

**Supplement Table E. The potential transcriptional regulatory elements
were scored by software**

Cutted result table

>1: hg38_refGene_NM_001166120 range=chr1:119412931-119423039 5'pad=0 3'pad=0 strand

Pos	66	0.846	direct	CAGCCAAAAATGTAAGATGAGTGCAA
Pos	161	<u>0.942</u>	direct	<u>AATTCGTTATCACTAGATACCTTTCC</u>
Pos	533	0.928	indirect	TTAAGGCCACAGTGTGATAAAGAGTC
Pos	489	0.898	indirect	GAACACTGGTCAGTTGATACCAGCTG
Pos	236	0.896	direct	GCAATTGAGGTTTTGGATATATTGGG
Pos	382	0.812	indirect	ATCCACCTGGAGGGAGATCTATTTTA
Pos	358	0.934	direct	CACTCTCAGAGAGTTGATAATGGGCT
Pos	375	0.820	direct	TAATGGGCTAAAATAGATCTCCCTCC
Pos	459	0.806	direct	TGGTTTAAGTTCACAGATTGCAGATC
Pos	160	0.925	indirect	GGAAAGGTATCTAGTGATAACGAATT
Pos	545	0.822	direct	ACACTGTGGCCTTAAGATTGGATTTC
Pos	550	0.812	direct	GTGGCCTTAAGATTGGATTTCCTTC
Pos	120	0.810	indirect	TAATACAAGTGTGGGGATTTGTAGTT
Pos	582	0.933	direct	CTGGGAAGAATTAGAGATATAACCTA
Pos	85	0.948	indirect	ATGACTCTAATCATAGATATTTGCAC
Pos	22	0.835	indirect	AATTGTTGAACTGAAGATGCTATGAA

Summarized length of all tested sequences = 700

Sum = 16
