Table 1. The highest ranked 240 oligonucleotide sequences utilized in ACESCAN

Rank	Upstream intron	Rank	Exon 5' end	Rank	Exon 3' end	Rank	Downstream intron	Rank	Aligned upstream intron	Rank	Aligned exon	Rank	Aligned downstream intron
12	tttc	11	cctcc	15	tccc	27	tgcat	10	tgcat	21	tgtag	2	gcatg
16	cttt	23	tccc	25	cctcc	80	gcatg	20	cgct	22	gtagt	6	tgcat
19	gccgc	30	cctc	39	ccctc	109	tcgca	28	gcat	26	actag	7	catg
47	tttt	46	ctccc	41	caatc	111	tccg	34	ccgc	31	tagaa	13	gcat
50	tttcc	61	ccctc	51	ctccc	136	cttt	37	gcatg	33	cctcc	17	catgc
63	ttgc	94	caatc	56	cctc	144	cgca	38	ctat	35	cgaag	18	tgca
65	tctct	119	tccct	67	ccct	165	tgtgc	43	ttgc	45	cccgc	24	ttgc
73	tctc	125	ctcc	74	aaag	168	cattg	48	cgtc	53	ctacg	29	acta
75	cgct	135	ccccc	96	tccct	171	tgccg	49	gtcg	55	taacg	58	atgca
78	ccgc	167	acata	110	gtccc	185	tcgcg	57	cgggg	64	taaac	60	ctaa
84	tccg	180	cggcg	113	tcctt	201	ccgc	59	acta	68	tctag	76	ctaac
97	tgtct	196	aaag	118	aggg	213	ctaac	72	caat	69	tagtg	77	gtttg
99	ttgtc	206	aggg	140	ctcc	217	gtttg	81	cggg	79	taacc	91	gccg
102	ctctt	207	cccc	152	tcccc	219	gacag	82	acgt	89	cgcgg	93	actaa
117	ctttc	215	cccgc	199	gaaa	184	ggaca	83	cacg	95	cgccc	122	ccaa
124	gccg	220	taacc	203	gaaag	194	atgat	86	atcc	101	taggc	123	cacta
126	tcttt	222	tctct	211	cccgc	198	agag	87	acact	103	cacga	139	cactt
132	tctt	223	caggg	225	tagg	141	aggg	90	ttaac	106	cgtag	166	cggt
133	cgccg	212	tgat	234	cgaag	98	caggg	100	actac	128	cccta	175	caat
134	tcctt	230	cgtgg	236	aaaag	85	gagg	105	cctat	129	gtcgt	176	caaat
146	tcct	162	gacc	238	tgaaa	88	cagg	107	gccg	130	ttacg	205	catgg
148	ccgct	114	ctgg	172	catca	42	tgag	115	caac	137	taggg	221	atgc
149	tgcat			195	gtac	32	gtgag	120	cgtt	138	cctcg	228	cact
151	ttcc			155	tggcc			127	cgca	142	cggcg	150	agag
159	ccttt			70	ctgg			145	tccat	143	tacga	92	taagt
169	ctct							154	catat	153	tctct	40	taaga
182	ttctc							160	tgcg	158	agtag	36	gagt
187	ctat							161	ggcg	163	ccgcg	14	tgagt
200	tttg							178	cccg	164	agtta	9	taag
204	tttgc							186	ccga	170	ttaat	8	gtaa
224	ttttt							188	cgat	173	tagga	5	gtga
232	gtttc							190	catc	174	actga	4	tgag
208	ggac							214	ctatt	177	tcctt	3	gtaag
210	gagg							226	cgga	183	gaaag	1	gtgag
227	aggc							240	tccg	189	ctcgc		
229	gacag							237	cctg	191	taatt		
179	ggctg							239	ccag	193	caatc		
181	cagg							192	aaaa	197	ccgct		
156	tggag							147	cagg	209	ccccc		
121	ggaca							157	gagg	216	ggcgg		
131	gagc							116	gtgag	218	ctagc		
62	tggg							104	ctgg	231	ctctc		
44	ggag							66	tgag	233	ccgaa		
										235	atcaa		
										202	tggag		
										108	catca		
										112	acctg		
										71	ctgga		
										52	gctgg		
										54	ctggc		

Oligonucleotide features are ranked from most significantly differentially represented between $S_{H,M}$ and $S_{h,m}$ (1) to least significantly differentially represented ($n = 240$) by the χ^2 statistic with Yates correction factor. Within each column, features are ordered by the level of enrichment in $S_{H,M}$ versus $S_{h,m}$ and represented according to pertinent sequence regions. Features in black and red represent oligonucleotides enriched in $S_{H,M}$ and $S_{h,m}$, respectively.

1. Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. (1990) *J. Mol. Biol.* **215,** 403-10.