

Table S4. Probe information used in TCGA to analyze CREB3L1 gene methylation in human breast tumor samples.

#	IlmnID-probe set	Methylated	Location	Feature	Source Sequence	Strand
14	cg24825027	variably	(-772)-(-723)	promoter	CGTGCAGGCTTTAGTATAAGGCTGGAAGGATGGAATAGCTCCCTCATCA	F
1	cg12256550	variably	(-717)-(-668)	promoter	CGGGACAGTGGTTGGTGAAGCCTTAAATGCCAATGTTCCAGGAACACTG	F
4	cg24644201	variably	(-597)-(-548)	promoter	GTGGCTCGAGGAATCCTCTCTCCTTTTTAAAGAGACATCTGCAACTTCG	R
6	cg25626312	variably	(-507)-(-458)	promoter	CGGGAACCCCTGGCTGGCTAGCCCAGCTGGCCAAGGCGCCACGCCCCAC	R
5	cg20981182	variably	(-495)-(-446)	promoter	TCTCTGTGAAACCGGGAACCCCTGGCTGGCTAGCCCAGCTGGCCAAGGCG	R
7	cg07700369	variably	(-395)-(-346)	5' UTR	GGAGCCGGGGCGGGGAGCTAAGTGTCTCCCCGAGACTGGGTGGCTGCCG	R
8	cg03044069	variably	(-113)-(-64)	5' UTR	AGTCCAGAGCTCTGCCTGAGCGCTGGCAAACGGGCGGGGGCAGGTCCG	R
2	cg15917625	variably	238-287	intron 1	ATTCAAAGATTGAGCCCCAGGAGGGGCGCTTAGCTCCAACACATGTCTG	R
3	cg06859463	variably	553-602	intron 1	CGGGGAAGCCAGGCCAGAAATTTTCAGGGTGTACCCTGGCAGCCCCAGG	F
15	cg25963429	variably	1700-1749	intron 1	CGGCCGAGTTCATTGAGAAGAAAGCCCAACTCAGAGCTGCCAAGGGCCGA	R
17	cg16012690	variably	15146-15195	intron 1	AGGGCTGGGATTAGCTGTGTCTGGCACCTCCGAGGGCACAGCAGCCCACG	R
18	cg09709565	variably	16620-16669	intron 1	CGCCCCCTAGGCACAGCAGTACTCAGACTGAAGGCCCTTCAGCTTGAAA	F
10	cg02364610	variably	17373-17422	intron 1	CGGCCAGGCCATTTCTGCCTCGGCCCCAGACGCAGAAGGGGTCCCATGCA	F
11	cg14547067	variably	17491-17540	intron 1	GCAGCAGCCGGTGGCGGCGTGGAGGGCACCGGAGGAGTGCAGGGCTCGCG	R
13	cg03131732	variably	17812-17861	intron 1	AGACTTTTTCTATAGTCGTGCCAATATAAGCTCCTTCTCGGCTGTCACG	R
12	cg09896120	variably	17916-17963	intron 1	AGGGTTCTGCAGGGGTGAGCGTCTACAGGGTGCCTTTCAGGCAACG	R
19	cg20068058	variably	18148-18197	intron 1	GTCTGAGGTCTCCAAAATGGGCTTTCAGGGATGGGGCCAAGTGGATGCG	F
20	cg22902089	variably	18560-18609	intron 1	CGCCCACCGTCCACCCAGCACCTGAAGAAGCCCGGCGCAAAGAGGACCTG	F
16	cg07008193	variably	18816-18865	intron 1	CGGATCTGGGCTGGACTCCCTGAAGGCCTTGGCTCAGGCAGATGACCCAG	R
9	cg21690489	variably	30549-30598	intron 3	CGCTCCCATCTAGGGATTTTAAGATGCTGCTCATCCTGTGGAATCCCAGG	R
	cg00352031	no	(-1302)-(-1253)	5' UTR	CGGTATACACCCACAGGGCATCATGTGCTCACCTCCACTGTTCCAGTCT	R
	cg06588284	no	6015-6064	intron 1	TGCCAGGGTAACCCAGATGAAGAAAACACACTTGACCCTCCAGTCAATCG	R
	cg06884875	no	13340-13389	intron 1	CGGACCTGGTTCTAATCCTGGTTCTGCTATACACTGTGCAGGCTTTGGAC	R
	cg16795564	no	3393-3442	intron 1	CGGGTGTGCTGGGCAAACATCCTTGCAGCTTCTGCTGCTCCCCTCTGAG	R
	cg18857647	no	21524-21573	intron 1	CGCTCACCATTGTTATCTGCAAGGGTGAAGTCTCAGGATGGGATCAAAAAC	R
	cg04424721	yes; both tumor & normal	42751-42800	intron 10	TTTCTCTGGAATGGGAAGCTCCAGGAGGCAGGGGCACGAGGCGGATCCG	F

- number assigned to each region.

IlmnID-probe set - TCGA probe name.

Methylated - if region is methylated in normal and/or tumor breast tissue.

Location - location of the 50 bp probe region within the CREB3L1 gene, relative to the translational start site.

Feature - location of the 50 bp probe region with regards to the gene structure.

Source Sequence - sequence of the 50 bp region analyzed.

Strand - F = forward strand; R = reverse strand, to which the source sequence corresponds.