA0604.1	Chr13:34392209-34392216	GACGTCAC	-	712/0/198/90	71.2/0.0/19.8/9.0	14.06/13.03	0.93	50.21/43.43	0.86
	MITF	bHLH-ZIP factors	Basic helix-loop-helix factors (bHLH)	MA0620.2	Chr13:34392208-34392225	TGACGTACAGAGATTTGG	-	9601/3103/4895/6354	40.1/13.0/20.4/26.5	26.59/26.2	0.99	41.55/39.7	0.96
	NR3C1	Steroid hormone receptors (NR3)	Nuclear receptors with C4 zinc fingers	MA0113.3	Chr13:34392206-34392222	AGTGACGTACAGAGATT	+	18207/8/9/10	99.9/0.0/0.0/0.1	17.63/15.91	0.90	30.4/26.52	0.87
	ATF7	Jun-related factors	Basic leucine zipper factors (bZIP)	MA0834.1	Chr13:34392205-34392218	TAGTGACGTCACGA	-	19329/77/16/25	99.4/0.4/0.1/0.1	22.24/20.25	0.91	44.47/38.94	0.88
	CREB1	CREB-related factors	Basic leucine zipper factors (bZIP)	MA0018.3	Chr13:34392206-34392217	AGTGACGTCAAG	+	8337/95/292/150	93.9/1.1/3.3/1.7	21.1/19.29	0.91	50.24/43.84	0.87
RFC4 chr3:186524157:G>A NM_002916.3:c.-90C>T PhastCons/phyloP: 0/1.013	AR	Steroid hormone receptors (NR3)	Nuclear receptors with C4 zinc fingers	MA0007.3	Chr3:186524145-186524161	AAGGACGAGATGCTCTC	-	3/3/5/2167	0.1/0.1/0.2/99.5	23.05/23.07	1.00	39.74/41.19	1.04