Characteristics of 50 randomly chosen human genes

				Alu Population Across *Alu* Landscape				Raw Stability Scores		
								Coding Exon Scores		
Gene	Locus	Coding Region Length (bp)	Coding Exons	250 kbp 5’ Flanking	Gene	250 kbp 3’ Flanking	Total	Lowest	Highest	Gene Score
ADGB	chr6:146,920,136-147,136,597	216,177	36	30	48	48	126	0.954	0.995	0.779
ARSH	chrX:2,924,654-2,951,426	26,773	9	239	28	158	425	0.884	0.935	0.726
BLK	chr8:11,351,521-11,422,108	20,884	12	80	24	101	205	0.969	0.987	0.950
C19orf76	chr19:50,191,942-50,194,247	656	2	361	0	300	661	0.925	0.928	0.925
CDH13	chr16:82,660,399-83,830,215	1,167,938	15	41	317	129	487	0.954	0.994	0.802
CHAMP1	chr13:115,079,965-115,092,803	2,439	1	95	9	6	110	only coding exon = 0.968		
CHRNA1	chr2:175,612,323-175,629,200	16,271	10	99	9	120	228	0.949	0.979	0.911
CHST9	chr18:24,495,595-24,765,289	226,551	5	60	47	82	189	0.979	.994	0.959
CYB5B	chr16:69,458,498-69,500,167	37,835	3	350	38	285	673	0.906	0.934	0.828
DCAF6	chr1:167,905,797-168,045,083	138,524	19	201	67	147	415	0.930	0.978	0.773
DTNBP1	chr6:15,523,032-15,663,289	139,895	10	158	16	129	303	0.943	0.983	0.841
GDPD2	chrX:69,642,881-69,653,241	8,102	16	142	2	185	329	0.072	0.966	0.071
GFI1	chr1:92,940,318-92,951,628	7,459	6	130	3	117	250	0.946	0.967	0.938
GRPEL2	chr5:148,724,977-148,734,146	5,743	4	59	6	236	301	0.928	0.964	0.913
H2AFB3	chrX:154,113,317-154,113,833	348	1	92	0	76	168	only coding exon = 0.986		
HDGFL1	chr6:22,569,678-22,570,750	756	1	60	0	39	99	only coding exon = 0.995		
HSPB9	chr17:40,274,756-40,275,371	480	1	289	0	285	574	only coding exon = 0.911		
IL17D	chr13:21,277,482-21,297,237	17,953	2	194	9	257	460	0.955	0.961	0.940
JMY	chr5:78,531,925-78,623,038	79,657	10	212	92	189	493	0.896	0.949	0.726
KCNA6	chr12:4,918,342-4,960,278	1,590	1	81	9	43	133	only coding exon = 0.991		
KEAP1	chr19:10,596,796-10,614,054	13,382	5	493	43	454	990	0.784	0.830	0.621
KIAA1598	chr10:118,644,306-118,765,088	118,736	15	140	44	96	280	0.946	0.986	0.821
MADCAM1	chr19:496,490-505,343	8,466	5	163	11	268	442	0.897	0.940	0.861
MAP9	chr4:156,263,812-156,298,122	28,068	13	81	6	34	121	0.972	0.989	0.934
MFSD4	chr1:205,538,112-205,572,046	31,392	10	153	14	192	359	0.943	0.969	0.882
MIA3	chr1:222,791,444-222,841,351	47,509	28	132	16	126	274	0.960	0.980	0.885
MRPS9	chr2:105,654,483-105,716,418	61,667	11	64	17	91	172	0.976	0.989	0.942
MUT	chr6:49,398,073-49,431,041	27,739	12	100	8	41	149	0.969	0.990	0.951
NANOS3	chr19:13,988,063-13,991,571	3,255	2	429	6	393	828	0.872	0.896	0.858
NCF1	chr7:74,188,309-74,203,659	15,126	11	432	21	466	919	0.876	0.893	0.723
NGB	chr14:77,731,834-77,737,655	4,402	4	215	1	152	368	0.974	0.978	0.970
OPRD1	chr1:29,138,654-29,190,208	50,900	3	473	72	301	846	0.898	0.928	0.844
OR6P1	chr1:158,532,441-158,533,394	954	1	36	0	42	78	only coding exon = 0.993		
PACSIN1	chr6:34,482,649-34,504,039	6,225	9	323	0	320	643	0.950	0.951	0.973
PATE4	chr11:125,703,211-125,709,967	5,068	3	95	0	110	205	0.980	0.988	0.977
PHKA2	chrX:18,910,416-19,002,480	90,448	33	147	47	187	381	0.898	0.971	0.724
PSG2	chr19:43,568,362-43,586,893	16,013	5	47	3	71	121	0.971	0.990	0.961
SET	chr9:131,451,509-131,458,675	10,769	8	403	2	377	782	0.872	0.907	0.821
SF3B3	chr16:70,557,691-70,611,571	45,157	25	447	64	168	679	0.840	0.926	0.499
SFRP5	chr10:99,526,508-99,531,756	4,320	3	80	1	257	338	0.960	0.965	0.952
SPATA7	chr14:88,851,742-88,904,804	52,604	12	75	20	164	259	0.968	0.980	0.924
TAGLN2	chr1:159,887,903-159,895,284	1,710	4	80	0	58	138	0.984	0.987	0.984
THYN1	chr11:134,118,173-134,123,260	4,445	7	62	0	108	170	0.906	0.913	0.978
TMEM136	chr11:120,195,838-120,204,388	3,140	3	73	2	129	204	0.975	0.979	0.973
TRNP1	chr1:27,320,195-27,327,377	684	1	317	4	334	655	only coding exon = 0.917		
TUBA1C	chr12:49,658,865-49,667,113	8,046	4	333	9	307	649	0.873	0.899	0.817
USMG5	chr10:105,148,809-105,156,270	264	2	168	8	376	552	0.893	0.902	0.892
XPNPEP3	chr22:41,253,085-41,328,823	69,254	10	332	109	416	857	0.859	0.926	0.563
ZNF296	chr19:45,574,758-45,579,688	4,773	3	333	6	407	746	0.896	0.917	0.885
ZNF567	chr19:37,180,303-37,212,225	8,199	3	282	29	270	581	0.888	0.917	0.853