Table legends: comparisons between the different categories of 5'ss. A, authentic 5'ss, C; cryptic 5'ss; M, mutant 5'ss; P1 and P2, pseudo 5'ss. S&S represents the score of the various 5'ss as calculated by the Shapiro and Senapathy matrix (33,34). S&S (A–C) refers to the difference between the S&S scores of the pairs of A and C 5'ss. Dist (A–C) is the distance in nucleotides between the pairs of A and C 5'ss. Numbers in bold are those that are an exception of the general trend (see text for details). Underlined numbers in Table S1 indicate first exons. In the 'S&S (M)' columns, N/A (not applicable) refers to those mutations that eliminate most of the 5'ss, hence their S&S score cannot be calculated. Averages (AVG) and standard deviations (SD) of every group of numbers are shown at the bottom of each table. In Table S6, Splice Id indicates the unique identifier number for alternative splicing events that is provided by the ASAP database. Alt 5'ss: alternative 5'ss.

Gene	Exon	Seq A	Seq C	S&S (A)	S&S (C)	S&S (A-C)	Dist (A-C)	DG (A)	DG (C)	DG(A)-DG(C)	Exon length A	Exon length C
ABCD1	1	GAGGTGGGG	CAGGTTGGG	79.05	75.74	3.31	9	-11.2	-11.8	**0.6**	**1286**	**1295**
APOB	24	AAGGTAAAA	AAAGTAAAT	79.93	73.47	6.46	40	-9.8	-4.4	-5.4	146	186
AR	4	CTGGTAAGG	CAGGTGTAG	88.13	67.88	20.25	-123	-9.8	-10.7	**0.9**	**288**	165
ATM	45	CAGGTAACT	AGAGTGACT	86.38	63	23.38	71	-11.9	-4.5	-7.4	218	**289**
		CAGGTAACT	TTGGTCTTT	86.38	53.92	32.46	79	-11.9	-5.5	-6.4	218	**297**
BRCA1	5	AAGGTATAT	TATGTAAGA	74.52	78.01	**-3.49**	-22	-8.9	-7.5	-1.4	78	56
	16	TTTGTGAGT	TAGGTATTG	72.77	66.66	6.11	69	-8.8	-9.9	1.1	**311**	**380**
CFTR	4	AAGGTAATA	ATTGTGAGG	79.93	71.9	8.03	-93	-9.8	-6.6	-3.2	216	123
	20	CAGGTGAGC	AAGGCAACT	91.27	68.06	23.21	29	-14.1	-6.3	-7.8	156	185
COL1A1	8	CCTGTGAGT	TTGGTAAGA	76.78	82.72	**-5.94**	96	-8.8	-9.8	**1**	**45**	141
		CCTGTGAGT	CTGGTGAGC	76.78	83.76	**-6.98**	186	-8.8	-9.9	**1.1**	**45**	231
	34	AAGGTGAGG	CTGGTGACA	91.62	70.33	21.29	-8	-12	-7.8	-4.2	108	100
COL3A1	16	CCTGTAAGT	GGAGTAAGC	79.93	71.9	8.03	23	-8.7	-6.5	-2.2	99	122
	20	CGCGTAAGT	CTGGTTATT	79.58	69.1	10.48	24	-10.1	-5.5	-4.6	54	78
	42	GATGTGAGT	CAGGTAGAA	81.5	70.5	11	30	-8.8	-11.6	**2.8**	108	138
COL6A1	3	GGGGTGAGT	CAAGTACTT	86.21	63.35	22.86	-66	-14.2	-5.6	-8.6	201	135
COL7A1	3	AAGGTGATC	TCCGTGAGC	76.61	66.14	10.47	-104	-9.9	-6.6	-3.3	160	56
	73	AGGGTGAGG	CTGGTATTC	84.11	62.3	21.81	-62	-12	-6.8	-5.2	201	139
	95	GTGGTGAGT	GGGGTCAGT	86.21	79.75	6.46	-7	-12.1	-11.9	-0.2	72	65
C3	18	TGGGTAAGG	GAAGTGAGT	83.76	81.84	1.92	-61	-12.2	-8.8	-3.4	109	**48**
CYP19	6	TGTGTAAGT	CAGGTAACT	75.91	86.38	**-10.47**	87	-9	-11.9	**2.9**	115	202
CYP27A1	6	GCGGTAGGA	GTGGTGGGT	73.29	75.91	**-2.62**	-89	-9.5	-11.3	**1.8**	167	78
DMD	64	GCTGTAAGT	AAAGTAGGT	76.78	76.96	**-0.18**	57	-8.7	-8.4	-0.3	75	132
	26	AAGGTAAAA	GAGGTTGAT	79.93	63.17	16.76	116	-9.8	-7.6	-2.2	171	**287**
FAH	12	CCGGTGAGT	GAGGTGGGT	89	83.42	5.58	105	-12.1	-13.4	**1.3**	102	207
FBN1	46	TAGGTGCGT	GAAGTCAGT	81.5	75.39	6.11	33	-11.8	-6.5	-5.3	117	150
F5	10	CAGGTATTT	TCTGTAAGA	75.39	70.15	5.24	-35	-11	-6.5	-4.5	215	180
FGA	4	GAGGTAAGT	AAAGTACAG	96.85	58.11	38.74	-66	-14.1	-3.5	-10.6	146	80
		GAGGTAAGT	AATGTTAGA	96.85	71.9	24.95	-36	-14.1	-4.3	-9.8	146	110
		GAGGTAAGT	GGAGTTAAG	96.85	49.73	47.12	-1	-14.1	-2.2	-11.9	146	145
		GAGGTAAGT	TAAGTATTA	96.85	72.94	23.91	4	-14.1	-4.5	-9.6	146	150
F7	7	TGGGTGGGT	TGGGTGGGT	74.69	74.69	0	37	-13.7	-13.7	0	124	161
GCK	4	AAGGTGGGC	CCTGTGAGG	80.1	72.42	7.68	-24	-11.2	-6.6	-4.6	120	96
GHV	2	TTTGTAAGC	TGGGTAATG	70.33	69.98	0.35	12	-6.5	-10.1	**3.6**	161	173
HBA2	1	GAGGTGAGG	GGGGTAAGG	89.35	84.99	4.36	-49	-12	-11.9	-0.1	132	83
HBB	1	CAGGTTGGT	AAGGTGAAC	80.1	76.61	3.49	-38	-14	-9.9	-4.1	135	97
		CAGGTTGGT	GTGGTGAGG	80.1	81.84	**-1.74**	-16	-14	-9.9	-4.1	135	119
		CAGGTTGGT	AAGGTTACA	80.1	70.5	9.6	13	-14	-7.6	-6.4	135	148
	2	AGGGTGAGT	AAGGTGAAG	88.48	77.83	10.65	-135	-14.2	-9.9	-4.3	223	88
		AGGGTGAGT	ATGGTTAAG	88.48	63.87	24.61	47	-14.2	-5.5	-8.7	223	**270**
HEXA	9	GACGTGAGG	AGGGTGGGT	76.43	78.18	**-1.75**	17	-6.6	-13.4	**6.8**	87	104
HEXB	8	TTGGTAAGA	AATGTTGGT	82.72	67.01	15.71	-4	-9.8	-6.5	-3.3	181	177
HMGCL	7	ACGGTAAGC	GGGGTATTT	85.68	64.74	20.94	78	-9.8	-8.9	-0.9	126	204
HPRT	1	GTGGTGAGC	CAGGTGGCG	80.62	68.58	12.04	49	-9.9	-11.2	**1.3**	112	161
	5	GAAGTAAGT	AAGGTAAGC	84.99	93.54	**-8.55**	67	-8.7	-11.9	**3.2**	**18**	85
IDS	7	ATGGTAAGC	CTGGTGAGT	86.03	89.35	**-3.32**	22	-9.8	-12.1	**2.3**	127	149
ITGB2	7	TTCGTAAGT	AGGGTGGGG	75.21	73.82	1.39	64	-8.7	-11.2	**2.5**	156	220
		TTCGTAAGT	GAGGTATAG	75.21	67.88	7.33	298	-8.7	-8.9	**0.2**	156	**454**
ITGB3	4	GATGTGAGT	CAGGTGTGG	81.5	81.67	**-0.17**	27	-8.8	-10.7	**1.9**	163	190
KRT5	1	AAGGTGAGC	AGGGTGAGG	90.4	84.11	6.29	-66	-12	-12	0	**946**	**880**
LDLR	12	GAGGTGTGG	TACGTACGA	78.53	66.31	12.22	11	-8.6	-4.5	-4.1	140	151
LPL	2	ACGGTAAGG	ATGGTGATC	86.91	69.1	17.81	-18	-9.8	-7.8	-2	161	143
		ACGGTAAGG	GAGGTATCC	86.91	66.84	20.07	42	-9.8	-8.9	-0.9	161	203
		ACGGTAAGG	CAGGTGGGA	86.91	81.15	5.76	142	-9.8	-13.3	**3.5**	161	**303**
		ACGGTAAGG	GAGGTTGGT	86.91	76.96	9.95	246	-9.8	-11.9	**2.1**	161	**407**
		ACGGTAAGG	AGAGTGAGG	86.91	72.25	14.66	382	-9.8	-6.6	-3.2	161	**543**
MTHFR	4	CAGGTGAGG	AAGGCATGC	92.49	65.27	27.22	-57	-14.1	-5.4	-8.7	194	137
NF1	27b	GAGGTAAGA	AACGTTAAG	91.44	58.46	32.98	-69	-11.9	-2.2	-9.7	111	**42**
	28	AAAGTAAGT	AAGGTATTC	87.26	68.93	18.33	-54	-8.7	-8.9	**0.2**	**433**	**379**
NF2	7	CGGGTGTGT	GATGTACGG	78.53	69.28	9.25	-28	-12.2	-3.5	-8.7	76	**48**
		CGGGTGTGT	ACGGTGTGA	78.53	71.9	6.63	-23	-12.2	-6.5	-5.7	76	53
	12	GAGGTGAGG	AAGGTGCTG	89.35	66.84	22.51	-53	-12	-8.6	-3.4	218	165
		GAGGTGAGG	GAGGTGCTG	89.35	64.57	24.78	-38	-12	-8.6	-3.4	218	180
PBGD	1	GCGGTGAGT	CAGGTTGCC	85.86	60.9	24.96	67	-12.1	-9.7	-2.4	60	127
	10	CAGGTAGGG	CGGGTGGGG	85.34	74.69	10.65	-9	-13.7	-12.6	-1.1	114	105
PGK1	4	AAGGTAGGA	GGGGTGAGG	83.42	81.84	1.58	30	-11.6	-12	**0.4**	145	175
PKD1	43	AAGGTGAGG	CAGGTGGCG	91.62	68.58	23.04	-66	-12	-11.2	-0.8	**291**	225
PTEN	4	GAGGTAGGT	CAGGTATGA	86.56	83.76	2.8	4	-13.8	-11	-2.8	44	48
	7	AAGGTTTGT	CATGTAAGG	78.7	83.42	**-4.72**	75	-9.8	-8.6	-1.2	167	242
PYGM	14	ACCGTGAGT	CAGGTGAAG	75.21	78.7	**-3.49**	-67	-8.8	-12	**3.2**	148	81
RPGR	5	CTGGTGAGA	CATGTAATT	83.94	73.99	9.95	-76	-9.9	-6.5	-3.4	159	83
SERPINA1	2	AAGGTAAGG	AGGGTACTC	94.76	61.25	33.51	-84	-11.9	-8.9	-3	**650**	**566**
TP53	5	ATGGTGAGC	GAGGTTGTG	82.89	58.81	24.08	-46	-9.9	-7.6	-2.3	184	138
	6	GAGGTCTGG	CTGGTTTGC	72.07	66.49	5.58	5	-7.6	-5.5	-2.1	113	118
TSC2	37	AAGGTGAGT	CCGGTGAGG	95.98	84.64	11.34	-29	-14.2	-9.9	-4.3	140	111
UGT1A1	1	CAGGTGTGT	GAGGTGACT	86.03	80.1	5.93	-141	-12.9	-9.9	-3	**879**	**738**
AVG=				82.96	72.38	11.22	10.92	-10.8	-8.6	-2.4	200.03	201.58
SD=				6.31	8.53	11.78	88.93	2.0	2.9	3.9	217.44	195.18
AVG (Abs)=							62.58			AVG. (int ex)=	160.22	174.21
										SD. (int ex)=	98.88	111.56

Table S1: Comparison between Authentic (A) and Cryptic (C) 5'ss.

Gene	Exon	Seq A	Seq M	S&S (A)	S&S (M)	S&S (A-M)
ABCD1	1	GAGGTGGGG	GAAGTGGGG	79.05	67.19	11.86
APOB	24	AAGGTAAAA	AAGGCAAAA	79.93	62.47	17.46
AR	4	CTGGTAAGG	CTGTTAAGG	88.13	70.68	17.45
ATM	45	CAGGTAACT	CAGATAACT	86.38	68.93	17.45
BRCA1	5	AAGGTATAT	AGGGTATAT	74.52	67.01	7.51
	16	TTTGTGAGT	TTTGTGAGC	72.77	67.19	5.58
CFTR	4	AAGGTAATA	AAGTTAATA	79.93	62.47	17.46
	20	CAGGTGAGC	CACGTGAGC	91.27	78.35	12.92
COL1A1	8	CCTGTGAGT	CCTATGAGT	76.78	59.33	17.45
		CCTGTGAGT	CCTGTGAAT	76.78	63	13.78
	34	AAGGTGAGG	-	91.62	N/A	N/A
COL3A1	16	CCTGTAAGT	CCTATAAGT	79.93	62.47	17.46
	20	CGCGTAAGT	CGCATAAGT	79.58	62.12	17.46
	42	GATGTGAGT	GATATGAGT	81.5	64.04	17.46
COL6A1	3	GGGGTGAGT	GGGATGAGT	86.21	68.76	17.45
COL7A1	3	AAGGTGATC	AGGGTGATC	76.61	69.1	7.51
	73	AGGGTGAGG	AGGGTGAGG	84.11	84.11	**0**
	95	GTGGTGAGT	GTAGTGAGT	86.21	74.34	11.87
C3	18	TGGGTAAGG	TGGATAAGG	83.76	66.31	17.45
CYP19	6	TGTGTAAGT	TGTGCAAGT	75.91	58.46	17.45
CYP27	6	GCGGTAGGA	GAGGTAGGA	73.29	81.15	**-7.86**
		GCGGTAGGA	GCAGTAGGA	73.29	61.43	11.86
DMD	64	GCTGTAAGT	GCTGTAACT	76.78	63.17	13.61
	26	AAGGTAAAA	AAGGGAAAA	79.93	62.47	17.46
FAH	12	CCGGTGAGT	CCGGTGAAT	89	75.21	13.79
FBN1	46	TAGGTGCGT	TAGATGCGT	81.5	64.04	17.46
F5	10	CAGGTATTT	CATGTATTT	75.39	63.17	12.22
FGA	4	GAGGTAAGT	GAGTTAAGT	96.85	79.4	17.45
F7	7	TGGGTGGGT	TGGGTGGAT	74.69	60.9	13.79
		TGGGTGGGT	TGGGTGGGT	74.69	74.69	**0**
		TGGGTGGGT	TGGGTACCA	74.69	58.11	16.58
GCK	4	AAGGTGGGC	-	80.1	N/A	N/A
GHV	2	TTTGTAAGC	TTTATAAGC	70.33	52.87	17.46
HBA2	1	GAGGTGAGG	GAGGCTCCC	89.35	39.61	49.74
HBB	1	CAGGTTGGT	CACGTTGGT	80.1	67.19	12.91
		CAGGTTGGT	CAGATTGGT	80.1	62.65	17.45
		CAGGTTGGT	CAGTTTGGT	80.1	62.65	17.45
		CAGGTTGGT	CAGGCTGGT	80.1	62.65	17.45
		CAGGTTGGT	CAGGTTGAT	80.1	66.31	13.79
		CAGGTTGGT	CAGGTTGCT	80.1	66.49	13.61
		CAGGTTGGT	CAGGTTGTT	80.1	66.31	13.79
		CAGGTTGGT	CAGGTTGGC	80.1	74.52	5.58
	2	AGGGTGAGT	AGGGTGTCT	88.48	64.04	24.44
HEXA	9	GACGTGAGG	GACATGAGG	76.43	58.98	17.45
HEXB	8	TTGGTAAGA	TTGGTAACA	82.72	69.1	13.62
HMGCL	7	ACGGTAAGC	ACGCTAAGC	85.68	68.23	17.45
HPRT	1	GTGGTGAGC	GTGGTGAAC	80.62	66.84	13.78
		GTGGTGAGC	GTGGTGATC	80.62	66.84	13.78
		GTGGTGAGC	-	80.62	N/A	N/A
	5	GAAGTAAGT	GAAGGAAGT	84.99	67.53	17.46
		GAAGTAAGT	GAAGTGTGT	84.99	71.02	13.97
		GAAGTAAGT	GAAGTAAAT	84.99	71.2	13.79
		GAAGTAAGT	GAATAAGTT	84.99	26	58.99
IDS	7	ATGGTAAGC	ATTTTAAGC	86.03	56.36	29.67
ITGB2	7	TTCGTAAGT	TTCATAAGT	75.21	57.76	17.45
ITGB3	4	GATGTGAGT	GATATGAGT	81.5	64.04	17.46
KRT5	1	AAGGTGAGC	AAGATGAGC	90.4	72.94	17.46
LDLR	12	GAGGTGTGG	GAGGCGTGG	78.53	61.08	17.45
LPL	2	ACGGTAAGG	ACGATAAGG	86.91	69.45	17.46
MTHFR	4	CAGGTGAGG	CAGATGAGG	92.49	75.04	17.45
NF1	27b	GAGGTAAGA	-	91.44	N/A	N/A
	28	AAAGTAAGT	AAAATAAGT	87.26	69.8	17.46
NF2	7	CGGGTGTGT	-	78.53	N/A	N/A
		CGGGTGTGT	CGGGTGTAT	78.53	64.74	13.79
	12	GAGGTGAGG	-	89.35	N/A	N/A
		GAGGTGAGG	GAGATGAGG	89.35	71.9	17.45
PBGD	1	GCGGTGAGT	GCGATGAGT	85.86	68.41	17.45
		GCGGTGAGT	GCGGAGAGT	85.86	68.41	17.45
		GCGGTGAGT	GCGGTGACT	85.86	72.25	13.61
		GCGGTGAGT	GCGGTTAGT	85.86	79.4	6.46
	10	CAGGTAGGG	CATGTAGGG	85.34	67.88	17.46
PGK1	4	AAGGTAGGA	AAGTTAGGA	83.42	65.96	17.46
PKD1	43	AAGGTGAGG	Not specified	91.62	N/A	N/A
PTEN	4	GAGGTAGGT	GAGGCAGGT	86.56	69.1	17.46
	7	AAGGTTTGT	AAGATTTGT	78.7	61.25	17.45
PYGM	14	ACCGTGAGT	ACCATGAGT	75.21	57.76	17.45
RPGR	5	CTGGTGAGA	CTGTTGAGA	83.94	66.49	17.45
SERPINA1	2	AAGGTAAGG	AAGTTAAGG	94.76	77.31	17.45
TP53	5	ATGGTGAGC	ATGGTGACC	82.89	69.28	13.61
	6	GAGGTCTGG	GAAGTCTGG	72.07	60.2	11.87
		GAGGTCTGG	GAGATCTGG	72.07	54.62	17.45
TSC2	37	AAGGTGAGT	AAGGATGAG	95.98	43.63	52.35
UGT1A1	1	CAGGTGTGT	CAGCTGTGT	86.03	68.58	17.45
AVG=				82.96	65.59	16.40
SD=				6.31	8.71	9.20

Table S2: Comparison between Authentic (A) and Mutant (M) 5'ss.

Gene	Exon	Seq M	Seq C	S&S (M)	S&S (C)	S&S (C-M)
ABCD1	1	GAAGTGGGG	CAGGTTGGG	67.19	75.74	8.55
APOB	24	AAGGCAAAA	AAAGTAAAT	62.47	73.47	11.00
AR	4	CTGTTAAGG	CAGGTGTAG	70.68	67.88	**-2.80**
ATM	45	CAGATAACT	AGAGTGACT	68.93	63	**-5.93**
		CAGATAACT	TTGGTCTTT	68.93	53.92	**-15.01**
BRCA1	5	AGGGTATAT	TATGTAAGA	67.01	78.01	11.00
	16	TTTGTGAGC	TAGGTATTG	67.19	66.66	**-0.53**
CFTR	4	AAGTTAATA	ATTGTGAGG	62.47	71.9	9.43
	20	CACGTGAGC	AAGGCAACT	78.35	68.06	**-10.29**
COL1A1	8	CCTATGAGT	TTGGTAAGA	59.33	82.72	23.39
		CCTATGAGT	CTGGTGAGC	59.33	83.76	24.43
		CCTGTGAAT	CTGGTGAGC	63	82.72	19.72
		CCTGTGAAT	CTGGTGAGC	63	83.76	20.76
	34	-	CTGGTGACA	N/A	70.33	N/A
COL3A1	16	CCTATAAGT	GGAGTAAGC	62.47	71.9	9.43
	20	CGCATAAGT	CTGGTTATT	62.12	69.1	6.98
	42	GATATGAGT	CAGGTAGAA	64.04	70.5	6.46
COL6A1	3	GGGATGAGT	CAAGTACTT	68.76	63.35	**-5.41**
COL7A1	3	AGGGTGATC	TCCGTGAGC	69.1	66.14	**-2.96**
	73	AGGGTGAGG	CTGGTATTC	84.11	62.3	N/A
	95	GTAGTGAGT	GGGGTCAGT	74.34	79.75	5.41
C3	18	TGGATAAGG	GAAGTGAGT	66.31	81.84	15.53
CYP19	6	TGTGCAAGT	CAGGTAACT	58.46	86.38	27.92
CYP27	6	GAGGTAGGA	GTGGTGGGT	81.15	75.91	**-5.24**
		GCAGTAGGA	GTGGTGGGT	61.43	75.91	14.48
DMD	64	GCTGTAACT	AAAGTAGGT	63.17	76.96	13.79
	26	AAGGGAAAA	GAGGTTGAT	62.47	63.17	0.70
FAH	12	CCGGTGAAT	GAGGTGGGT	75.21	83.42	8.21
FBN1	46	TAGATGCGT	GAAGTCAGT	64.04	75.39	11.35
F5	10	CATGTATTT	TCTGTAAGA	63.17	70.15	6.98
FGA	4	GAGTTAAGT	AAAGTACAG	79.4	58.11	**-21.29**
		GAGTTAAGT	AATGTTAGA	79.4	71.9	**-7.50**
		GAGTTAAGT	GGAGTTAAG	79.4	49.73	**-29.67**
		GAGTTAAGT	TAAGTATTA	79.4	72.94	**-6.46**
F7	7	TGGGTGGAT	TGGGTGGGT	60.9	74.69	13.79
		TGGGTGGGT	TGGGTGGGT	74.69	74.69	0.00
		TGGGTACCA	TGGGTGGGT	58.11	74.69	16.58
GCK	4	-	CCTGTGAGG	N/A	72.42	N/A
GHV	2	TTTATAAGC	TGGGTAATG	52.87	69.98	17.11
HBA2	1	GAGGCTCCC	GGGGTAAGG	39.61	84.99	45.38
HBB	1	CACGTTGGT	AAGGTGAAC	67.19	76.61	9.42
		CACGTTGGT	GTGGTGAGG	67.19	81.84	14.65
		CACGTTGGT	AAGGTTACA	67.19	70.5	3.31
		CAGATTGGT	AAGGTGAAC	62.65	76.61	13.96
		CAGATTGGT	GTGGTGAGG	62.65	81.84	19.19
		CAGATTGGT	AAGGTTACA	62.65	70.5	7.85
		CAGTTTGGT	AAGGTGAAC	62.65	76.61	13.96
		CAGTTTGGT	GTGGTGAGG	62.65	81.84	19.19
		CAGTTTGGT	AAGGTTACA	62.65	70.5	7.85
		CAGGCTGGT	AAGGTGAAC	62.65	76.61	13.96
		CAGGCTGGT	GTGGTGAGG	62.65	81.84	19.19
		CAGGCTGGT	AAGGTTACA	62.65	70.5	7.85
		CAGGTTGAT	AAGGTGAAC	66.31	76.61	10.30
		CAGGTTGAT	GTGGTGAGG	66.31	81.84	15.53
		CAGGTTGAT	AAGGTTACA	66.31	70.5	4.19
		CAGGTTGCT	AAGGTGAAC	66.49	76.61	10.12
		CAGGTTGCT	GTGGTGAGG	66.49	81.84	15.35
		CAGGTTGCT	AAGGTTACA	66.49	70.5	4.01
		CAGGTTGTT	AAGGTGAAC	66.31	76.61	10.30
		CAGGTTGTT	GTGGTGAGG	66.31	81.84	15.53
		CAGGTTGTT	AAGGTTACA	66.31	70.5	4.19
		CAGGTTGGC	AAGGTGAAC	74.52	76.61	2.09
		CAGGTTGGC	GTGGTGAGG	74.52	81.84	7.32
		CAGGTTGGC	AAGGTTACA	74.52	70.5	**-4.02**
	2	AGGGTGTCT	AAGGTGAAG	64.04	77.83	13.79
		AGGGTGTCT	ATGGTTAAG	64.04	63.87	**-0.17**
HEXA	9	GACATGAGG	AGGGTGGGT	58.98	78.18	19.20
HEXB	8	TTGGTAACA	AATGTTGGT	69.1	67.01	**-2.09**
HMGCL	7	ACGCTAAGC	GGGGTATTT	68.23	64.74	**-3.49**
HPRT	1	GTGGTGAAC	CAGGTGGCG	66.84	68.58	1.74
		GTGGTGATC	CAGGTGGCG	66.84	68.58	1.74
		-	CAGGTGGCG	N/A	68.58	N/A
	5	GAAGGAAGT	AAGGTAAGC	67.53	93.54	26.01
		GAAGTGTGT	AAGGTAAGC	71.02	93.54	22.52
		GAAGTAAAT	AAGGTAAGC	71.2	93.54	22.34
		GAATAAGTT	AAGGTAAGC	26	93.54	67.54
IDS	7	ATTTTAAGC	CTGGTGAGT	56.36	89.35	32.99
ITGB2	7	TTCATAAGT	AGGGTGGGG	57.76	73.82	16.06
		TTCATAAGT	GAGGTATAG	57.76	67.88	10.12
ITGB3	4	GATATGAGT	CAGGTGTGG	64.04	81.67	17.63
KRT5	1	AAGATGAGC	AGGGTGAGG	72.94	84.11	11.17
LDLR	12	GAGGCGTGG	TACGTACGA	61.08	66.31	5.23
LPL	2	ACGATAAGG	ATGGTGATC	69.45	69.1	**-0.35**
		ACGATAAGG	GAGGTATCC	69.45	66.84	**-2.61**
		ACGATAAGG	CAGGTGGGA	69.45	81.15	11.70
		ACGATAAGG	GAGGTTGGT	69.45	76.96	7.51
		ACGATAAGG	AGAGTGAGG	69.45	72.25	2.80
MTHFR	4	CAGATGAGG	AAGGCATGC	75.04	65.27	**-9.77**
NF1	27b	-	AACGTTAAG	N/A	58.46	N/A
	28	AAAATAAGT	AAGGTATTC	69.8	68.93	**-0.87**
NF2	7	-	GATGTACGG	N/A	69.28	N/A
		-	ACGGTGTGA	N/A	71.9	N/A
		CGGGTGTAT	GATGTACGG	64.74	69.28	4.54
		CGGGTGTAT	ACGGTGTGA	64.74	71.9	7.16
	12	-	AAGGTGCTG	N/A	66.84	N/A
		-	GAGGTGCTG	N/A	64.57	N/A
		GAGATGAGG	AAGGTGCTG	71.9	66.84	**-5.06**
		GAGATGAGG	GAGGTGCTG	71.9	64.57	**-7.33**
PBGD	1	GCGATGAGT	CAGGTTGCC	68.41	60.9	**-7.51**
		GCGGAGAGT	CAGGTTGCC	68.41	60.9	**-7.51**
		GCGGTGACT	CAGGTTGCC	72.25	60.9	**-11.35**
		GCGGTTAGT	CAGGTTGCC	79.4	60.9	**-18.50**
	10	CATGTAGGG	CGGGTGGGG	67.88	74.69	6.81
PGK1	4	AAGTTAGGA	GGGGTGAGG	65.96	81.84	15.88
PKD1	43	Not specified	CAGGTGGCG	N/A	68.58	N/A
PTEN	4	GAGGCAGGT	CAGGTATGA	69.1	83.76	14.66
	7	AAGATTTGT	CATGTAAGG	61.25	83.42	22.17
PYGM	14	ACCATGAGT	CAGGTGAAG	57.76	78.7	20.94
RPGR	5	CTGTTGAGA	CATGTAATT	66.49	73.99	7.50
SERPINA1	2	AAGTTAAGG	AGGGTACTC	77.31	61.25	**-16.06**
TP53	5	ATGGTGACC	GAGGTTGTG	69.28	58.81	**-10.47**
	6	GAAGTCTGG	CTGGTTTGC	60.2	66.49	6.29
		GAGATCTGG	CTGGTTTGC	54.62	66.49	11.87
TSC2	37	AAGGATGAG	CCGGTGAGG	43.63	84.64	41.01
UGT1A1	1	CAGCTGTGT	GAGGTGACT	68.58	80.1	11.52
AVG=				65.59	72.38	7.98
SD=				8.71	8.53	13.60

Table S3: Comparison between Mutant (M) and Cryptic (C) 5'ss.

Gene	Exon	Seq A	S&S (A)	Seq P1	S&S (P1)	Dist (A-P1)	Seq P2	S&S (P2)	Dist (A-P2)	S&S (A-P1)	S&S (A-P2)
ABCD1	1	GAGGTGGGG	79.05								
APOB	24	AAGGTAAAA	79.93								
AR	4	CTGGTAAGG	88.13	GAAGTGGGA	66.14	15	CAAGTGGGCC	69.11	-20	21.99	19.02
ATM	45	CAGGTAACT	86.38	TGAGTGAGT	73.12	48	GAAGTAGGT	74.69	-37	13.26	11.69
BRCA1	5	AAGGTATAT	74.52	TTGGTAATG	69.98	12				4.54	
	16	TTTGTGAGT	72.77	TATGTAGGT	73.12	65	AGGGTCAAC	62.65	-51	**-0.35**	10.12
CFTR	4	AAGGTAATA	79.93	TAGGTAGTG	67.19	81				12.74	
	20	CAGGTGAGC	91.27								
COL1A1	8	CCTGTGAGT	76.78								
	34	AAGGTGAGG	91.62								
COL3A1	16	CCTGTAAGT	79.93								
	20	CGCGTAAGT	79.58	GTGGTGAAC	66.84	-8				12.74	
	42	GATGTGAGT	81.5	CTGGTGAAC	69.98	-17	CTGGTACAG	63.35	-26	11.52	18.15
COL6A1	3	GGGGTGAGT	86.21	GGGGTTGGC	63.87	63	CTCGTGGGG	61.78	-5	22.34	24.43
COL7A1	3	AAGGTGATC	76.61								
	73	AGGGTGAGG	84.11	AGAGTGAGG	72.25	25	GGGGTGTGG	71.02	-32	11.86	13.09
	95	GTGGTGAGT	86.21								
C3	18	TGGGTAAGG	83.76	AGAGTCAGA	64.74	37	CCGGTACAA	61.95	20	19.02	21.81
CYP19	6	TGTGTAAGT	75.91	AAAGTATGA	71.02	-15	TAAGTAATA	64.57	4	4.89	11.34
CYP27A1	6	GCGGTAGGA	73.29	CAGGTGGGC	80.97	81	TGGGTGTGG	69.8	-85	**-7.68**	3.49
DMD	64	GCTGTAAGT	76.78								
	26	AAGGTAAAA	79.93	TAAGTAAAA	64.57	25				15.36	
FAH	12	CCGGTGAGT	89								
FBN1	46	TAGGTGCGT	81.5								
F5	10	CAGGTATTT	75.39	GAAGTAACC	65.79	16				9.6	
FGA	4	GAGGTAAGT	96.85								
F7	7	TGGGTGGGT	74.69								
GCK	4	AAGGTGGGC	80.1								
GHV	2	TTTGTAAGC	70.33								
HBA2	1	GAGGTGAGG	89.35	ATGGTGCGG	73.12	-19	AAGGTCGGC	73.63	-44	16.23	15.72
HBB	1	CAGGTTGGT	80.1								
	2	AGGGTGAGT	88.48								
HEXA	9	GACGTGAGG	76.43								
HEXB	8	TTGGTAAGA	82.72								
HMGCL	7	ACGGTAAGC	85.68	CTGGTGGCG	61.08	20				24.6	
HPRT	1	GTGGTGAGC	80.62								
	5	GAAGTAAGT	84.99								
IDS	7	ATGGTAAGC	86.03								
ITGB2	7	TTCGTAAGT	75.21								
ITGB3	4	GATGTGAGT	81.5								
KRT5	1	AAGGTGAGC	90.4	ACTGTGGGT	65.61	30	TGGGTCTGA	62.3	34	24.79	28.1
LDLR	12	GAGGTGTGG	78.53								
LPL	2	ACGGTAAGG	86.91								
MTHFR	4	CAGGTGAGG	92.49								
NF1	27b	GAGGTAAGA	91.44								
	28	AAAGTAAGT	87.26								
NF2	7	CGGGTGTGT	78.53								
	12	GAGGTGAGG	89.35	GGAGTCAGA	62.47	-12				26.88	
PBGD	1	GCGGTGAGT	85.86	CCGGTGACC	69.8	15	TTGGTAACG	70.15	-26	16.06	15.71
	10	CAGGTAGGG	85.34								
PGK1	4	AAGGTAGGA	83.42	CCTGTGATT	63	9				20.42	
PKD1	43	AAGGTGAGG	91.62	CCGGTGGGC	73.12	15				18.5	
PTEN	4	GAGGTAGGT	86.56								
	7	AAGGTTTGT	78.7	GTGGTGATA	67.01	-50	CCTGTGTGT	65.96	-57	11.69	12.74
PYGM	14	ACCGTGAGT	75.21								
RPGR	5	CTGGTGAGA	83.94								
SERPINA1	2	AAGGTAAGG	94.76	CTGGTGAAT	75.56	-22	AAGGTTGCT	65.61	5	19.2	29.15
TP53	5	ATGGTGAGC	82.89	GTTGTGAGG	69.63	-43				13.26	
	6	GAGGTCTGG	72.07								
TSC2	37	AAGGTGAGT	95.98	TGAGTGAGG	68.76	4	TCAGTGAGG	68.41	18	27.22	27.57
UGT1A1	1	CAGGTGTGT	86.03	GAAGTGACT	68.23	-92				17.8	
AVG=			82.96	AVG (P)=	68.10				AVG (P)=	15.87	
SD=			6.26	SD (P)=	4.49				SD (A-P)=	8.00	

Table S4: Comparison between Authentic (A) and Pseudo (P) 5'ss.

Gene	Exon	Seq C	S&S (C)	Dist (A-C)	Seq P1	S&S (P1)	Dist (A-P1)	Seq P2	S&S (P2)	Dist (A-P2)	S&S (C-P1)	S&S (C-P2)
ABCD1	1	CAGGTTGGG	75.74	9								
APOB	24	AAAGTAAAT	73.47	40								
AR	4	CAGGTGTAG	67.88	-123	GAAGTGGGA	66.14	15	CAAGTGGGCC	69.11	-20	1.74	**-1.23**
ATM	45	AGAGTGACT	63	71	TGAGTGAGT	73.12	48	GAAGTAGGT	74.69	-37	**-10.12**	**-11.69**
		TTGGTCTTT	53.92	79								
BRCA1	5	TATGTAAGA	78.01	-22	TTGGTAATG	69.98	12				8.03	
	16	TAGGTATTG	66.66	69	TATGTAGGT	73.12	65	AGGGTCAAC	62.65	-51	**-6.46**	4.01
CFTR	4	ATTGTGAGG	71.9	-93	TAGGTAGTG	67.19	81				4.71	
	20	AAGGCAACT	68.06	29								
COL1A1	8	TTGGTAAGA	82.72	96								
		CTGGTGAGC	83.76	186								
	34	CTGGTGACA	70.33	-8								
COL3A1	16	GGAGTAAGC	71.9	23								
	20	CTGGTTATT	69.1	24	GTGGTGAAC	66.84	-8				2.26	
	42	CAGGTAGAA	70.5	30	CTGGTGAAC	69.98	-17	CTGGTACAG	63.35	-26	0.52	7.15
COL6A1	3	CAAGTACTT	63.35	-66	GGGGTTGGC	63.87	63	CTCGTGGGG	61.78	-5	**-0.52**	1.57
COL7A1	3	TCCGTGAGC	66.14	-104								
	73	CTGGTATTC	62.3	-62	AGAGTGAGG	72.25	25	GGGGTGTGG	71.02	-32	**-9.95**	**-8.72**
	95	GGGGTCAGT	79.75	-7								
C3	18	GAAGTGAGT	81.84	-61	AGAGTCAGA	64.74	37	CCGGTACAA	61.95	20	17.1	19.89
CYP19	6	CAGGTAACT	86.38	87	AAAGTATGA	71.02	-15	TAAGTAATA	64.57	4	15.36	21.81
CYP27A1	6	GTGGTGGGT	75.91	-89	CAGGTGGGC	80.97	81	TGGGTGTGG	69.8	-85	**-5.06**	6.11
DMD	64	AAAGTAGGT	76.96	57								
	26	GAGGTTGAT	63.17	116	TAAGTAAAA	64.57	25				**-1.4**	
FAH	12	GAGGTGGGT	83.42	105								
FBN1	46	GAAGTCAGT	75.39	33								
F5	10	TCTGTAAGA	70.15	-35	GAAGTAACC	65.79	16				4.36	
FGA	4	AAAGTACAG	58.11	-66								
		AATGTTAGA	71.9	-36								
		GGAGTTAAG	49.73	-1								
		TAAGTATTA	72.94	4								
F7	7	TGGGTGGGT	74.69	37								
GCK	4	CCTGTGAGG	72.42	-24								
GHV	2	TGGGTAATG	69.98	12								
HBA2	1	GGGGTAAGG	84.99	-49	ATGGTGCGG	73.12	-19	AAGGTCGGC	73.63	-44	11.87	11.36
HBB	1	AAGGTGAAC	76.61	-38								
		GTGGTGAGG	81.84	-16								
		AAGGTTACA	70.5	13								
	2	AAGGTGAAG	77.83	-135								
		ATGGTTAAG	63.87	47								
HEXA	9	AGGGTGGGT	78.18	17								
HEXB	8	AATGTTGGT	67.01	-4								
HMGCL	7	GGGGTATTT	64.74	78	CTGGTGGCG	61.08	20				3.66	
HPRT	1	CAGGTGGCG	68.58	49								
	5	AAGGTAAGC	93.54	67								
IDS	7	CTGGTGAGT	89.35	22								
ITGB2	7	AGGGTGGGG	73.82	64								
		GAGGTATAG	67.88	298								
ITGB3	4	CAGGTGTGG	81.67	27								
KRT5	1	AGGGTGAGG	84.11	-66	ACTGTGGGT	65.61	30	TGGGTCTGA	62.3	34	18.5	21.81
LDLR	12	TACGTACGA	66.31	11								
LPL	2	ATGGTGATC	69.1	-18								
		GAGGTATCC	66.84	42								
		CAGGTGGGA	81.15	142								
		GAGGTTGGT	76.96	246								
		AGAGTGAGG	72.25	382								
MTHFR	4	AAGGCATGC	65.27	-57								
NF1	27b	AACGTTAAG	58.46	-69								
	28	AAGGTATTC	68.93	-54								
NF2	7	GATGTACGG	69.28	-28								
		ACGGTGTGA	71.9	-23								
	12	AAGGTGCTG	66.84	-53	GGAGTCAGA	62.47	-12				4.37	
		GAGGTGCTG	64.57	-38								
PBGD	1	CAGGTTGCC	60.9	67	CCGGTGACC	69.8	15	TTGGTAACG	70.15	-26	**-8.9**	**-9.25**
	10	CGGGTGGGG	74.69	-9								
PGK1	4	GGGGTGAGG	81.84	30	CCTGTGATT	63	9				18.84	
PKD1	43	CAGGTGGCG	68.58	-66	CCGGTGGGC	73.12	15				**-4.54**	
PTEN	4	CAGGTATGA	83.76	4								
	7	CATGTAAGG	83.42	75	GTGGTGATA	67.01	-50	CCTGTGTGT	65.96	-57	16.41	17.46
PYGM	14	CAGGTGAAG	78.7	-67								
RPGR	5	CATGTAATT	73.99	-76								
SERPINA1	2	AGGGTACTC	61.25	-84	CTGGTGAAT	75.56	-22	AAGGTTGCT	65.61	5	**-14.31**	**-4.36**
TP53	5	GAGGTTGTG	58.81	-46	GTTGTGAGG	69.63	-43				**-10.82**	
	6	CTGGTTTGC	66.49	5								
TSC2	37	CCGGTGAGG	84.64	-29	TGAGTGAGG	68.76	4	TCAGTGAGG	68.41	18	15.88	16.23
UGT1A1	1	GAGGTGACT	80.1	-141	GAAGTGACT	68.23	-92				11.87	
AVG=			72.38		AVG (P)=	68.1				AVG (C-P)=	4.28	
SD=			8.53		SD (P)=	4.49				SD (C-P)=	10.71	

Table S5: Comparison between Cryptic (C) and Pseudo (P) 5'ss.

GENE	EXON	SEQUENCE	S&S	Splice Id
ACRBP	exon 2 (alt 5'ss)	ATGGTGAGG	84.11	239966
	exon 2 (alt 5'ss)	AAGGTGAGG	91.62	239967
AD-017	exon 1 (alt 5'ss)	GGGGTATCT	64.92	34024
	exon 1 (alt 5'ss)	AGTGTAAGG	75.04	34027
AGR2	exon 1 (alt 5'ss)	CAGGTGGGT	86.56	123603
	exon 1 (alt 5'ss)	CAGGTAAGG	95.63	123605
ALDOA	exon 6? (alt 5'ss)	CCGGTGAGT	89	186955
	exon 6? (alt 5'ss)	CAGGTGGGC	80.97	186956
ANAPC11	exon 1 (alt 5'ss)	CGCGTAGGG	64.92	70274
	exon 1 (alt 5'ss)	AAGGTGCGA	79.58	70277
	exon 1 (alt 5'ss)	CGGGTTGGT	72.6	70279
APEX	exon 1 (alt 5'ss)	TGAGTCAGG	62.3	144152
	exon 1 (alt 5'ss)	AGGGTACAA	61.43	144155
.APR-1	exon 1 (alt 5'ss)	GAGGTACAG	67.71	204889
	exon 1 (alt 5'ss)	CAGGTCCTG	61.25	204891
ATP5G1	exon 1 (alt 5'ss)	GAGGTGAGT	93.71	130278
	exon 1 (alt 5'ss)	CAGGTGACT	83.24	130280
BAT1	exon 3 (alt 5'ss)	TAGGTAAGC	90.05	217192
	exon 3 (alt 5'ss)	TTGGTTCGC	61.95	217194
	exon 3 (alt 5'ss)	TTGGTATTT	63.52	217195
BAT3	exon 1 (alt 5'ss)	CAGGTTTGG	75.21	44300
	exon 1 (alt 5'ss)	ACGGTCCGT	70.68	44301
BCAT2	exon 1 (alt 5'ss)	CAGGTGGGT	86.56	115901
	exon 1 (alt 5'ss)	GGGGTGAGG	81.84	115907
BCL2L1	exon 1 (alt 5'ss)	CAGGTAGGC	84.11	22668
	exon 1 (alt 5'ss)	CAGGTGAGA	91.44	22671
	exon 2 (alt 5'ss)	AATGTAGGT	76.61	22672
	exon 2 (alt 5'ss)	CTGGTACCT	67.88	22674
	exon 3 (alt 5'ss)	CAGGTAGTG	71.55	22675
	exon 3 (alt 5'ss)	TGGGTAAGA	82.72	22676
BTF3	exon 1 (alt 5'ss)	AAGGTACAA	68.93	120005
	exon 1 (alt 5'ss)	CAGGTACCG	71.02	120024
CES2	exon 10 (alt 5'ss)	ATGGTGATG	70.33	35788
	exon 10 (alt 5'ss)	ACAGTGAGT	76.26	35789
CD63	exon 2 (alt 5'ss)	GAGGTATAG	67.88	165404
	exon 2 (alt 5'ss)	CAGGTGAGG	92.49	165405
CDKN3	exon 2 (alt 5'ss)	CAAGTGAGT	84.99	126505
	exon 2 (alt 5'ss)	ATGGTATGT	80.8	126508
CNOT7	exon 1 (alt 5'ss)	CAAGTAGAT	64.04	58780
	exon 1 (alt 5'ss)	TGGGTAACT	74.52	58782
COLS7A	exon 1 (alt 5'ss)	CAGGTAGCG	71.72	224730
	exon 1 (alt 5'ss)	AGGGTACGA	75.21	224731
	exon 1 (alt 5'ss)	CGTGTAAGC	74.69	224732
CPNE1	exon 1 (alt 5'ss)	GGGGTAATT	75.56	89619
	exon 1 (alt 5'ss)	CCGGTAAGA	86.73	89622
CREM	(alt 5'ss)	TAGGTAAGT	95.63	3266
	(alt 5'ss)	ACAGTATGT	68.58	3267
	(alt 5'ss)	CAGGTAAGA	94.58	3271
	(alt 5'ss)	GTGGTAAGA	83.94	3272
	(alt 5'ss)	CTGGTGAGA	83.94	3274
DEDD	exon 7 (alt 5'ss)	GTGGTGAGG	81.84	82843
	exon 7 (alt 5'ss)	TCAGTGTGA	56.54	82844
DJ-1	exon 1 (alt 5'ss)	GGGGTGAGT	86.21	154063
	exon 1 (alt 5'ss)	CAGGTCAGC	84.81	154064
DPH2L2	exon 1 (alt 5'ss)	AGTGTACGA	63	16321
	exon 1 (alt 5'ss)	CGAGTGAGG	73.12	16323
E4F1	exon 12 (alt 5'ss)	AGTGTTGGT	59.51	158020
	exon 12 (alt 5'ss)	GAGGTGGGT	83.42	158021
FTS	exon 2 (alt 5'ss)	GGGGTGAGG	81.84	30442
	exon 2 (alt 5'ss)	TGGGTACGC	71.55	30443
GAS5	exon 7 (alt 5'ss)	TGGGTAAGG	83.76	29694
	exon 7 (alt 5'ss)	AAGGTACAT	74.34	29696
GMPPA	exon 1 (alt 5'ss)	GTGGTAAAG	71.2	231572
	exon 1 (alt 5'ss)	GAGGTTAGT	87.26	231576
GRB7	exon 1 (alt 5'ss)	CAGGTAAGG	95.63	125277
	exon 1 (alt 5'ss)	CAGGTAAGA	94.58	125279
HLA-B	(alt 5'ss)	GCTGTGGTG	45.2	148872
	(alt 5'ss)	GTGGTGCCT	61.6	148874
	(alt 5'ss)	GGGGTAAGG	84.99	148906
HMGIY	exon 3? (alt 5'ss)	CCGGTGAGT	89	105813
	exon 3? (alt 5'ss)	CAGGTGGGT	86.56	105823
HNRPF	exon 1 (alt 5'ss)	AAGGTGGGG	81.32	209525
	exon 1 (alt 5'ss)	CAGGTAGCA	70.68	209526
	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	209527
HNRPH3	exon 3 (alt 5'ss)	GAAGTATGT	74.17	37732
	exon 3 (alt 5'ss)	GTGGTATGT	78.53	37735
HNRPK	exon 1 (alt 5'ss)	GCGGTGAGG	81.5	105456
	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	105458
HSPC028	exon 1 (alt 5'ss)	CAGGTGAGA	91.44	218579
	exon 1 (alt 5'ss)	CAGGTGAGG	92.49	218580
HSPC126	exon 1 (alt 5'ss)	GTGGTGAGA	80.8	72724
	exon 1 (alt 5'ss)	TAGGTAATG	77.48	72726
HSPC142	exon 1 (alt 5'ss)	ACGGTGAGC	82.54	212339
	exon 1 (alt 5'ss)	AAGGTGGGT	85.68	212342
HSPC171	exon 4 (alt 5'ss)	AGAGTGAGT	76.61	37476
	exon 4 (alt 5'ss)	CAGGTGAGC	91.27	37477
HSPC274	exon 1 (alt 5'ss)	CCGGTAAGG	87.78	225995
	exon 1 (alt 5'ss)	CGGGTAGGA	76.78	225999
	exon 1 (alt 5'ss)	AACGTATGT	75.39	226002
IRF3	exon 1 (alt 5'ss)	GGGGTGGGT	75.91	139017
	exon 1 (alt 5'ss)	TAGGTAACG	77.66	139022
ITGB4	(alt 5'ss)	AACGTAAGG	81.84	126342
	(alt 5'ss)	TGGGTATGA	71.9	126343
KIAA0436	exon 1 (alt 5'ss)	TGGGTAAGT	88.13	251140
	exon 1 (alt 5'ss)	TGCGTATGT	64.39	251143
KIAA0852	exon 20 (alt 5'ss)	AAGGTGCAG	66.84	150107
	exon 20 (alt 5'ss)	GAGGTGAGC	88.13	150109
KIAA1118	exon 10 (alt 5'ss)	GAGGTGACC	74.52	60788
	exon 10 (alt 5'ss)	ACGGTGTGC	71.72	60789
LHX6	exon 9 (alt 5'ss)	CAGGTCAGG	86.03	115429
	exon 9 (alt 5'ss)	AAGGTAAAT	85.34	115431
LO51119	exon 2 (alt 5'ss)	TCTGTAAGC	69.98	110895
	exon 2 (alt 5'ss)	CAGGTGGGT	86.56	110899
LOC51053	exon 1 (alt 5'ss)	CCAGTAAGT	80.27	54576
	exon 1 (alt 5'ss)	TGGGTAAGG	83.76	54577
LOC51329	exon 1 (alt 5'ss)	GAGGTGGGA	78.01	115163
	exon 1 (alt 5'ss)	AGGGTAGGA	75.91	115164
	exon 1 (alt 5'ss)	GGGGTGGGT	75.91	115166
	exon 2 (alt 5'ss)	AAGGTCGCA	60.2	115169
	exon 2 (alt 5'ss)	AGGGTGAGG	84.11	115172
LOC51596	exon 1 (alt 5'ss)	CAGGTAAGA	94.58	113295
	exon 1 (alt 5'ss)	GTGGTGAGT	86.21	113306
	exon 1 (alt 5'ss)	GGTGTGAGT	73.99	113309
LOC51604	(alt 5'ss)	CAGGTGGGC	80.97	128004
	(alt 5'ss)	CCTGTAAGT	79.93	128044
LOC51645	exon 2 (alt 5'ss)	TTGGTAATC	68.76	69441
	exon 2 (alt 5'ss)	GAAGTAACT	71.37	69442
	exon 2 (alt 5'ss)	TAGGTAAGA	90.22	69444
LOC55871	exon 5 (alt 5'ss)	CAGGTGCAG	67.71	211412
	exon 5 (alt 5'ss)	ATGGTAAGT	91.62	211413
MAGED2	exon 9 (alt 5'ss)	CAAGTGAGA	79.58	219689
	exon 9 (alt 5'ss)	TAGGTATCT	71.2	219690
MAPK7	exon 2 (alt 5'ss)	CAAGTAAGT	88.13	228256
	exon 2 (alt 5'ss)	GGGGTGAGT	86.21	228257
MBD4	exon 3 (alt 5'ss)	CTGGTGAGA	83.94	225423
	exon 3 (alt 5'ss)	AAGGTATCC	69.1	225424
	exon 7 (alt 5'ss)	TTGGTAAAT	74.34	225428
	exon 7 (alt 5'ss)	CAGGTGAGG	92.49	225429
MLF1	exon 1 (alt 5'ss)	CTCGTGAGT	76.43	129086
	exon 1 (alt 5'ss)	AAGGTATCG	70.33	129089
MRPL36	exon 1 (alt 5'ss)	CGGGTAAGG	88.13	149572
	exon 1 (alt 5'ss)	CAGGTCAGG	86.03	149579
MRPS12	exon 1 (alt 5'ss)	GAGGTCGGT	76.96	204243
	exon 1 (alt 5'ss)	GAGGTATTT	72.25	204244
MTCH1	exon 9 (alt 5'ss)	AGCGTGAGT	75.56	39496
	exon 9 (alt 5'ss)	CAGGTTGGT	80.1	39498
MUS81	exon 10 (alt 5'ss)	AAGGTAATT	85.34	30232
	exon 10 (alt 5'ss)	CAGGTACCT	75.39	30233
NAP1L1	(alt 5'ss)	GAGGTCAGA	81.84	26873
	(alt 5'ss)	AGGGTGAGT	88.48	26888
NCF1	exon 8 (alt 5'ss)	GAGGTCATT	73.47	244196
	exon 8 (alt 5'ss)	CAGGTAGGA	84.29	244198
NNAT	exon 2 (alt 5'ss)	AAGGTGTTC	65.79	105773
	exon 2 (alt 5'ss)	GAGGTATAC	66.66	105777
NOP56	(alt 5'ss)	CAGGTACCA	69.98	27730
	(alt 5'ss)	CAGGTCAGC	84.81	27731
NOT56L	exon 1 (alt 5'ss)	GAGGTGGGC	77.83	158777
	exon 1 (alt 5'ss)	CATGTGAGT	84.64	158779
NUP62	exon 1 (alt 5'ss)	GAGGTAAGC	91.27	205088
	exon 1 (alt 5'ss)	AAGGTGGGA	80.27	205091
	exon 1 (alt 5'ss)	GTGGTGAGC	80.62	205092
OCIA	exon 1 (alt 5'ss)	GCCGTAAGT	76.09	97998
	exon 1 (alt 5'ss)	GCGGTACCT	64.39	97999
	exon 2 (alt 5'ss)	GAGGTGGGT	83.42	98001
	exon 2 (alt 5'ss)	CAGGTGGGA	81.15	98004
ODF2	(alt 5'ss)	AAGGTACCT	74.52	99687
	(alt 5'ss)	GAGGTAGGC	80.97	99689
PAEP	exon 6 (alt 5'ss)	TAGGTGAGC	86.91	128199
	exon 6 (alt 5'ss)	TGGGTAATG	69.98	128202
PCMT1	exon 8 (alt 5'ss)	CAGGTGGAA	67.36	133284
	exon 8 (alt 5'ss)	AAGGTGAAA	76.78	133285
PDCD10	exon 1 (alt 5'ss)	CTGGTAAGG	88.13	230871
	exon 1 (alt 5'ss)	GGCGTAAGC	70.85	230876
	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	230878
	exon 1 (alt 5'ss)	TTTGTAAGT	75.91	230880
PK1.3	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	137902
	exon 1 (alt 5'ss)	GTGGTAATG	71.2	137904
PLP1	exon 3 (alt 5'ss)	ACGGTAACA	72.25	243135
	exon 3 (alt 5'ss)	AAGGTGATC	76.61	243137
PPP1R7	exon 5? (alt 5'ss)	GAGGTACTG	67.71	225864
	exon 5? (alt 5'ss)	AAGGTGAGA	90.57	225866
PQBP1	exon 1 (alt 5'ss)	CAGGTATCG	71.2	228654
	exon 1 (alt 5'ss)	TTGGTAACG	70.15	228655
	exon 1 (alt 5'ss)	GGGGTGGGT	75.91	228656
PRAME	exon 1 (alt 5'ss)	CAGGTTTGT	79.58	228584
	exon 1 (alt 5'ss)	AGAGTAAGT	79.75	228585
PRKCSH	exon 12 (alt 5'ss)	GAGGTGCAG	64.57	247174
	exon 12 (alt 5'ss)	AAGGTCCGT	78.53	247176
PSEN1	exon 2 (alt 5'ss)	ACTGTACGT	68.06	228074
	exon 2 (alt 5'ss)	CAGGTACAG	70.85	228075
PYCR1	exon 1 (alt 5'ss)	GGGGTGGGT	75.91	132999
	exon 1 (alt 5'ss)	ACGGTAGCT	67.36	133001
RAB7L1	exon 1 (alt 5'ss)	TTGGTTTGT	67.71	107284
	exon 1 (alt 5'ss)	CCGGTGGGT	78.7	107286
RASSF1	exon 2 (alt 5'ss)	GTGGTGAGC	80.62	231854
	exon 2 (alt 5'ss)	CAGGTGGGA	81.15	231855
RNF7	exon 1 (alt 5'ss)	CAGGTGATG	78.7	152076
	exon 1 (alt 5'ss)	TGGGTAAGC	82.54	152079
RPL17	exon 1 (alt 5'ss)	GAGGTGAGT	93.71	132172
	exon 1 (alt 5'ss)	GGGGTCAGT	79.75	132176
	exon 1 (alt 5'ss)	GAGGTCCGC	70.68	132179
	exon 2 (alt 5'ss)	TTGGTGGGG	70.33	132181
	exon 2 (alt 5'ss)	AAAGTATGG	72.07	132182
	exon 2b? (alt 5'ss)	ACTGTAAGT	79.05	132184
	exon 2b? (alt 5'ss)	AATGTAAGT	86.91	132187
SEC13L1	exon 1 (alt 5'ss)	ATGGTGAGT	88.48	58363
	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	58364
	exon 1 (alt 5'ss)	AAGGTGCTA	65.79	58365
SEC23B	exon 1 (alt 5'ss)	TAGGTGAGC	86.91	80344
	exon 1 (alt 5'ss)	CAGGTGAGC	91.27	80345
SIRT3	exon 1 (alt 5'ss)	GATGTGAGT	81.5	240797
	exon 1 (alt 5'ss)	GAGGTATTT	72.25	240798
SLC25A1	exon 1 (alt 5'ss)	CAGGTGGGC	80.97	110428
	exon 1 (alt 5'ss)	GGGGTGAGG	81.84	110429
SLC25A14	exon 2 (alt 5'ss)	ATTGTAAGC	73.82	64990
	exon 2 (alt 5'ss)	GGAGTAAGC	71.9	64991
SMAC	exon 3? (alt 5'ss)	CAGGTACAG	70.85	83054
	exon 3? (alt 5'ss)	CAGGTACTG	70.85	83055
SMUG1	exon 1 (alt 5'ss)	CAGGTGAGG	92.49	216746
	exon 1 (alt 5'ss)	GGGGTAAGA	83.94	216749
	exon 1 (alt 5'ss)	GAGGTTTTG	58.28	216751
SPHK2	exon 1 (alt 5'ss)	GAGGTGAGG	89.35	24284
	exon 1 (alt 5'ss)	AAGGTCTAA	59.51	24290
SSBP1	exon 1 (alt 5'ss)	CAGGTGAGG	92.49	205845
	exon 1 (alt 5'ss)	TGTGTAGGT	65.61	205846
	exon 1 (alt 5'ss)	TCGGTAAAG	69.63	205848
TAZ	exon 1 (alt 5'ss)	CCAGTGAGT	77.13	132298
	exon 1 (alt 5'ss)	GAGGTGGGA	78.01	132313
TCEB1	exon 1 (alt 5'ss)	CAGGTACGG	84.64	70409
	exon 1 (alt 5'ss)	CGAGTGAGT	77.48	70413
TM4SF6	exon 1 (alt 5'ss)	CTCGTAAGT	79.58	104270
	exon 1 (alt 5'ss)	TGGGTGAGA	79.58	104271
VEZATIN	exon 3 (alt 5'ss)	AAGGTATCC	69.1	235968
	exon 3 (alt 5'ss)	TTGGTAAGT	88.13	235970
	exon 7 (alt 5'ss)	ACGGTTAGC	76.09	235978
	exon 7 (alt 5'ss)	TGAGTAAGT	76.26	235979
VPS29	exon 2 (alt 5'ss)	AGAGTAAGT	79.75	165902
	exon 2 (alt 5'ss)	AAGGTCTGT	78.7	165905
VRK2	exon 1 (alt 5'ss)	CAGGTAGGA	84.29	127703
	exon 1 (alt 5'ss)	CCGGTCAGT	82.54	127704
97 genes	230 alt 5'ss	AVG.=	78.26	
	120 alt 5'ss in exon 1	SD=	9.08	

Table S6: Complete list of alternative 5'ss (33).