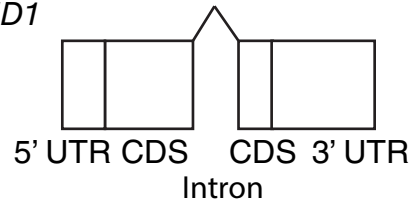


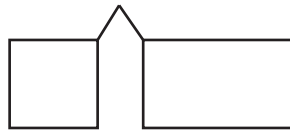
ID1



iCreERT2 cDNA

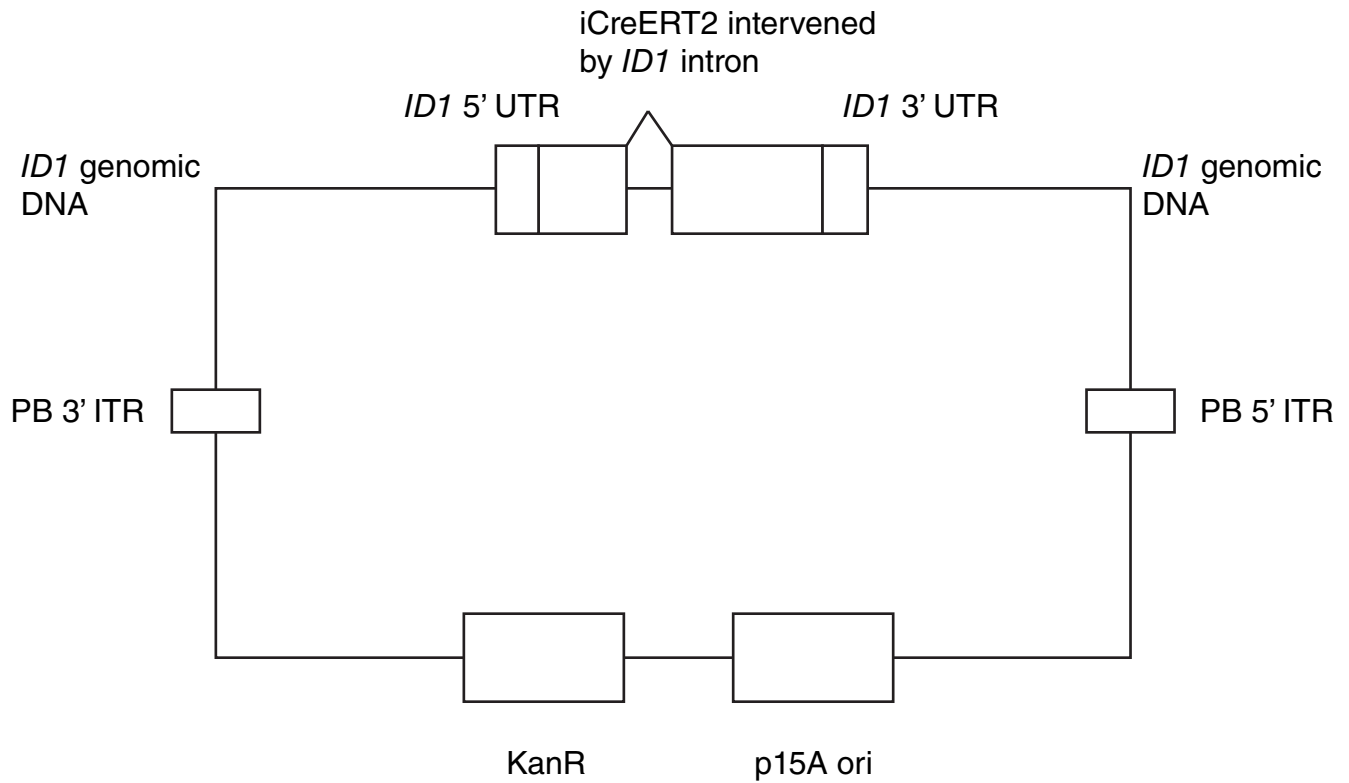


Seamlessly splice in
ID1 intron



iCreERT2 with *ID1* intron

Seamlessly clone into a p15A-PB
plasmid with *ID1* genomic DNA



Intron splice site prediction

NetGene2 World Wide Web Server
Center for Biological Sequence Analysis
The Technical University of Denmark
DK-2800 Lyngby, Denmark

***** NetGene2 v. 2.4 *****

The sequence: sequence1 has the following composition:

Length: 2222 nucleotides.

22.0% A, 28.1% C, 28.6% G, 21.3% T, 0.0% X, 56.7% G+C

Donor splice sites, direct strand

pos	5'->3'	phase	strand	confidence	5'	exon	intron	3'
597	2	+		0.95	ACATTGGCAG	^	GTGAGATCCA	H
1245	0	+		0.58	TGGGGCCATG	^	GTGAGGCTGC	
1380	0	+		0.46	CGACCAGATG	^	GTCAGTGCCT	

Donor splice sites, complement strand

pos	3'->5'	pos	5'->3'	phase	strand	confidence	5'	exon	intron	3'
1478		745	2	-		0.37	TGTCGTCCAG	^	GTGGTCAGT	
1470		753	1	-		0.55	AGGTTGGTCA	^	GTAAGCCCAT	
1435		788	0	-		0.55	GAAGGGTCTG	^	GTAGGATCAT	
1088		1135	2	-		0.55	ACCAGGCCAG	^	GTATCTCTGC	
1046		1177	0	-		0.70	AGATCAGGCG	^	GTGGGTGGCC	
950		1273	2	-		0.34	GGCAGAACAG	^	GATAGTTGTTG	
701		1522	1	-		0.34	GCATAGCCAG	^	GTACCCGCAA	
423		1800	0	-		0.71	CTTGGTCAAA	^	GTCAGTGCCT	
231		1992	0	-		0.71	TGGCTTGACG	^	GTACAGGAGG	
222		2001	0	-		0.46	GGTACAGGAG	^	GTAGTCCCTC	

Acceptor splice sites, direct strand

pos	5'->3'	phase	strand	confidence	5'	intron	exon	3'
149	2	+		0.25	CTGTGTGCAG	^	ATCCTGGGCT	
835	2	+		1.00	GTTTTCACAG	^	GACCAAGACC	H
842	0	+		0.34	CAGGACCAAG	^	ACCTGTGTGT	
858	1	+		0.40	GTGTCCACAG	^	CTGGTGTGGA	
1587	1	+		0.07	GCCTGGCTAG	^	AGATCCTGAT	
1589	0	+		0.07	CTGGCTAGAG	^	ATCCTGATGA	
1669	2	+		0.33	TCTTGGACAG	^	GAACCAAGGA	
1825	2	+		0.18	TTCTGTCCAG	^	CACCTGAAG	
1835	0	+		0.07	CACCTGAAG	^	TCTCTGAAG	
1978	2	+		0.53	CCCACATCAG	^	GCACATGAGT	

Acceptor splice sites, complement strand

pos	3'->5'	pos	5'->3'	phase	strand	confidence	5'	intron	exon	3'
2049		174	2	-		0.15	CCAGCAGCAG	^	GTCATAGAGG	
2040		183	2	-		0.07	GGTCATAGAG	^	GGGCACCACG	
2007		216	0	-		0.83	TGCTGTACAG	^	ATGCTCCATG	
1967		256	1	-		0.07	GATGTGGGAG	^	AGGATGAGGA	
1776		447	2	-		0.17	TAGATTTGAG	^	GCACACAAAC	
1752		471	2	-		1.00	CTCCCTGCAG	^	ATTTCATCATG	H
1732		491	1	-		0.07	CGGAACCGAG	^	ATGATGTAGC	
1605		618	0	-		0.07	GCCAGACGAG	^	ACCAATCATC	
1593		630	0	-		0.07	CAATCATCAG	^	GATCTCTAGC	
1584		639	0	-		0.07	GGATCTCTAG	^	CCAGGCACAT	
1580		643	1	-		0.19	CTCTAGCCAG	^	GCACATTCTA	
1511		712	0	-		0.32	CTTCGCCAG	^	TTGATCATGT	
1279		944	1	-		0.43	TCTCCAGCAG	^	ATGGCTCGAG	
1181		1042	0	-		0.07	ATTGGTCCAG	^	CCACGAGCCT	
1174		1049	1	-		0.17	CAGCCACCAG	^	CCTGCATGAT	
1159		1064	1	-		0.23	ATGATTTAG	^	GGATGGACAC	
1144		1079	1	-		0.18	GACACACCAG	^	CCCTGGCCAT	
859		1364	0	-		0.15	TCCACACCAG	^	CTGTGGACAC	
720		1503	1	-		0.31	GGCTCCTTAG	^	GCACCCCGC	
580		1643	2	-		0.19	TGTGGATCAG	^	CATTCTCCCA	
555		1668	1	-		0.19	GGTGCGGGAG	^	ATGTCCTTCA	
343		1880	2	-		0.43	TCATCACCCAG	^	GGACACAGCA	
203		2020	1	-		0.33	ACATCCTCAG	^	GTTTCAGCAGG	
172		2051	2	-		0.96	TGTTGTTTCA	^	GTTTCAGCAGG	
162		2061	0	-		0.34	CTTGACCCAG	^	GCAGCCAGG	
158		2065	1	-		0.20	CACCAGGCAG	^	CCCAGGATCT	
153		2070	0	-		0.19	GGCAGCCCAG	^	GATCTGCACA	
140		2083	1	-		0.19	CTGCACACAG	^	ACAGGAGCAT	
136		2087	2	-		0.18	ACACAGACAG	^	GAGCATCTTC	
133		2090	2	-		0.18	CAGACAGGAG	^	CATCTTCCAG	

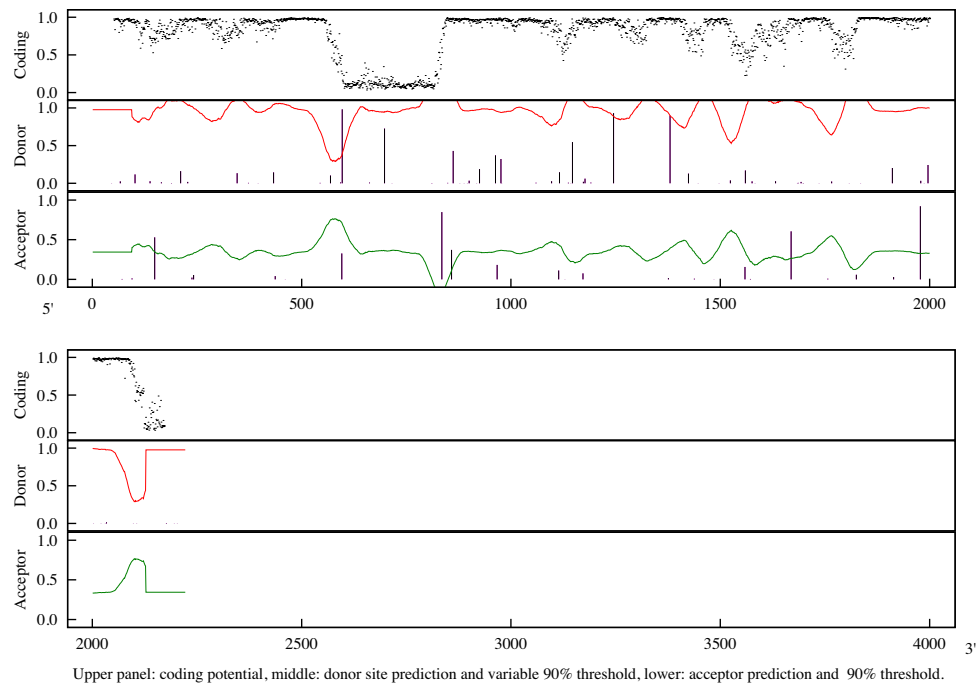
CUTOFF values used for confidence:

Highly confident donor sites (H): 95.0 %
Nearly all true donor sites: 50.0 %

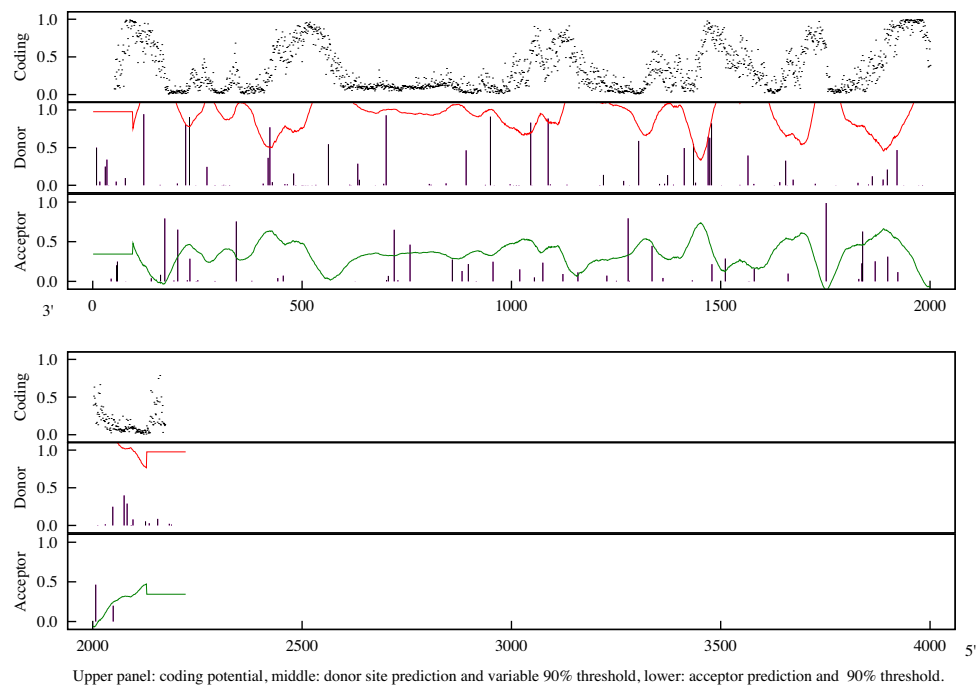
Highly confident acceptor sites (H): 95.0 %
Nearly all true acceptor sites: 20.0 %

Intron splice site prediction

NetGene2 H. sapiens output for sequence: sequence1 + strand. nucleotides: 2222

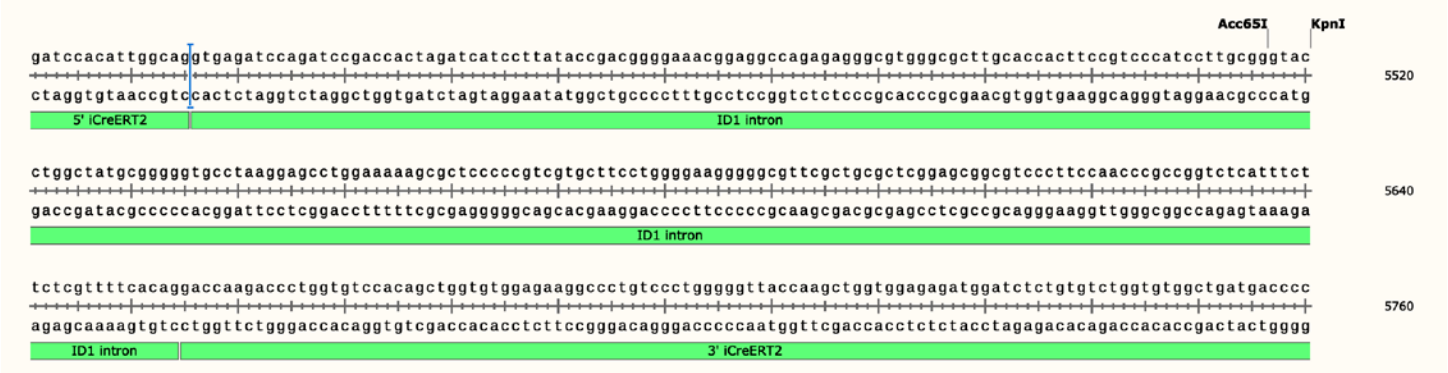


NetGene2 H. sapiens output for sequence: sequence1 - strand. nucleotides: 2222



Intron splice sites

ACATTGGCAG



GACCAAGACC