SUPPLEMENTAL TABLES

Tissue and cancer specific expression of DIEXF is

epigenetically mediated by an Alu repeat

NAME	SEQUENCE	LENGTH (bp)
CG rich region	F1:GTTTAGTTATTAAATATTAT	
	R1:CTTATACTACCATATTCTAT	
	F2:TGTTTGTATGTGTTTTTTATAT	291
	R2:ACAAAATACTTAAATCATAAAC	
	SeqF2:TGTTTGTATGTGTTTTTTATAT	
Aj2c1 (AluSq2)	F1:TAGATTTTAATGGGTAAAAGTA	
	R1:CAATAACTTTACAATATACTAC	
	F2:TGTGGTTGTATTAGTTAAGG	495
	R2:ACCAACATTTAAAAATACCTAA	
	SeqR2:ACCAACATTTAAAAATACCTAA	
CpGi	F1:ATATAAGTATAAAGTTTATGTTT	
	R1:TATCATAAAAAAAATACTCCTC	
	F2:GTTTTAGGGTTTTGAGAATAT	287
	R2:ATTAAATAACTAACTCTAACTC	
	SeqR2:ATTAAATAACTAACTCTAACTC	
Alu Sx	F1:GGTTTTTTTGTTGAGTTTGT	
	R1:ATATCTACAAAAAATTCCTAAA	
	F2:TGTAATTTTTTGTTAAGAGGTA	374
	R2:TCTCTAACCACAAAAATC	
	SeqF2:TGTAATTTTTTGTTAAGAGGTA	
Alu Sx II	F1:ATTTTTGTGTGGTTAGAGA	
	R1:CACTATATCCCACAAATATA	
	F2:TTTAGGAATTTTTTGTAGATAT	256
	R2:CACCCTAACTAACATAATAA	
	SeqF2:TTTAGGAATTTTTTGTAGATAT	
Alu Jo	F1:AATTAAGTGTATTAGTAGTT	
	R1:AAAATCACATAACAAACCC	
	F2:TGTTTTGTTATTAGTTAGGG	448
	R2:AAATCACACAAAACTCTCAT	
	SeqF2:TGTTTTGTTATTAGTTAGGG	

Supplemental Table 1. Primers for bisulfite sequencing PCR.

NAME	SEQUENCE	LENGTH (bp)
Exons 3_4	F: GACAGTATTGTAGATGATGC	212
	R: CTGAACAGTGACTCGTGT	
Exons 6_7	F: AGACGCCGAAGCCAGAAGTT	142
	R: CCTCGAGGAGGCTGATGAA	
Exons 8_9	F: TCATTGGTGGAGAAGGAGAG	155
	R: ATGTGAGTCCAGGGGTAGT	
Exons 11_12	F:CCTTCAAGGAGAGAAACAGT	151
	R:GGTGGCTCTCAGCATATTAC	
Exon 12-3'UTRa	F: GCAGGAAGTGGTATTTGGCA	478
	R: GGCTGGGGCAGAATAAGTTT	
3'UTRa	F:TCCTGTTTCCCTTCTGTGAG	169
	R:CCTGGAGCTCTGTTCTTTCT	
PPIA (Cyclophilin A)	F:CTCCTTTGAGCTGTTTGCAG	325
	R:CACCACATGCTTGCCATCC	
PSMC4	F:TGTTGGCAAAGGCGGTGGCA	182
	R:TCTCTTGGTGGCGATGGCAT	

Supplemental Table 2. Primers for RT-qPCR.

Supplemental Table 3. Northern blot probe sequences.

NAME	SEQUENCE	LENGTH cDNA (bp)	LENGTH DNA (bp)
A (exons 3-6)	F: TGAAGATGGTGGTAGCGATG	583	6077
	R: CTTCAGAGCAGTCCTTTCCG		
B (exons 7-9)	F:	393	3326
	GACAGCAAGAAGAAAATCATTGTG R: ATGTGAGTCCAGGGGTAGT		
C (exons 9-12)	F: CCAATGACAGGCTCTATCAG	435	8697
	R: GGTGGCTCTCAGCATATTAC		
D (exon 12-3'UTRa)	F: GCAGGAAGTGGTATTTGGCA	478	479
	R: GGCTGGGGCAGAATAAGTTT		
E (3'UTRa)	F: TCCTGTTTCCCTTCTGTGAG	169	169
	R: CCTGGAGCTCTGTTCTTTCT		
F (3'UTRa)	F: TGGAGTAGAGAAACCTGGA	418	418
	R: CCAAGTACAGAACCTGAACC		
G (3'UTRb)	F: GTCATTTGTCAGAGGAGGAA	189	189
	R: GGGCTTACAATTAACTTGCTG		
PPIA (Cyclophilin A)	F: CTCCTTTGAGCTGTTTGCAG	325	4988
	R: CACCACATGCTTGCCATCC		

Supplemental Table 4. siRNA sequences

NAME	TARGET SEQUENCE	LOCATION	STARTING POSITION
si <i>DIEXF</i> #1	CCACCTGGACTAAGACCAA	ORF (common to all transcripts)	840
si <i>DIEXF</i> #2	GCTACAGTCCAACAAGAAT	ORF (common to all transcripts)	2299
si <i>DIEXF</i> #3	GCTATTGTTTGCCCTATAT	3'UTR (specific for the long 8.5kb transcript)	7118
siCtrlª	MISSION siRNA Universal Negative Control#1 (Sigma-Aldrich)	non-targeting	

^a Non-targeting siRNA designed by Sigma-Aldrich with no homology to any known gene sequence and tested in vitro in human cells.

Supplemental Table 5. Primers for 3'/5' RACE.

NAME	SEQUENCE
UPM mix	Long: CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT Short: CTAATACGACTCACTATAGGGC
7R	GAAGAGCTGCACCACCCGCAAAGCA
3R	CCACACTGACATCGCTACCACCATC
12F	GGTCCTAGGCTCCCCTTACACCTCT
3'UTRaF	GGCCACGTGGACCTGCACTGTTCTC

Supplemental Table 6. Primers for ChIP.

NAME	SEQUENCE	LENGTH (pb)
CG rich region	F:CCAGCCTCTCCGAATCTAA	234
	R:GCTTAAATCATAAGCCGCAGAA	
Aj2c1 (AluSq2) 5'	F:TTGCATCAGTTAACGTTTTTCT	172
	R:ATATCAACCAACATTTAAGGGT	
Aj2c1 (AluSq2) 3'	F:TTGCATCAGTTAACGTTTTTCT	199
	R:ATATCAACCAACATTTAAGGGT	
CpGi	F:AACACTAGTGAACGAACT	153
	R:AGGAAGTTGTACCAGTCAA	
CpGi I	F:TTGACTGGACAACTTCCT	229
	R:CCAAACTCGAGGATACAT	
CpGi II	F:AGTCGCCAGAGATGTATC	180
	R:TGCCTCTTAGCAGGAAAT	
Alu Sx I	F:TAATTTCCTGCTAAGAGGCA	372
	R:TCTCTGACCACAAAAATC	
Alu Sx II	F:CGGATTTTTGTGTGGTCAGA	278
	R:ACCCTAGCTAACATGGTGA	
Alu Jo	F:ACTACTTTGGGCTGCTTTGT	350
	R:GAGCGGTGGCTCATATCT	
GAPDH	F:TTGCAACCGGGAAGGAAA	120
	R:TAGCCTCCGTCCAGCTGACTT	
16CEN	F: CAGTTTGCCAGATAGTCTCTTT	211
	R: GAGACATTTGGGAAGGTCACTGAAT	
CPLX2	F: CCTCCAGACCCCACCCATCC	173
	R: AGGCTTCCCCGCGGGCTTCTCAG	
DRD1	F: GAGGACGCCCCGGTGAGTGC	245
	R: GCCGGCCGTTCTAGGAGTTGGTT	